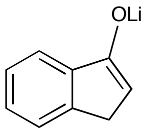
Supporting Information

Lithium Enolates of Simple Ketones:
Structure Determination Using the Method of Continuous Variation

Lara R. Liou, Anne J. McNeil, Antonio Ramirez, Gilman E. S. Toombes, Jocelyn M. Gruver, and David B. Collum*
Contribution from the Department of Chemistry and Chemical Biology
Baker Laboratory, Cornell University
Ithaca, New York 14853-1301



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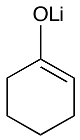

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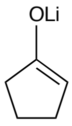

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$X_{\mathbf{A}\text{ or }\mathbf{B}}$ = the mole fraction of enolate subunits **A** or **B**

ϕ_n = a measure of the relative stability for an aggregate with n subunits of **A**

ϕ_{Nn} = a measure of the relative stability for an aggregate with N total subunits and with n subunits of **A**

rms = the root mean square of the sum of the squares of the residuals

I. Experimental Methods

II. TMEDA experimental observations

III. THF experimental observations

IV. DME experimental observations

V. Crystal Structures

VI. Mathematical Descriptions of Ensembles

VII. Simulated Ensembles: Influence of Aggregate Stability

VIII. Fitting Program Code and Instructions

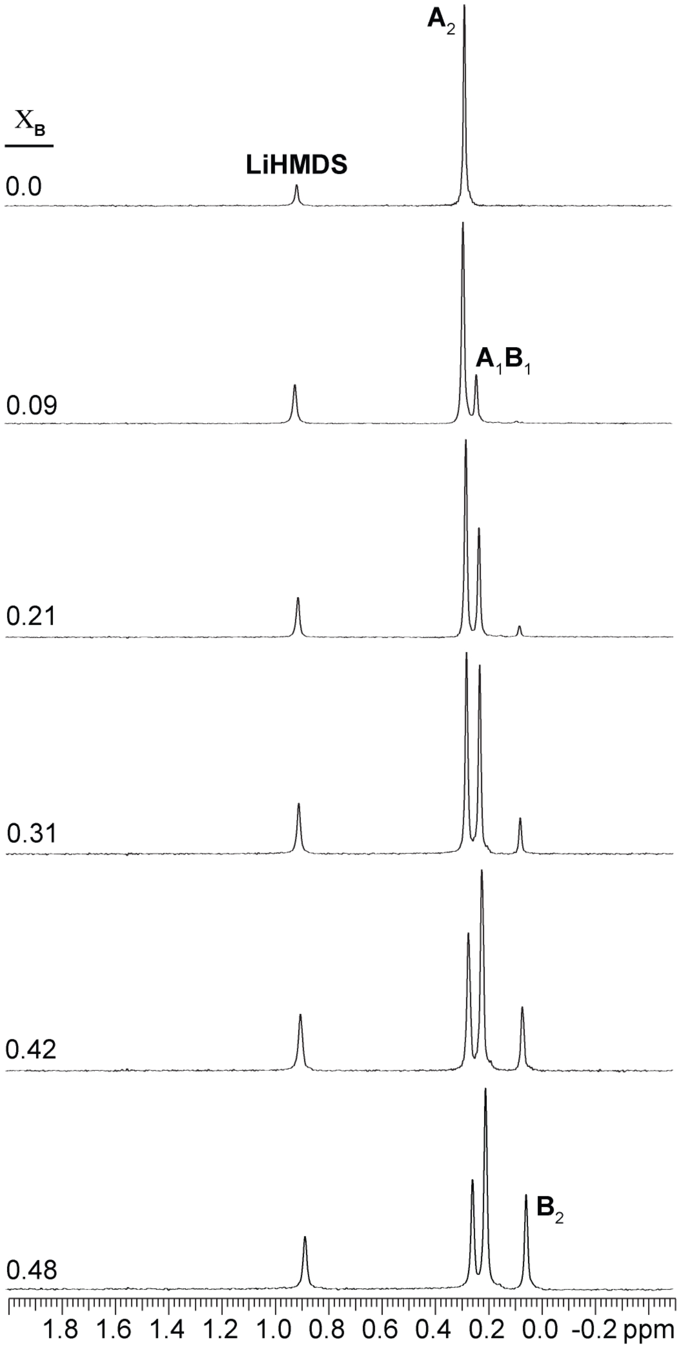
I. Experimental Methods

a. Preparation of NMR spectroscopy samples

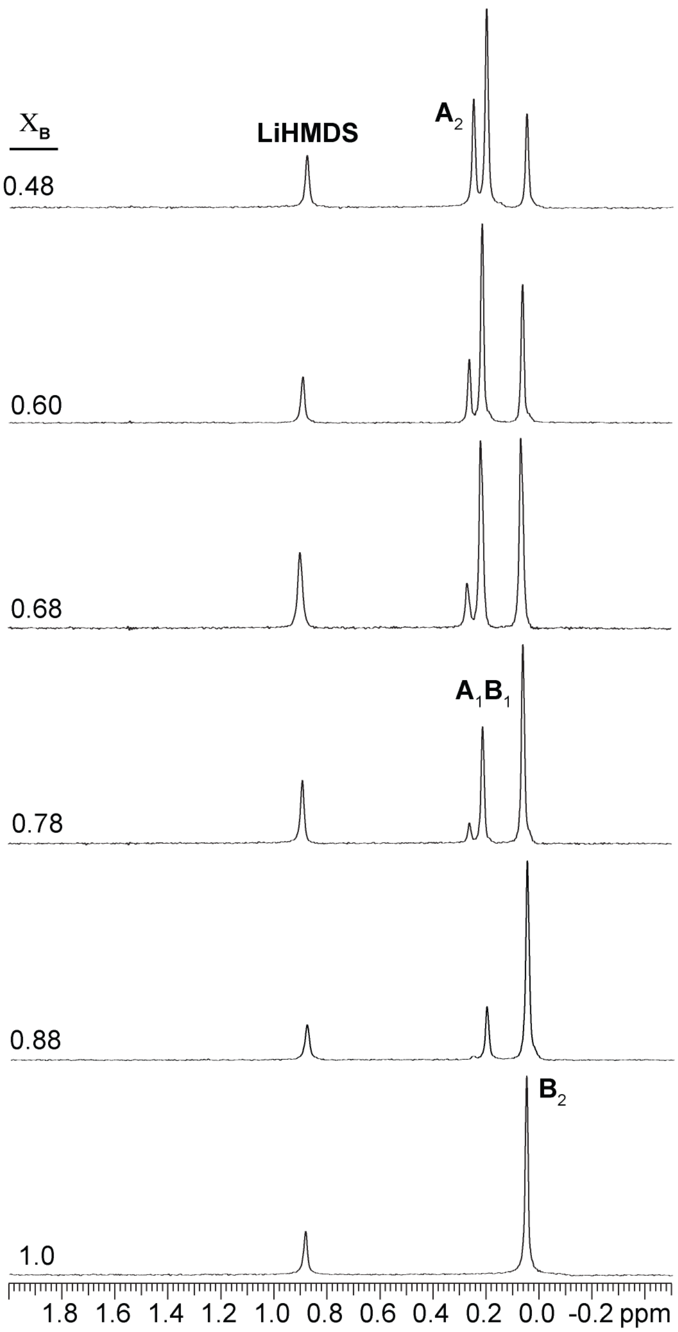
Cyclohexanone and cyclopentanone were stored over 3 or 4 Å molecular sieves and distilled under vacuum prior to use. Indanone was used directly as commercially provided by the Sigma-Aldrich Company. Stock solutions were prepared at room temperature. After flame drying the NMR tube on a Schlenk line and placing it under argon, the tube was placed in a -78 °C dry ice/acetone bath. The appropriate amounts of the base followed by the ketones and other components needed were added via syringe allowing about 30 seconds to one minute between additions. All samples had a total volume of 0.60 mL. The best results were obtained when between 100 and 300 μL were added at a time and when large concentration differences between the stock solutions and final concentrations were avoided. The tube was sealed under partial vacuum and immediately vortexed for 10 - 15 seconds before being replaced into a -78 °C bath. The samples were quickly vortexed twice more being careful to avoid excessive warming (above -20 °C). Inverting the NMR tubes to mix the samples or allowing them to warm often resulted in low quality spectra or significant deviations from the expected result.

b. Integration of NMR resonances by deconvolution

NMR resonances were integrated using Varian's software, VNMR. After weighted Fourier transform with 64,000 points and phasing, line broadening was set between 0 and 0.2 and a baseline correction was applied if appropriate. Deconvolution was performed in the absolute intensity mode, with application of a drift correction, with the default parameters for contributions from Lorentzian and Gaussian line shapes, and using the line list for well resolved spectra. For poorly resolved spectra, the resonances were indicated using the "mark" and "use mark" commands.



II.a. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 1.2 M TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.12 M LiHMDS.



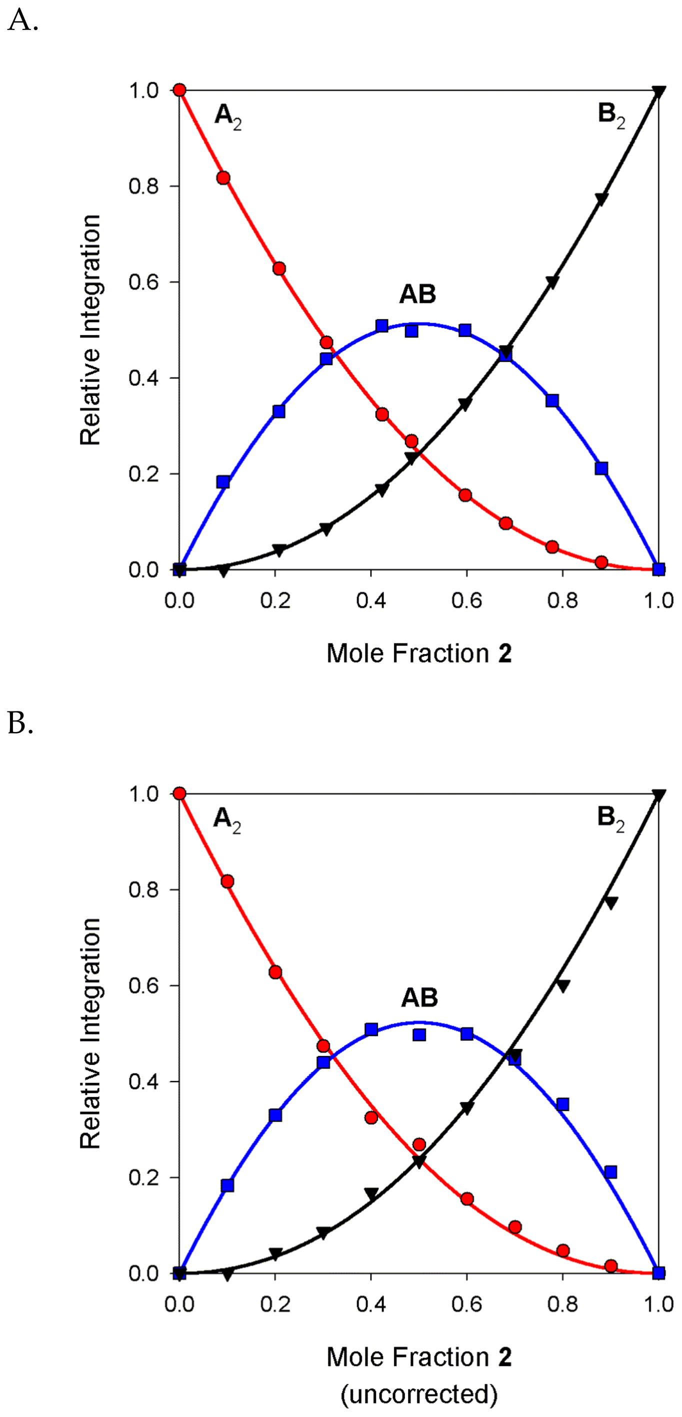
II.a. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 1.2 M TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.12 M LiHMDS.

II.b. Resonance integrations for each aggregate in an ensemble of $[^6Li]$**1** (**A**) and $[^6Li]$**2** (**B**) at various mole fractions of **A** and **B**. Spectra (see **II.a.**) were recorded on a 0.10 M mixture of enolates in 10 equivalents of TMEDA/toluene at -90 °C.

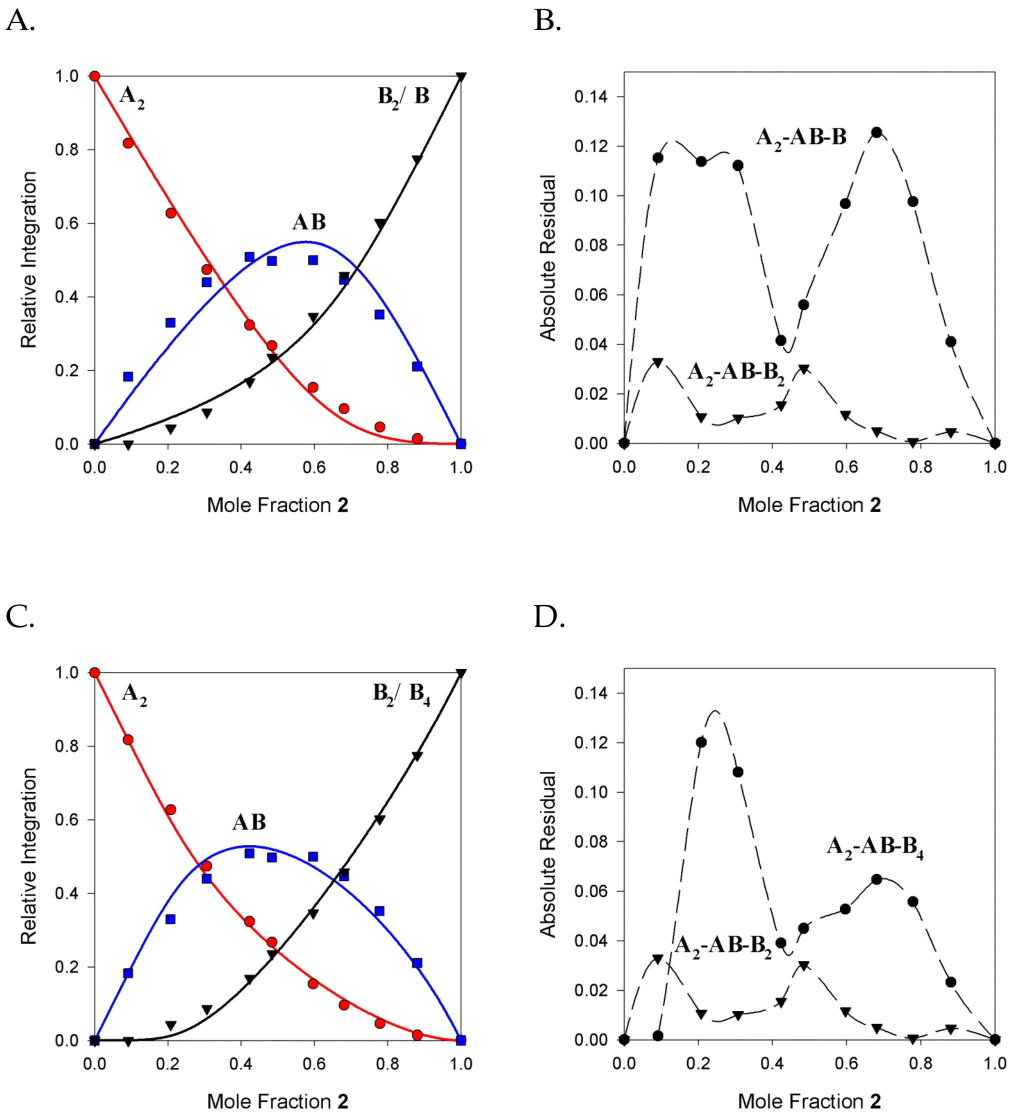
Uncorrected X_B	Calculated X_B	Resonance Integrations			
		A_2	**A_1B_1**	**B_2**	LiHMDS
0.00	0.00	1.00	0.00	0.00	0.00
0.10	0.09	155.05	34.74	0.00	40.84
0.20	0.21	144.59	75.92	9.95	38.98
0.30	0.31	145.61	135.16	26.71	49.90
0.40	0.42	117.84	185.16	61.48	67.14
0.50	0.48	95.83	178.16	84.38	56.57
0.60	0.60	52.61	170.32	118.26	48.87
0.70	0.68	46.46	216.81	222.38	105.09
0.80	0.78	13.52	103.30	176.87	66.63
0.90	0.88	3.60	53.16	195.81	44.05
1.00	1.00	0.00	0.00	1.00	0.00

II.c. Relative integrations for aggregates in an ensemble of **1** (**A**) and **2** (**B**) at various mole fractions of **A** and **B**. Integrations were measured (see **II.a** and **II.b**) for a 0.10 M enolate ensemble in 10 equivalents of TMEDA/toluene at -90 °C.

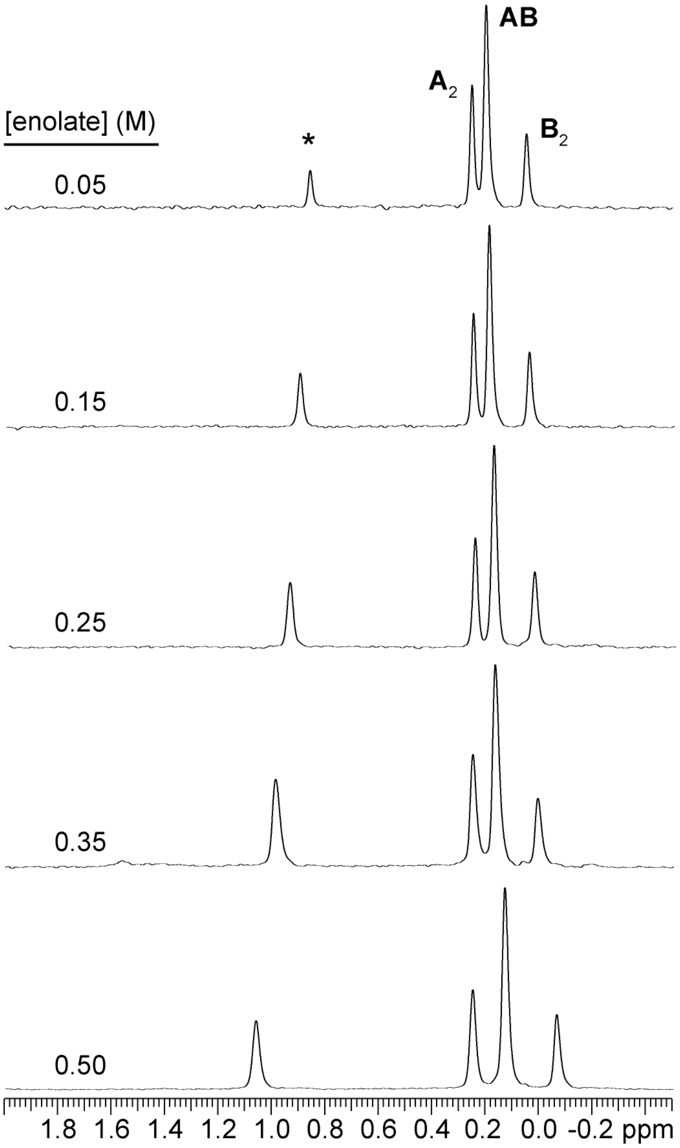
Uncorrected X_B	Calculated X_B	Relative Integrations		
		A_2	**A_1B_1**	**B_2**
0.00	0.00	1.00	0.00	0.00
0.10	0.09	0.82	0.18	0.00
0.20	0.21	0.63	0.33	0.04
0.30	0.31	0.47	0.44	0.09
0.40	0.42	0.32	0.51	0.17
0.50	0.48	0.27	0.50	0.24
0.60	0.60	0.15	0.50	0.35
0.70	0.68	0.10	0.45	0.46
0.80	0.78	0.05	0.35	0.60
0.90	0.88	0.01	0.21	0.78
1.00	1.00	0.00	0.00	1.00



II.d. Plot of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of TMEDA/toluene at -90 °C (see **II.c**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2**; ϕ_0 = 0.95; ϕ_1 = 1.0; ϕ_2 = 0.95; rms = 0.005. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **2**; ϕ_0 = 0.91; ϕ_1 = 1.0; ϕ_2 = 0.91; rms = 0.015.



II.e. Plots of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of TMEDA/toluene at -90 °C (see **II.c**) fit to an ensemble of **A_2-AB-B** and **A_2-AB-B_4**. A) Plot and fit of the relative integration versus the calculated mole fraction of **2** fit to **A_2-AB-B**; $\phi_{10} = 0.57$; $\phi_{11} = 0.00$; $\phi_{20} = 0.00$; $\phi_{21} = 1.25$; $\phi_{22} = 0.18$; rms = 0.03. B) Plot of the sum of the absolute residuals for **A_2-AB-B_2** and **A_2-AB-B** versus the mole fraction of **2**. C) Plot and fit of the relative integration versus the calculated mole fraction of **2** fit to **A_2-AB-B_4**. $\phi_{20} = 0.00$; $\phi_{21} = 0.53$; $\phi_{22} = 1.40$; $\phi_{40} = 1.20$; $\phi_{41} = \phi_{42} = \phi_{43} = \phi_{44} = 1.00$; rms = 0.03. D) Plot of the sum of the absolute residuals for **A_2-AB-B_2** and **A_2-AB-B_4** versus the mole fraction of **2**.



II.f. ^{6}Li NMR spectra of equimolar mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with 0.02 M excess LiHMDS (*).

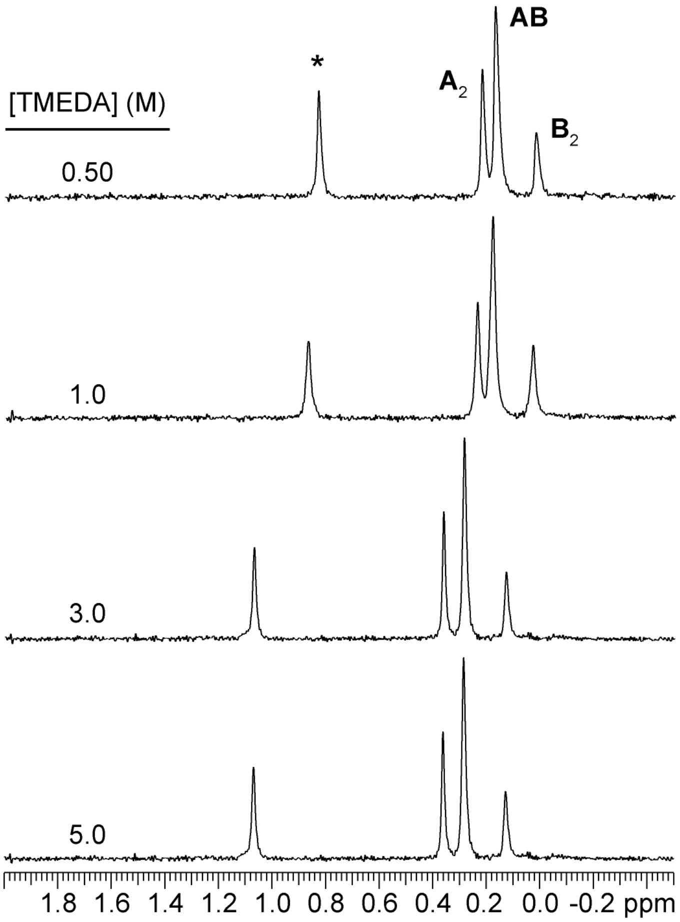
II.g. Resonance integrations for each aggregate in an ensemble of $[^6\text{Li}]$**1** (**A**) and $[^6\text{Li}]$**2** (**B**) at various absolute Li concentrations and the corresponding equilibrium constants for the ensemble. Spectra (see **II.f.**) were recorded on an equimolar mixture of **1** and **2** in 10 equivalents of TMEDA/toluene at -90 °C. K_{eq}'s and $\Delta G°$ were calculated according to the following equation: $K_{eq} = [\mathbf{AB}]^2/[\mathbf{A}_2][\mathbf{B}_2]$.

[Total Li] (M)	[Ketone] (M)	Resonance Integrations				X_B	K_{eq}	$\Delta G°$ (Kcal)
		LiHMDS	$\mathbf{A}_2$	**AB**	$\mathbf{B}_2$			
0.06	0.050	54.29	154.75	340.91	115.12	0.47	6.52	-0.68
0.18	0.15	97.73	150.68	326.18	123.00	0.48	5.74	-0.64
0.29	0.25	138.36	162.15	360.09	142.98	0.49	5.59	-0.63
0.41	0.35	227.93	223.11	430.04	143.20	0.45	5.79	-0.64
0.58	0.50	166.73	194.54	416.56	153.53	0.47	5.81	-0.64

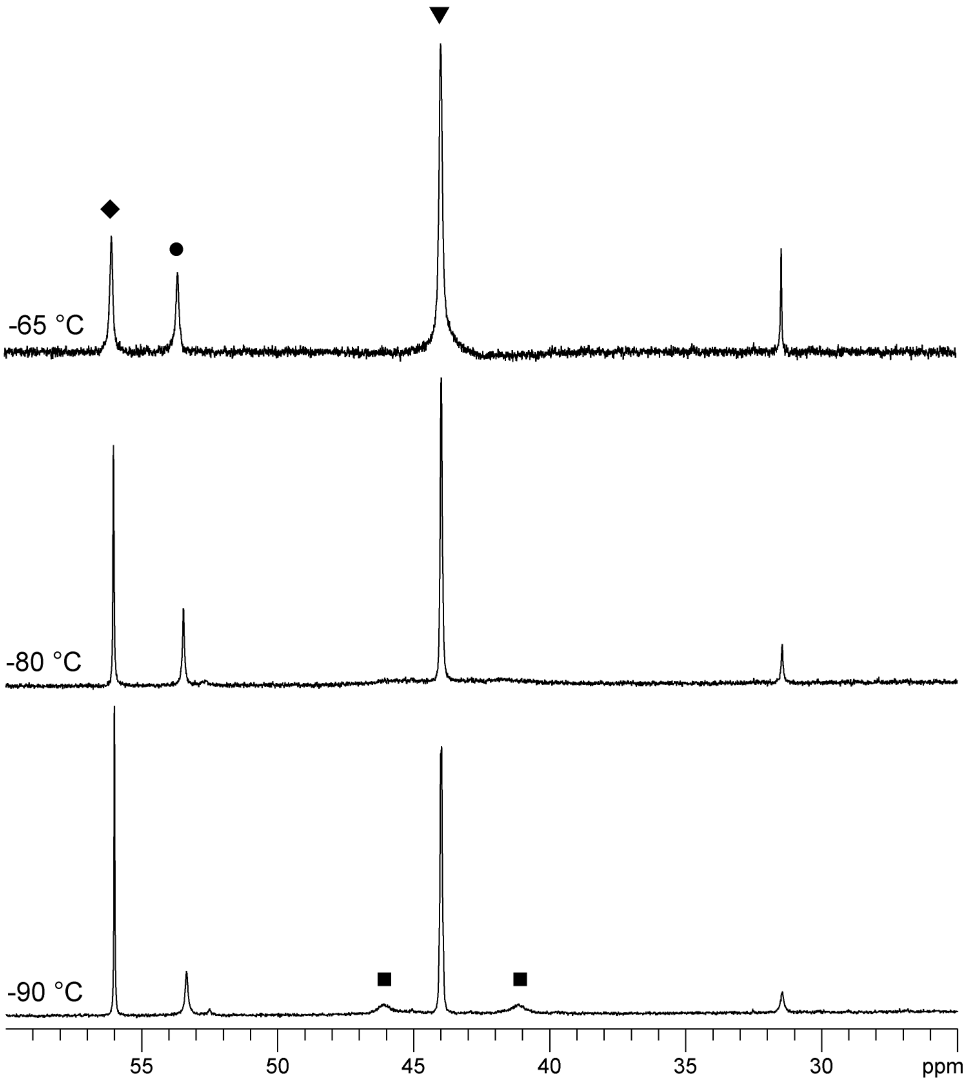
II.h. Resonance integrations for each aggregate in an ensemble of $[^6\text{Li}]$**1** (**A**) and $[^6\text{Li}]$**2** (**B**) at various TMEDA concentrations and the corresponding equilibrium constants. Spectra (see **II.i.**) were recorded on a 0.10 M equimolar mixture of **1** and **2** at -90 °C. K_{eq}'s and $\Delta G°$ were calculated according to the following equation: $K_{eq} = [\mathbf{AB}]^2/[\mathbf{A}_2][\mathbf{B}_2]$.

[TMEDA] (M)*	X_B	Resonance Integrations				K_{eq}	$\Delta G°$ (Kcal)
		LiHMDS	$\mathbf{A}_2$	**AB**	$\mathbf{B}_2$		
0.4	0.46	156.04	161.75	339.77	107.77	6.62	-0.69
0.9	0.46	132.65	167.00	351.63	122.01	6.07	-0.66
2.9	0.46	114.2	130.49	261.16	92.29	5.66	-0.63
4.9	0.45	121.36	199.89	376.36	130.36	5.44	-0.62

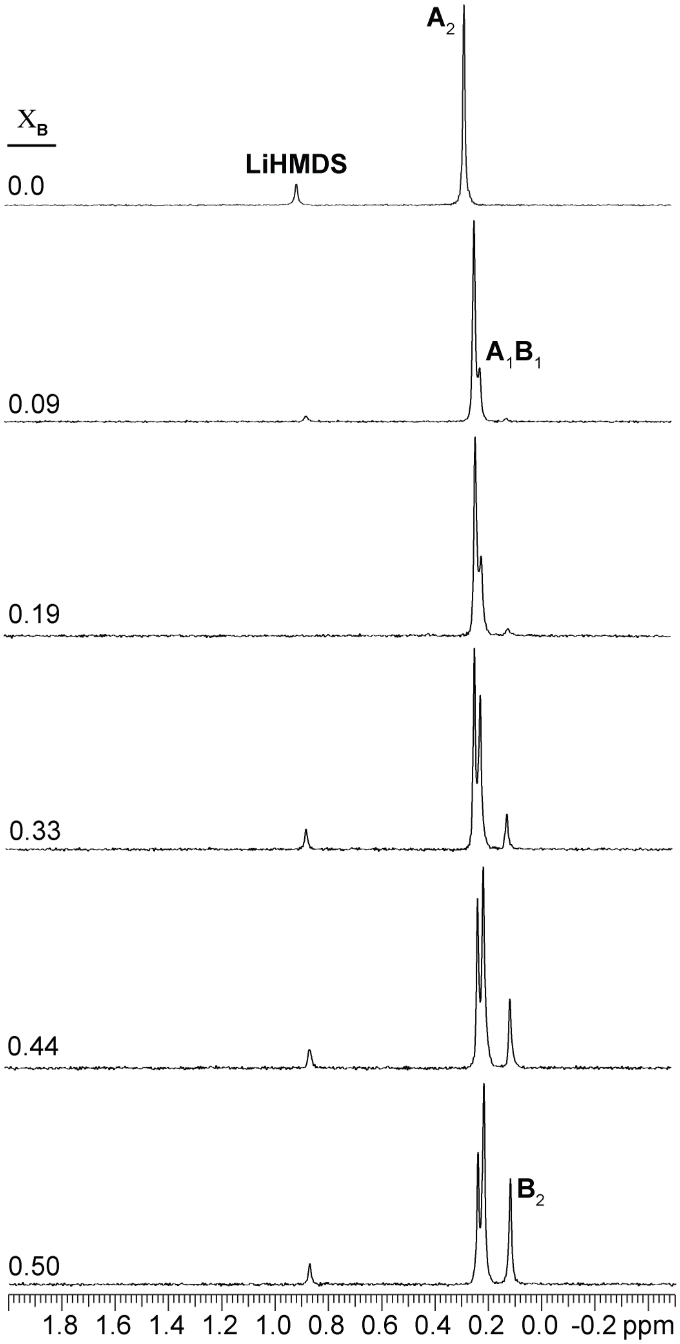
* Indicates the concentration of free TMEDA.



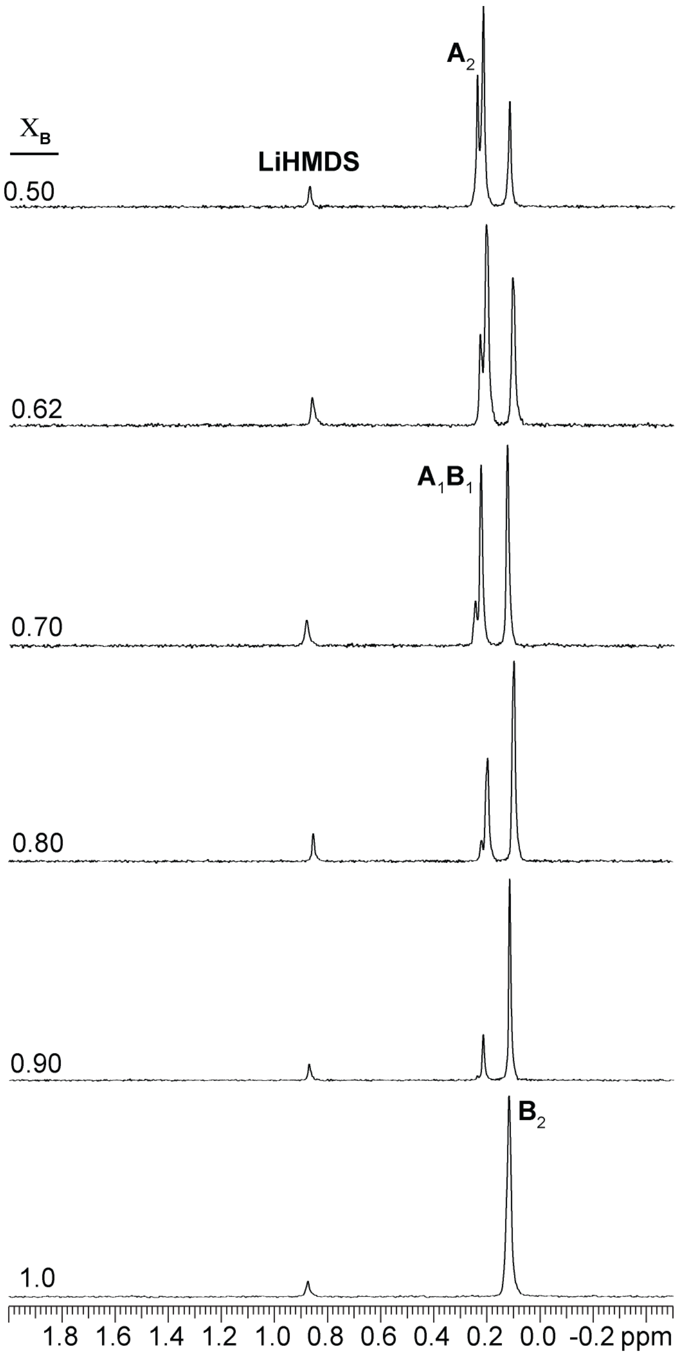
II.i. ^{6}Li NMR spectra of equimolar mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various concentrations of TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.12 M LiHMDS (*). Total TMEDA concentration is noted on spectra.



II.j. ^{13}C NMR spectra of 0.10 M [^{6}Li]**1** in 0.20 M TMEDA/toluene at various temperatures. (■) bound $\underline{C}H_3$-N-; (●) bound -$\underline{C}H_2$-; (◆) free $\underline{C}H_3$-N; (▼) free -$\underline{C}H_2$-



II.k. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 1.2 M TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.12 M LiHMDS.



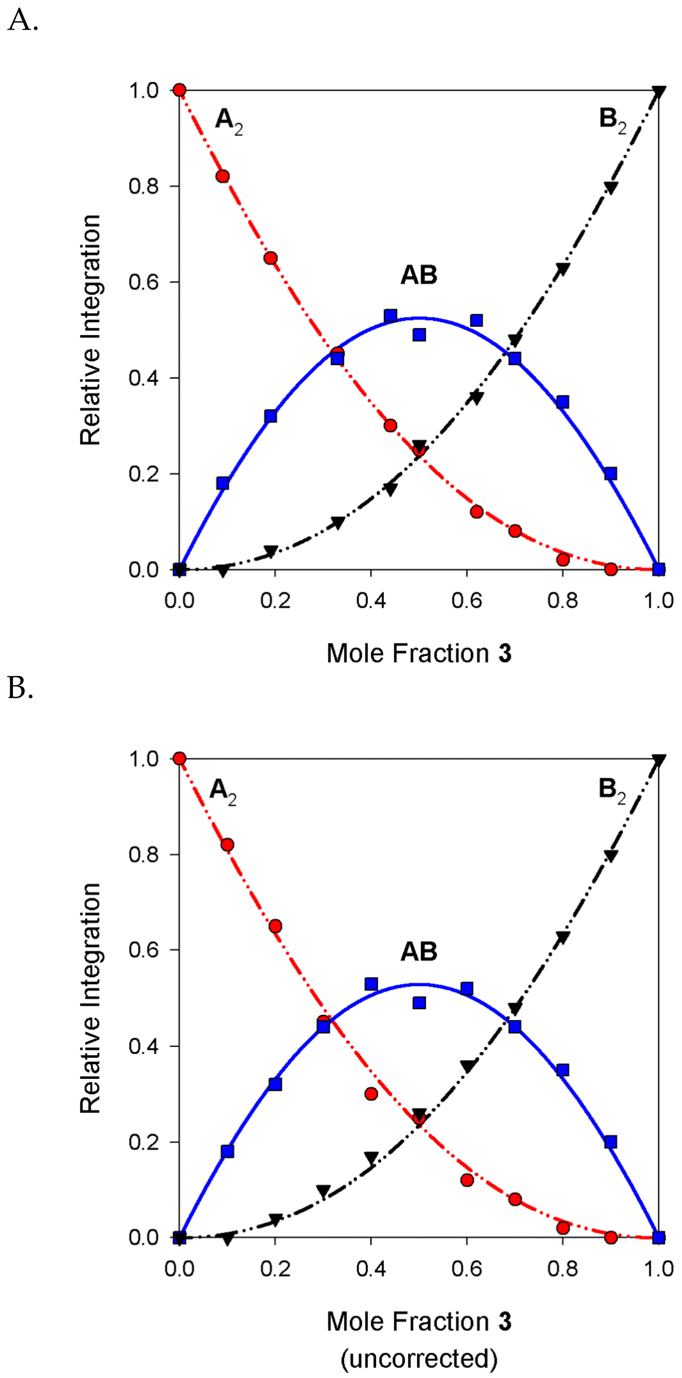
II.k. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 1.2 M TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.12 M LiHMDS.

II.l. Resonance integrations for each aggregate in an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions of **A** and **B**. Spectra (see **II.k.**) were recorded on a 0.10 M mixture of enolates in 10 equivalents of TMEDA/toluene at -90 °C.

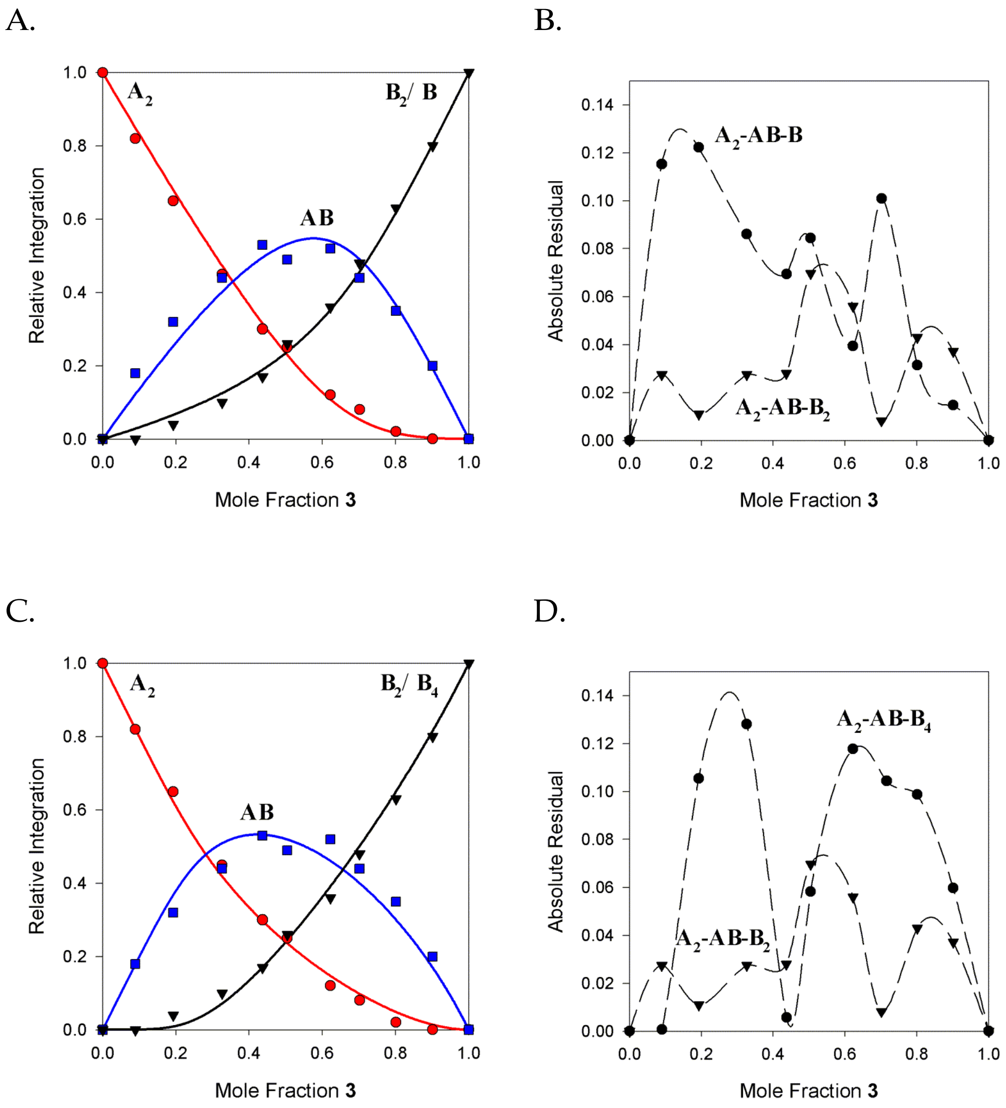
Uncorrected X_B	Calculated X_B	Resonance Integrations			
		A_2	**AB**	**B_2**	LiHMDS
0.00	0.00	1.00	0.00	0.00	0.00
0.10	0.09	184.51	40.45	0.00	7.00
0.20	0.19	182.47	88.53	9.87	0.00
0.30	0.33	149.2	146.55	34.54	19.52
0.40	0.44	114.67	204.8	65.88	24.11
0.50	0.50	92.83	185.08	96.21	20.12
0.60	0.62	59.93	270.97	186.38	32.79
0.70	0.70	31.91	176.38	194.18	32.16
0.80	0.80	8.81	125.6	225.48	23.26
0.90	0.90	0.00	37.25	150.93	15.02
1.00	1.00	0.00	0.00	1.00	0.00

II.m. Relative integrations for aggregates in an ensemble of **1** (**A**) and **3** (**B**) at various mole fractions of **A** and **B**. Integrations were measured (see **II.k** and **II.l**) for a 0.10 M enolate ensemble in 10 equivalents of TMEDA/toluene at -90 °C.

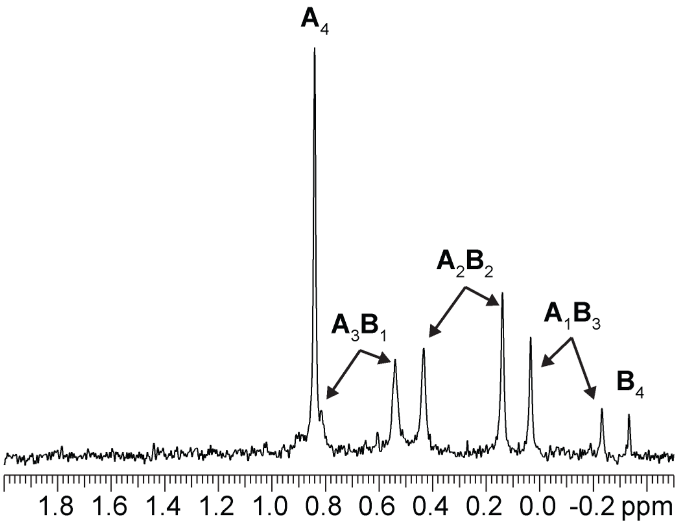
Uncorrected X_B	Calculated X_B	Relative Integrations		
		A_2	**AB**	**B_2**
0.00	0.00	1.00	0.00	0.00
0.10	0.09	0.82	0.18	0.00
0.20	0.19	0.65	0.32	0.04
0.30	0.33	0.45	0.44	0.10
0.40	0.44	0.30	0.53	0.17
0.50	0.50	0.25	0.49	0.26
0.60	0.62	0.12	0.52	0.36
0.70	0.70	0.08	0.44	0.48
0.80	0.80	0.02	0.35	0.63
0.90	0.90	0.00	0.20	0.80
1.00	1.00	0.00	0.00	1.00



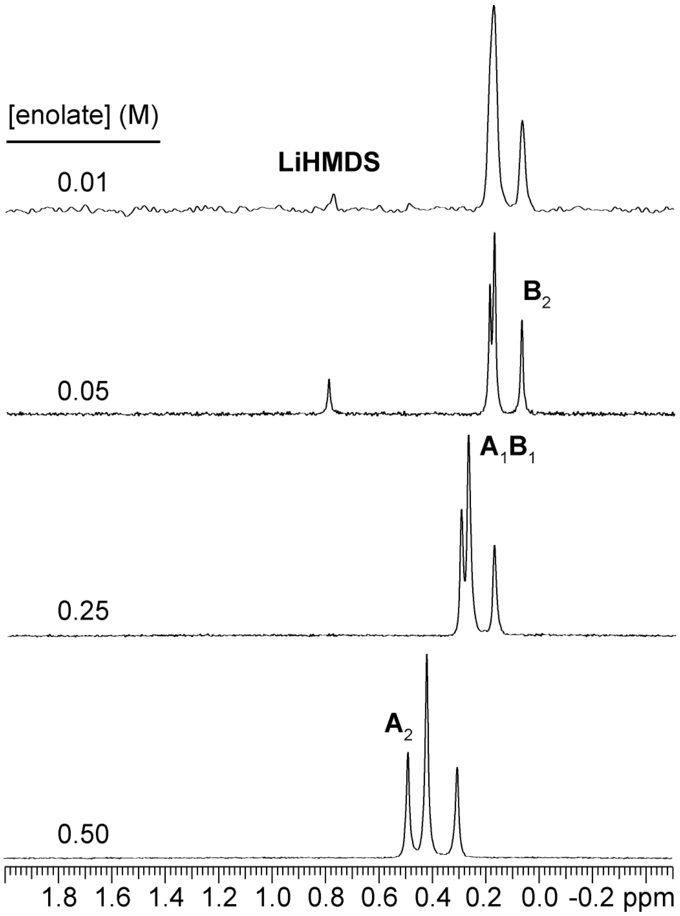
II.n. Plot of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 10 equivalents of TMEDA/toluene at -90 °C (see **II.l**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3**; $\phi_0 = 0.91$; $\phi_1 = 1.0$; $\phi_2 = 0.91$; rms = 0.013. B) Plot and fit of the relative populations versus the uncorrected mole fraction of **3**; $\phi_0 = 0.89$; $\phi_1 = 1.0$; $\phi_2 = 0.89$; rms = 0.017.



II.o. Plots of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 10 equivalents of TMEDA/toluene at -90 °C (see **II.k**) fit to an ensemble of **A_2-AB-B** and **A_2-AB-B_4**. A) Plot and fit of the relative integration versus the calculated mole fraction of **3** fit to **A_2-AB-B**; $\phi_{10} = 0.60$; $\phi_{11} = 0.00$; $\phi_{20} = 0.00$; $\phi_{21} = 1.32$; $\phi_{22} = 0.18$; rms = 0.03. B) Plot of the sum of the absolute residuals for **A_2-AB-B_2** and **A_2-AB-B** versus the mole fraction of **3**. C) Plot and fit of the relative integration versus the calculated mole fraction of **3** fit to **A_2-AB-B_4**. $\phi_{20} = 0.00$; $\phi_{21} = 0.53$; $\phi_{22} = 1.41$; $\phi_{40} = 1.16$; $\phi_{41} = \phi_{42} = \phi_{43} = \phi_{44} = 0.00$; rms = 0.03. D) Plot of the sum of the absolute residuals for **A_2-AB-B_2** and **A_2-AB-B_4** versus the mole fraction of **3**.



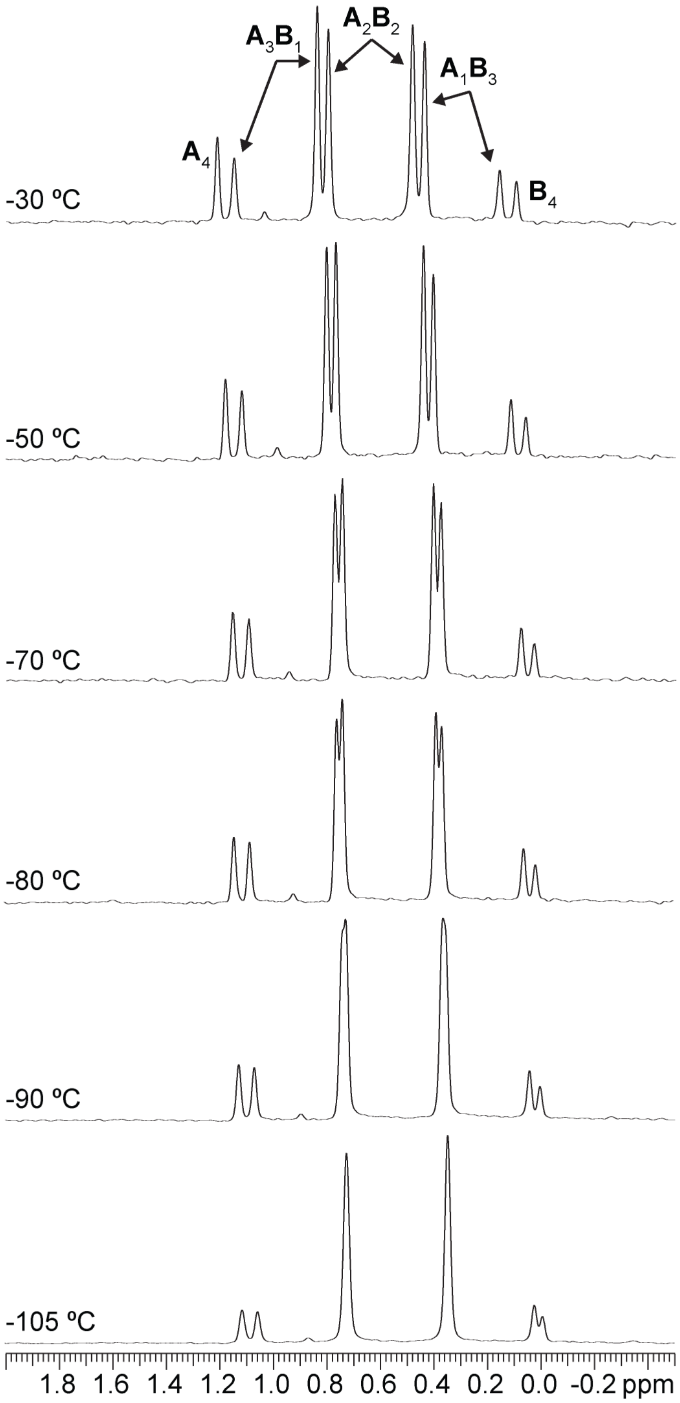
II.p. ^{6}Li NMR spectrum of an equimolar mixture of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) in 2.0 M DMEA at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.10 M LiHMDS.



II.q. ^{6}Li NMR spectra of equimolar mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents TMEDA/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with 0.05 equivalents excess LiHMDS.

II.r. Resonance integrations for each aggregate in an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations. Spectra (see **II.p.**) were recorded on an equimolar mixture of **1** and **3** in 10 equivalents of TMEDA/toluene at -90 °C. K_{eq}'s and $\Delta G°$ were calculated according to the following equation: $K_{eq} = [\mathbf{AB}]^2/[\mathbf{A}_2][\mathbf{B}_2]$.

[Total Li] (M)	[Ketone] (M)	Resonance Integrations $\mathbf{A}_2$	$\mathbf{AB}$	$\mathbf{B}_2$	$X_\mathbf{B}$	K_{eq}	$\Delta G°$ (Kcal)
0.53	0.50	110.40	218.65	105.11	0.49	4.12	-0.51
0.26	0.25	104.76	240.96	104.37	0.50	5.31	-0.61
0.053	0.05	92.94	163.65	87.50	0.49	3.29	-0.43
0.011	0.01	100.47	194.88	110.53	0.51	3.42	-0.45

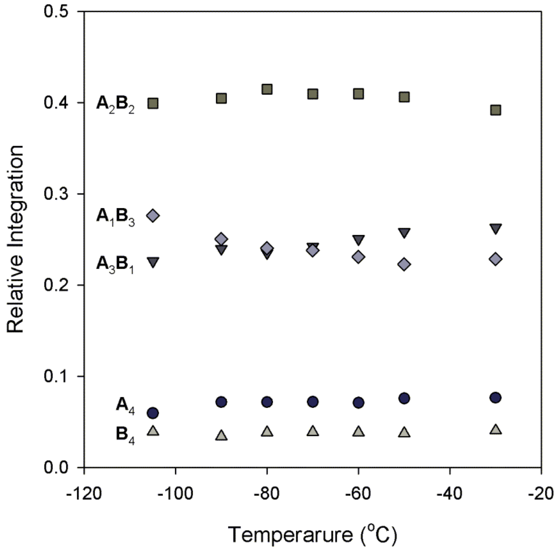


III.a. ^{6}Li NMR spectra of an equimolar mixture [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various temperatures in 2.4 M THF/toluene. Sample was prepared via in situ enolization of 0.20 M total ketone with 0.24 M LiHMDS.

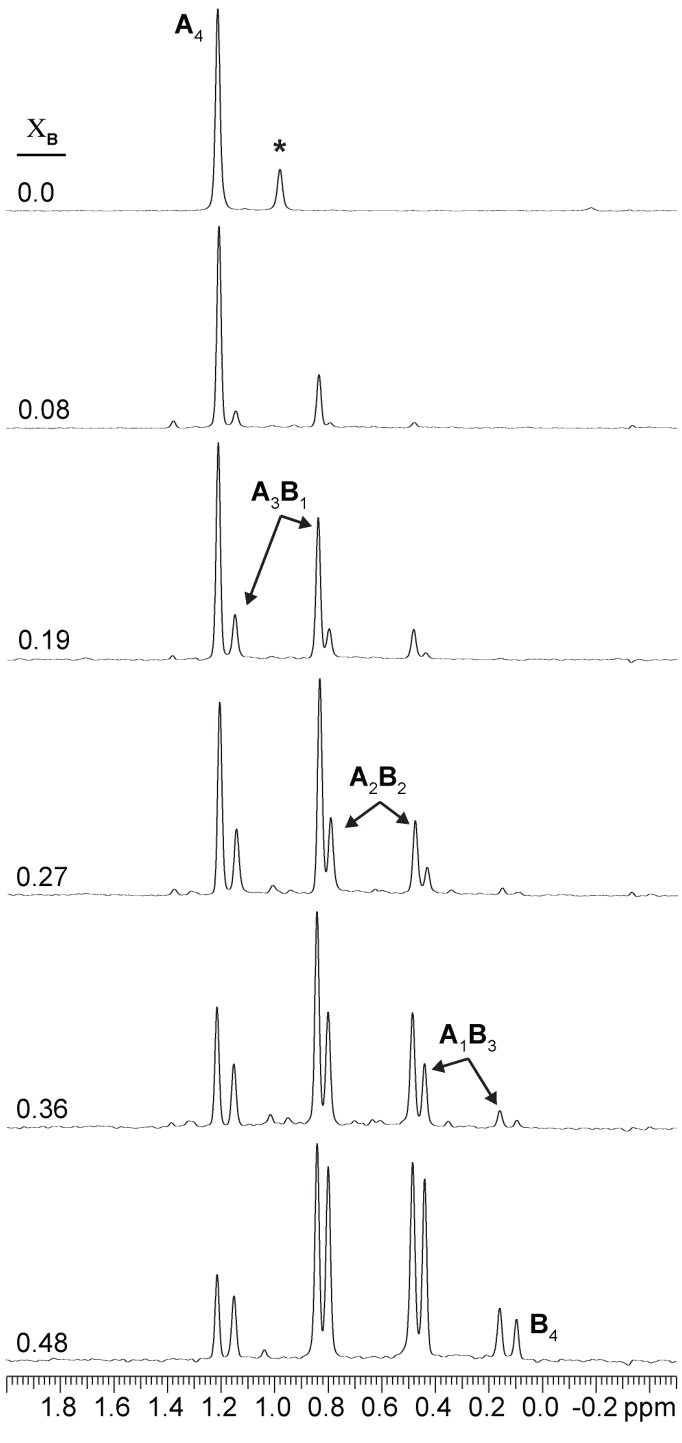
III.b. Resonance integrations and relative integrations for a 0.20 M equimolar mixture of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various temperatures in 2.4 M THF/toluene (see **III.a)**. Sample was prepared via in situ enolization of 0.20 M total ketone with 0.24 M LiHMDS.

Temp.	Resonance Integrations							
		$\mathbf{B}_1$ $\mathbf{A}_3$		$\mathbf{B}_2\mathbf{A}_2$		$\mathbf{B}_3\mathbf{A}_1$		
°C	$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{B}_2$	$\mathbf{A}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$
-30	89.45	76.02	232.41	220.69	238.78	198.22	69.91	47.39
-50	82.99	74.50	209.44	221.14	225.2	180.10	64.30	41.05
-60	79.93	76.56	206.6	231.69	231.24	187.59	73.09	43.40
-70	78.64	74.23	190.96	234.69	213.75	196.80	63.81	42.43
-80	71.79	66.25	169.58	220.69	195.72	181.01	60.54	38.51
-90	72.41	71.03	171.57	221.04	188.56	192.14	61.17	34.47
-105	46.79	44.53	301.45	0.00	309.7	0.00	54.39	30.62

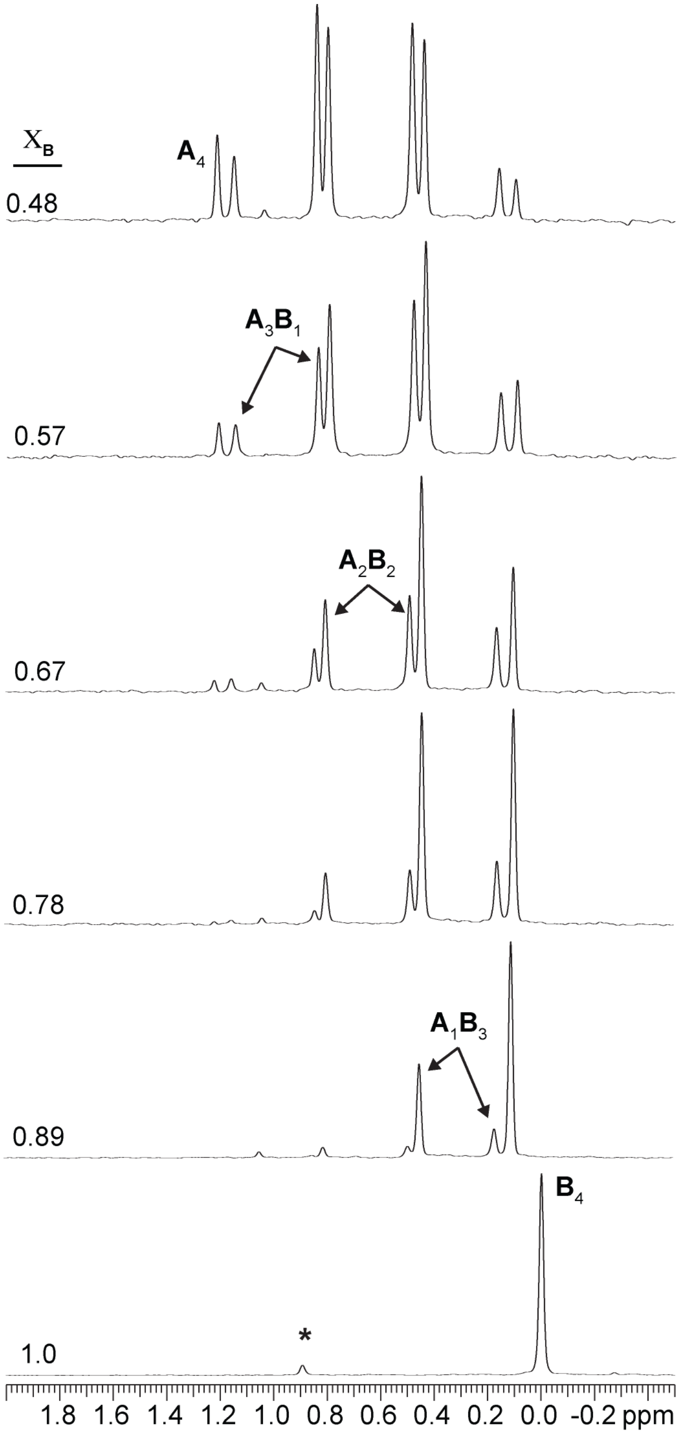
	Relative Integrations				
Temp. (°C)	$\mathbf{A}_4$	$\mathbf{B}_1$ $\mathbf{A}_3$	$\mathbf{B}_2\mathbf{A}_2$	$\mathbf{B}_3\mathbf{A}_1$	$\mathbf{B}_4$
-30	0.08	0.26	0.39	0.23	0.04
-50	0.08	0.26	0.41	0.22	0.04
-60	0.07	0.25	0.41	0.23	0.04
-70	0.07	0.24	0.41	0.24	0.04
-80	0.07	0.24	0.42	0.24	0.04
-90	0.07	0.24	0.41	0.25	0.03
-105	0.06	0.23	0.40	0.28	0.04



III.c. Plot of relative integration versus temperature for an equimolar mixture **1** (**A**) and **2** (**B**) at various temperatures in 2.4 M THF/toluene (see **III.b**). Sample was prepared via in situ enolization of 0.20 M total ketone with 0.24 M LiHMDS.



III.d. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.4 M THF/toluene at -30 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.24 M LiHMDS. * denotes the LiHMDS resonance.



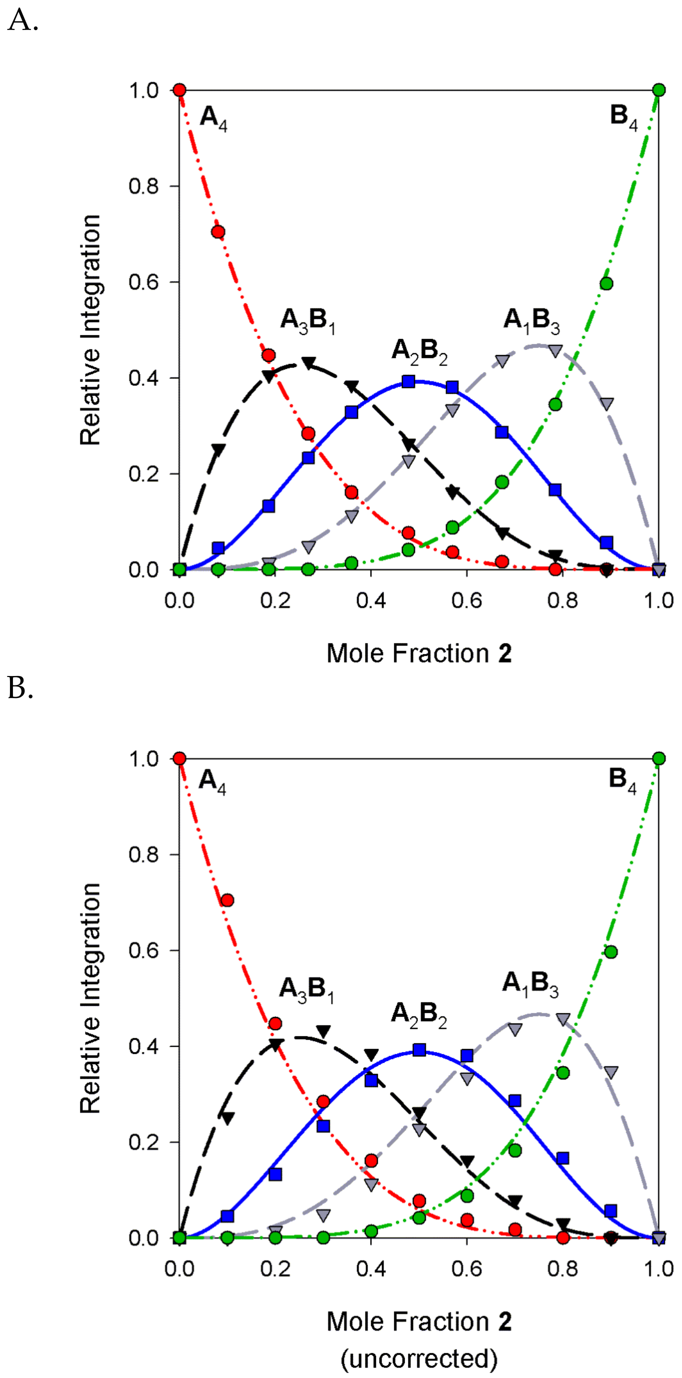
III.d. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.4 M THF/toluene at -30 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.24 M LiHMDS. * denotes the LiHMDS resonance.

III.e. Resonance integrations for an ensemble of $[^{6}\text{Li}]$**1** (**A**) and $[^{6}\text{Li}]$**2** (**B**) at various mole fractions of **A** and **B**. Spectra (see **III.d.**) were recorded on a 0.20 M mixture of enolates in 10 equivalents of THF/toluene at -30 °C.

		Resonance Integrations							
Uncorrected	Calc.		$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		
X_B	X_B	$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.10	0.08	219.50	15.15	63.38	3.85	10.06	0.00	0.00	0.00
0.20	0.19	209.39	44.10	146.15	25.71	36.19	6.90	0.00	0.00
0.30	0.27	215.95	78.69	252.03	81.13	96.23	29.93	8.09	0.00
0.40	0.36	129.17	70.59	239.08	123.23	140.39	67.57	23.80	10.17
0.50	0.48	89.45	76.02	232.41	220.69	238.78	198.22	69.91	47.39
0.60	0.57	32.29	37.80	107.44	169.79	170.54	223.68	76.23	77.77
0.70	0.67	11.68	16.78	39.94	108.85	98.80	240.73	76.77	132.02
0.80	0.78	0.00	8.21	12.66	62.96	50.20	241.50	71.09	233.79
0.90	0.89	0.00	0.00	0.00	14.30	7.75	108.79	28.40	234.57
1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00

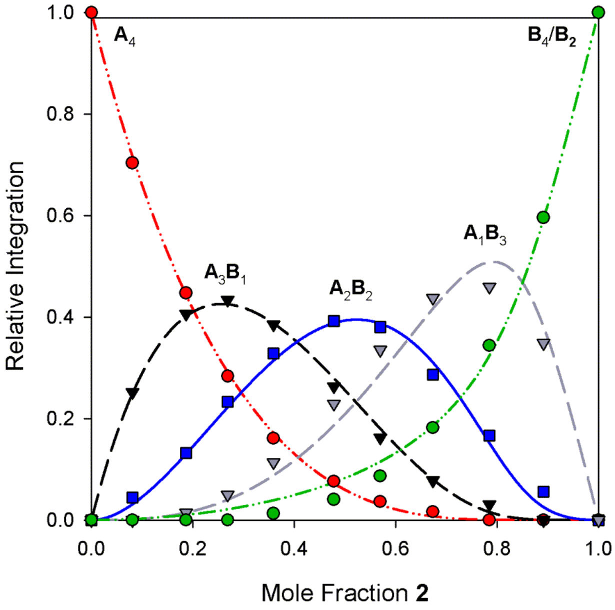
III.f. Relative integrations for aggregates in an ensemble of **1** (**A**) and **2** (**B**) at various mole fractions of **A** and **B**. Populations were measured (see **III.d** and **III.e**) for a 0.20 M enolate ensemble in 10 equivalents of THF/toluene at -30 °C.

		Relative Integrations				
Uncorrected X_B	Calculated X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.08	0.70	0.25	0.04	0.00	0.00
0.20	0.19	0.45	0.41	0.13	0.01	0.00
0.30	0.27	0.28	0.43	0.23	0.05	0.00
0.40	0.36	0.16	0.39	0.33	0.11	0.01
0.50	0.48	0.08	0.26	0.39	0.23	0.04
0.60	0.57	0.04	0.16	0.38	0.33	0.09
0.70	0.67	0.02	0.08	0.29	0.44	0.18
0.80	0.78	0.00	0.03	0.17	0.46	0.34
0.90	0.89	0.00	0.00	0.06	0.35	0.60
1.00	1.00	0.00	0.00	0.00	0.00	1.00

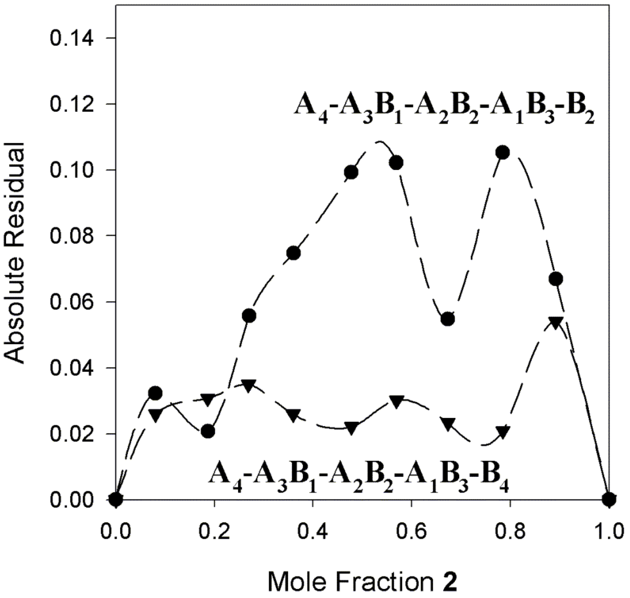


III.g. Plot of the relative integrations versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of THF/toluene at -30 °C (see **III.f**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2**; $\phi_0 = 0.94$; $\phi_1 = 1.09$; $\phi_2 = 1.23$; $\phi_3 = 1.31$; $\phi_4 = 1.00$; rms = 0.007. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **2**; $\phi_0 = 0.83$; $\phi_1 = 0.94$; $\phi_2 = 1.11$; $\phi_3 = 1.24$; $\phi_4 = 1.00$; rms = 0.023.

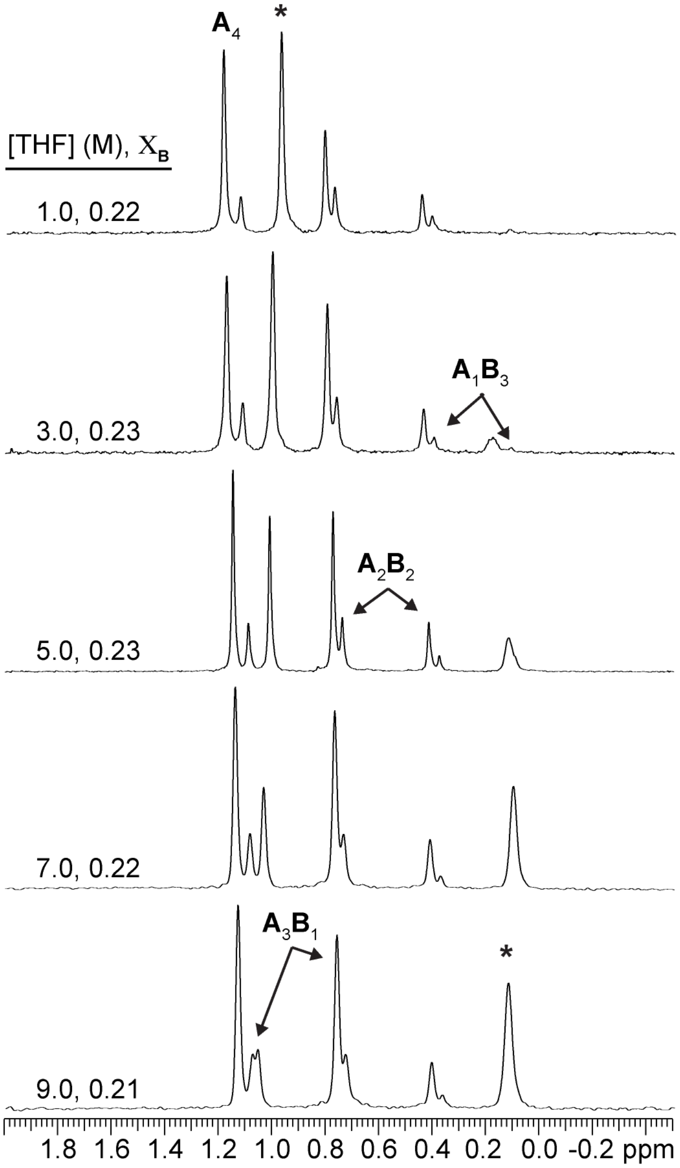
A.



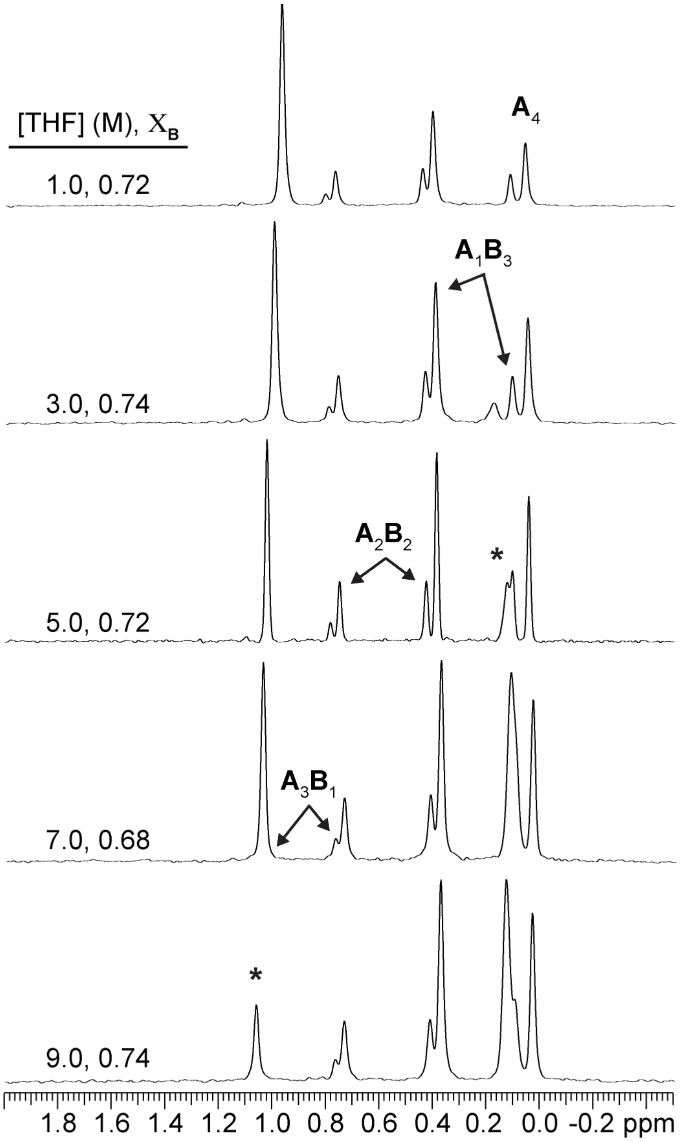
B.



III.h. Plots of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of THF/toluene at -30 °C fit to an ensemble of **A_4-A_3B_1-A_2B_2-A_1B_3-B_2** (see **III.d** and **g**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2** fit to **A_4-A_3B_1-A_2B_2-A_1B_3-B_2**; ϕ_{20} = 0.18; $\phi_{21} = \phi_{22}$ = 0.00; ϕ_{40} = 0.00; ϕ_{41} = 1.11; ϕ_{42} = 1.11; ϕ_{43} = 0.88; ϕ_{44} = 0.60; rms = 0.02. B) Plot of the sum of the absolute residuals for **A_4-A_3B_1-A_2B_2-A_1B_3-B_4** and **A_4-A_3B_1-A_2B_2-A_1B_3-B_2** versus the mole fraction of **2**.



III.i. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various concentrations of THF/toluene at -30 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.02 M excess LiHMDS (*).



III.i. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various concentrations of THF/toluene at -30 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.02 M excess LiHMDS (*).

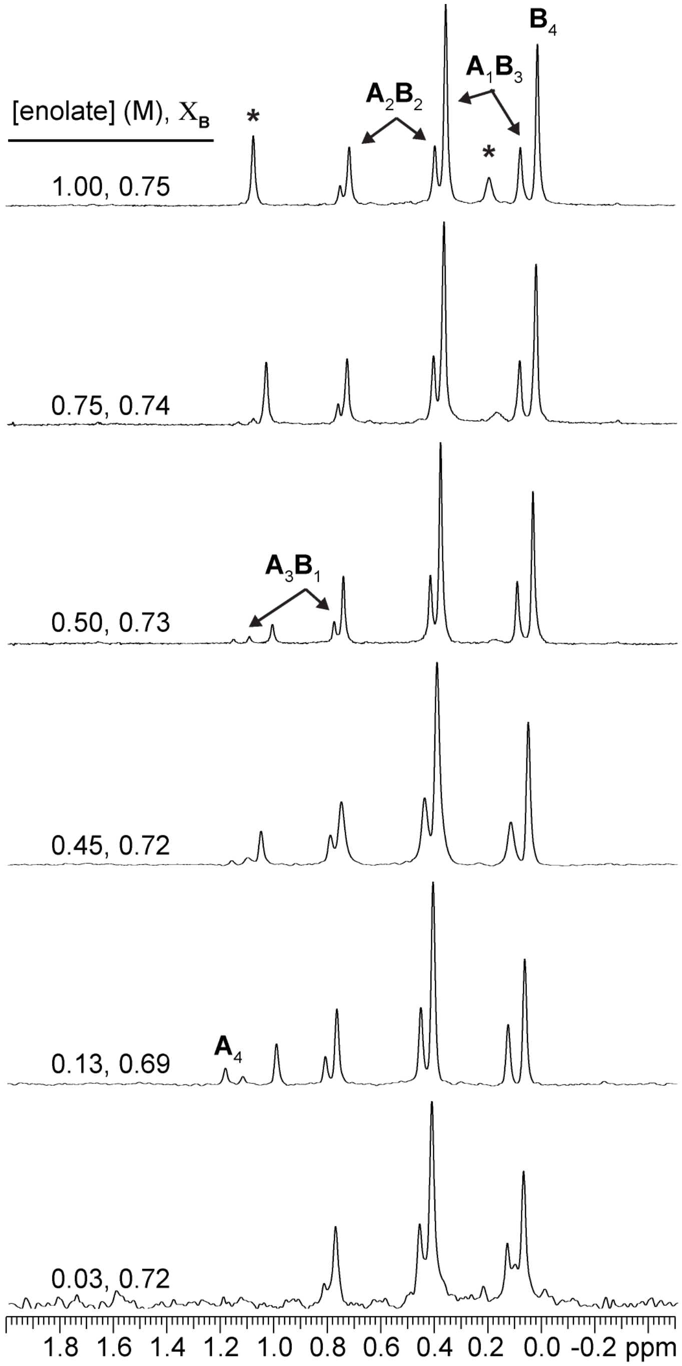
III.j. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various THF concentrations. Spectra (see **III.i**.) were recorded on a 0.10 M mixture of **1** and **2** at -30 °C.

[THF]	Calc.	Resonance Integrations								
		$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		LiHMDS	
(M)	$X_\mathbf{B}$		$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	dimer	mono.
1.0	0.22	186.86	32.35	100.39	41.79	40.71	19.15	0.00	218.78	0
3.0	0.23	201.49	54.14	167.98	58.05	52.62	17.69	0.00	243.42	44.44
5.0	0.23	261.81	61.86	220.99	79.19	78.57	22.92	0.00	219.93	128.74
7.0	0.22	284.23	72.76	268.58	85.73	86.09	17.47	0.00	156.47	245.01
9.0	0.21	300.49	65.82	277.51	100.88	89.03	21.45	0.00	100.14	331.82

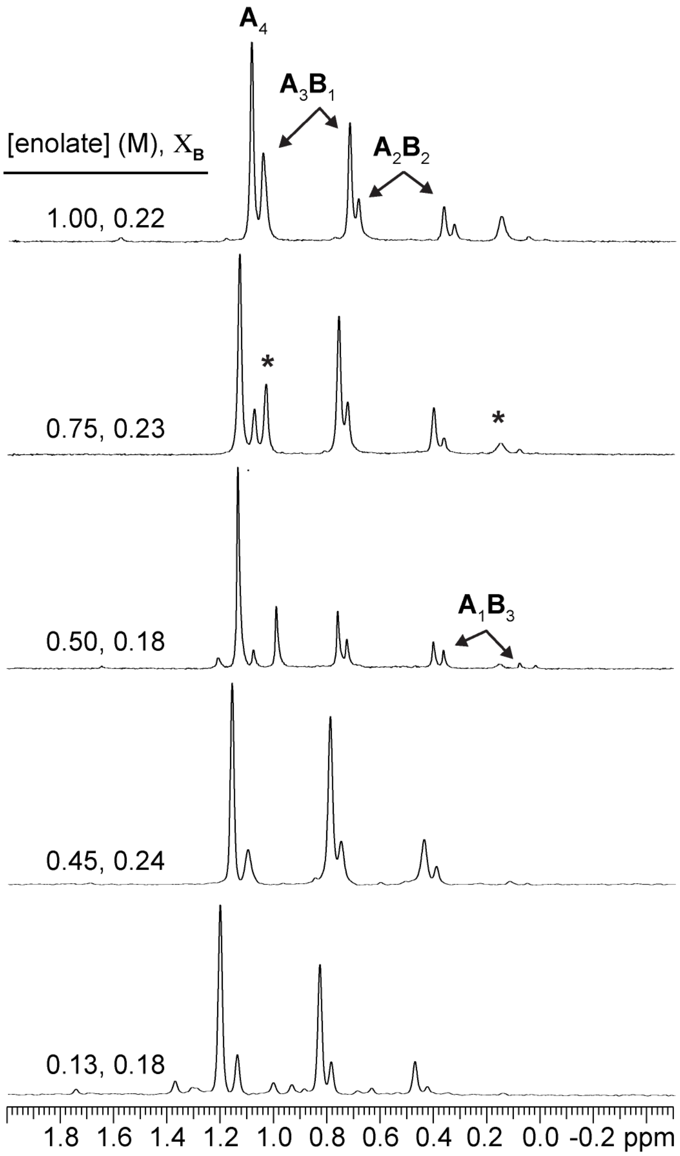
[THF]	Calc.	Resonance Integrations								
		$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$	LiHMDS	
(M)	$X_\mathbf{B}$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$		dimer	mono.
1.0	0.72	0.00	13.01	55.97	48.39	154.62	46.56	98.19	330.66	0.00
3.0	0.74	0.00	19.59	83.76	63.64	241.96	67.13	173.51	343.43	51.16
5.0	0.72	0.00	20.05	79.52	66.95	224.66	74.89	167.41	249.91	114.90
7.0	0.68	0.00	35.60	112.81	101.48	314.94	151.18	224.93	314.49	366.30
9.0	0.74	0.00	25.03	119.86	84.63	341.03	93.26	251.26	134.95	464.36

III.k. Relative integrations for each aggregate in ensembles of **1** (**A**) and **2** (**B**) at various THF concentrations (see **III.i** and **j**.). Spectra were recorded on a 0.10 M mixture of **1** and **2** at -30 °C.

[THF] (M)	Calculated $X_\mathbf{B}$	Calculated X_{LiHMDS}	Relative Integrations				
			$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.0	0.22	0.34	0.44	0.32	0.20	0.05	0.00
3.0	0.23	0.34	0.37	0.40	0.20	0.03	0.00
5.0	0.23	0.32	0.36	0.39	0.22	0.03	0.00
7.0	0.22	0.33	0.35	0.42	0.21	0.02	0.00
9.0	0.21	0.34	0.35	0.40	0.22	0.03	0.00
1.0	0.72	0.44	0.00	0.03	0.25	0.48	0.24
3.0	0.74	0.38	0.00	0.03	0.23	0.48	0.27
5.0	0.72	0.37	0.00	0.03	0.23	0.47	0.26
7.0	0.68	0.42	0.00	0.04	0.23	0.50	0.24
9.0	0.74	0.40	0.00	0.03	0.22	0.47	0.27



III.1. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene at -30 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS (*).



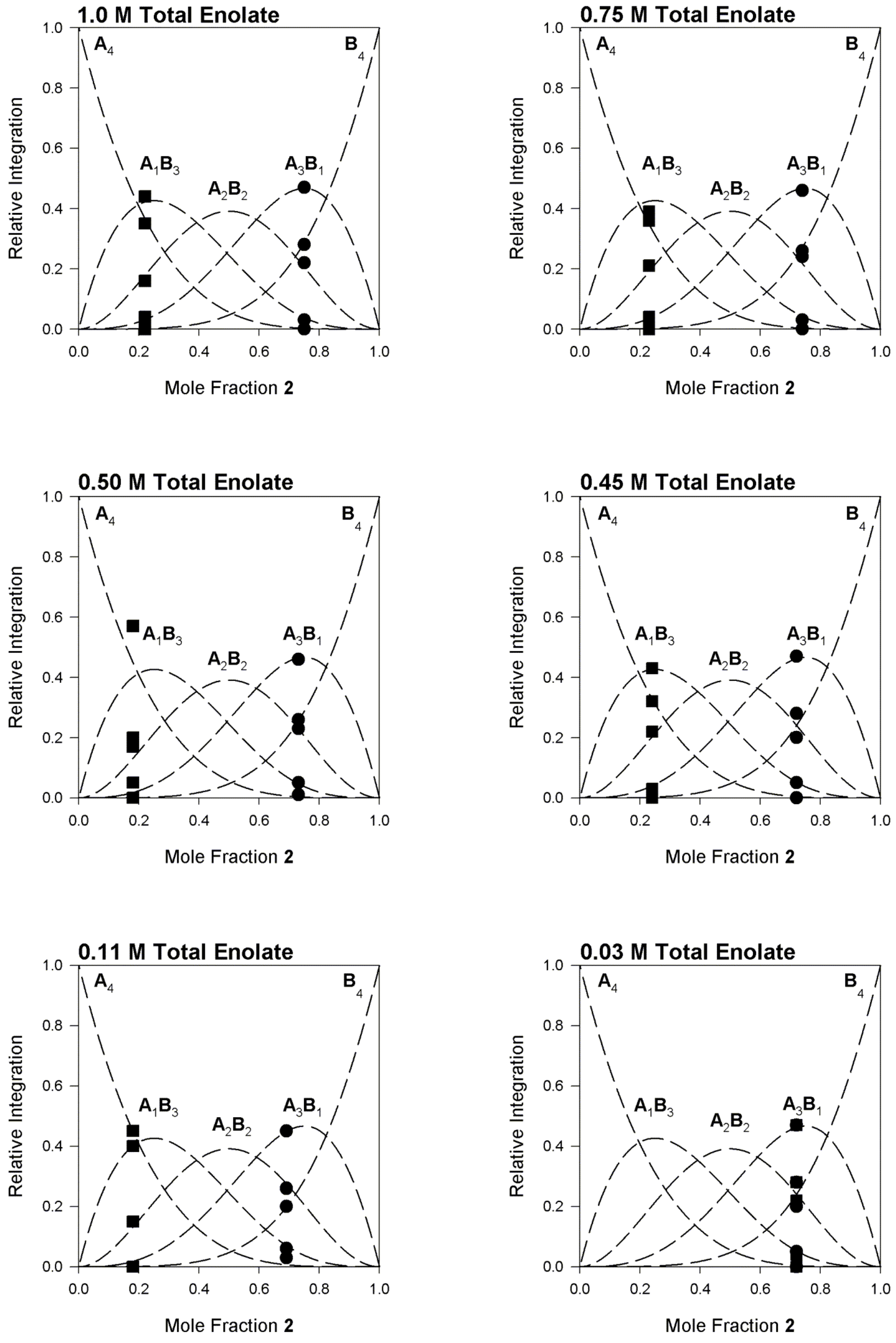
III.1 (cont.). ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene at -30 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS (*).

III.m. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene with excess LiHMDS. Spectra (see **III.l**) were recorded at -30 °C.

		Resonance Integrations							
Calc.	[enolate]	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$
$X_{\mathbf{B}}$	(M)		$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	
0.75	1.00	0.00	0.00	17.92	77.98	68.76	237.67	70.99	179.61
0.74	0.75	0.00	4.28	20.58	86.19	85.23	248.32	79.41	187.91
0.73	0.50	4.30	7.42	21.11	73.99	71.84	218.02	67.45	162.60
0.72	0.45	3.83	10.93	35.02	147.10	113.73	355.63	89.31	185.85
0.69	0.13	20.78	11.11	30.27	98.07	90.95	250.78	74.27	146.82
0.72	0.03	0.00	0.00	35.30	134.05	141.50	334.25	125.60	212.23
0.22	1.00	226.70	144.22	143.48	57.67	46.85	21.54	6.98	0.00
0.23	0.75	252.94	49.30	180.62	67.29	66.33	21.71	5.93	0.00
0.18	0.50	188.94	13.83	54.09	31.09	26.20	14.71	3.38	0.00
0.24	0.45	237.51	61.55	257.76	63.90	95.18	21.61	0.00	0.00
0.18	0.11	253.94	45.08	181.41	33.92	53.40	74.27	0.00	0.00

III.n. Relative integrations for each aggregate in ensembles of **1** (**A**) and **2** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene with excess LiHMDS. Spectra (see **III.l**) were recorded at -30 °C.

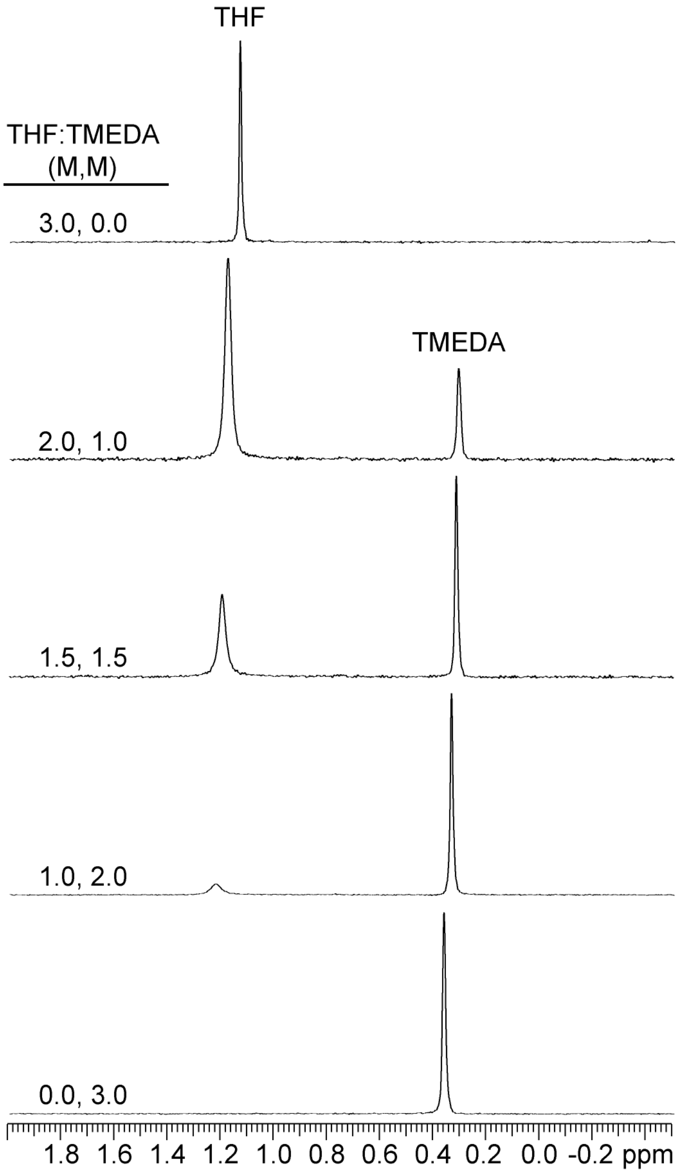
[Li]	[enolate]	Calc.	Relative Integrations				
(M)	(M)	$X_{\mathbf{B}}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.16	1.00	0.75	0.00	0.03	0.22	0.47	0.28
0.82	0.75	0.74	0.00	0.03	0.24	0.46	0.26
0.58	0.50	0.73	0.01	0.05	0.23	0.46	0.26
0.50	0.45	0.72	0.00	0.05	0.28	0.47	0.20
0.11	0.13	0.69	0.03	0.06	0.26	0.45	0.20
0.03	0.03	0.72	0.00	0.04	0.28	0.47	0.22
1.16	1.00	0.22	0.35	0.44	0.16	0.04	0.00
0.82	0.75	0.23	0.39	0.36	0.21	0.04	0.00
0.58	0.50	0.18	0.57	0.20	0.17	0.05	0.00
0.50	0.45	0.24	0.32	0.43	0.22	0.03	0.00
0.13	0.11	0.18	0.45	0.40	0.15	0.00	0.00



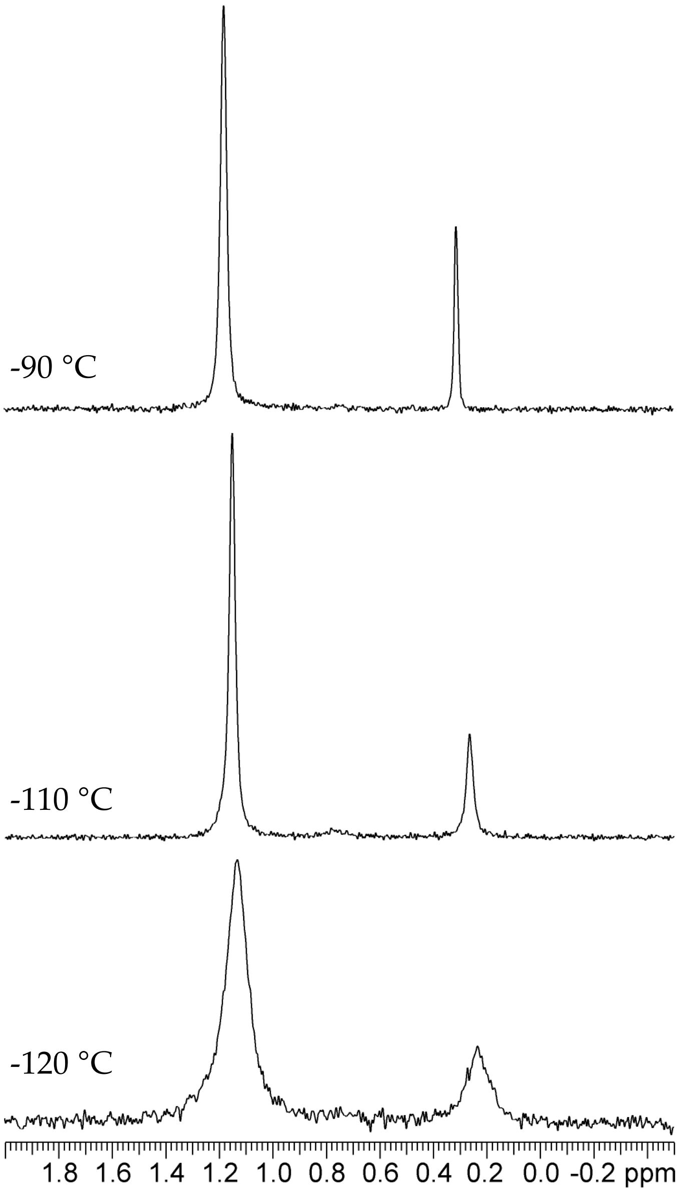
III.o. Relative integrations of mixtures of **1** (**A**) and **2** (**B**) at various absolute Li concentrations in 10 equivalents of THF/toluene at -30 °C plotted on the curves for a fit to the Job plot of an ensemble of tetramers (**III.g**).

III.p. Absolute residuals for the deviation of the relative integrations of ensembles of **1** and **2** in 10 equivalents THF/toluene at various absolute Li concentrations from the expected relative integrations based on the fit in **III.g**.

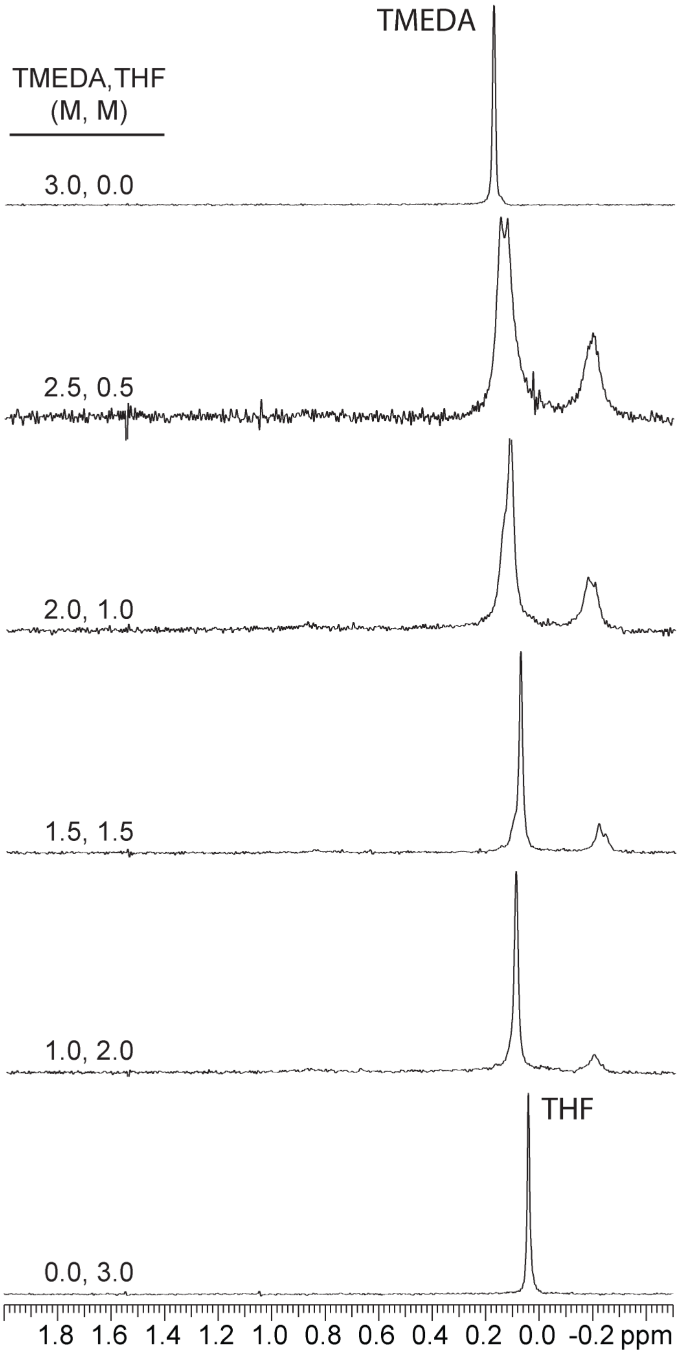
[enolate] (M)	Calc. X_B	Absolute Residuals				
		$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.00	0.75	0.00	0.01	0.02	0.01	0.01
0.75	0.74	0.00	0.01	0.02	0.01	0.01
0.50	0.73	0.00	0.00	0.00	0.01	0.01
0.45	0.72	0.00	0.01	0.02	0.02	0.02
0.13	0.69	0.02	0.02	0.02	0.00	0.01
0.03	0.72	0.01	0.02	0.04	0.01	0.02
1.00	0.22	0.01	0.03	0.03	0.01	0.00
0.75	0.23	0.03	0.06	0.02	0.01	0.00
0.50	0.18	0.11	0.19	0.04	0.04	0.00
0.45	0.24	0.02	0.02	0.01	0.01	0.00
0.11	0.18	0.01	0.01	0.02	0.02	0.00



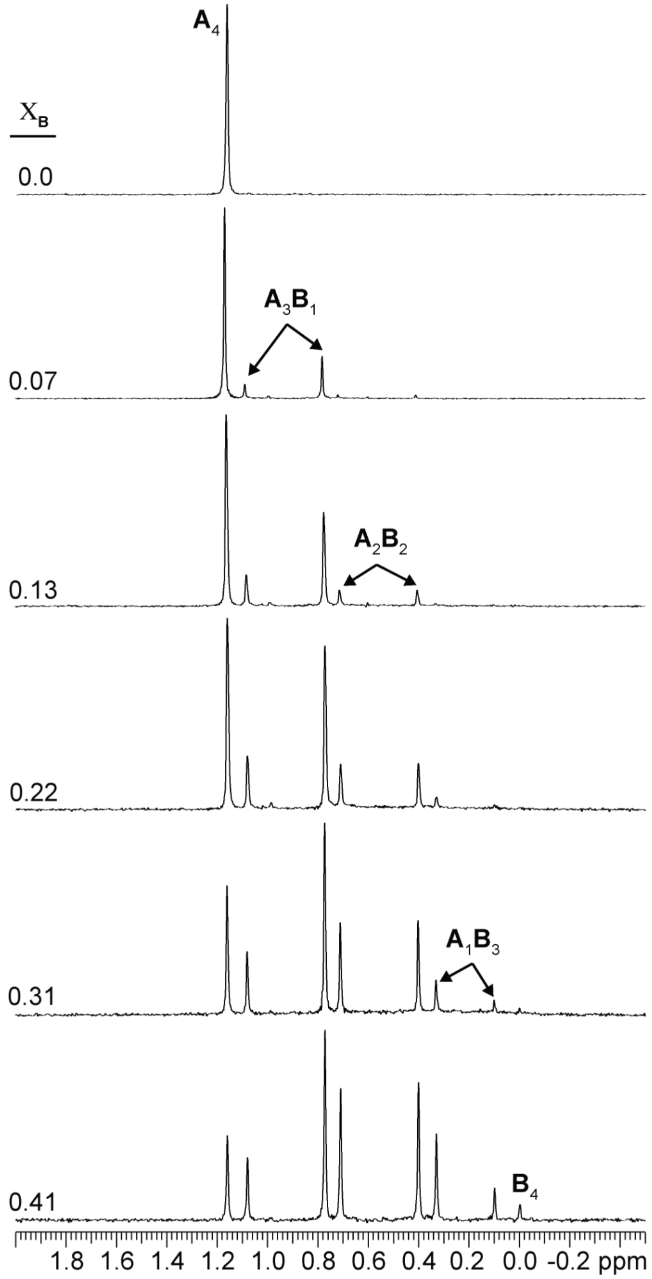
III.q. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** in various mole fractions of TMEDA and THF/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone, 0.10 M [^{6}Li] LiHMDS and 3.0 M total ligand (30 equivalents).



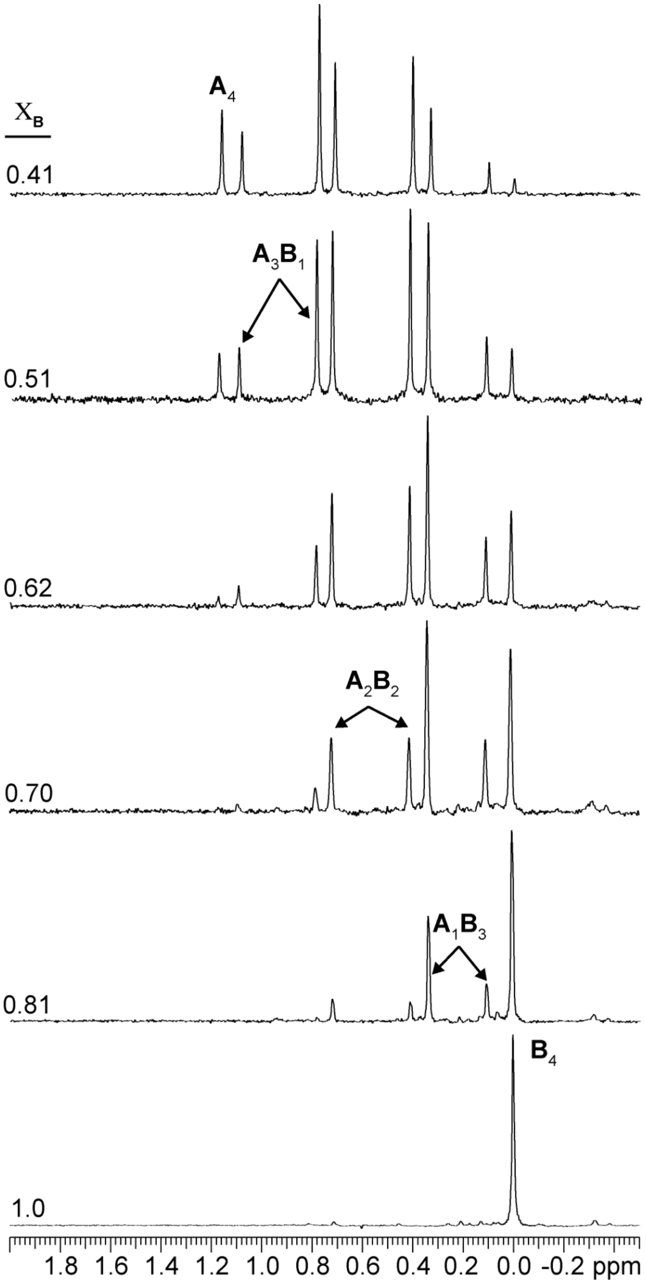
III.r. ^{6}Li NMR spectra of [^{6}Li]**1** in 2.0 M TMEDA and 1.0 M THF/toluene at various temperatures. Samples are 0.10 M [^{6}Li]**1** and 3.0 M total ligand (30 equivalents).



III.s. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**2** in various mole fractions of TMEDA and THF/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone, 0.10 M [^{6}Li] LiHMDS and 3.0 M total ligand (30 equivalents).



III.t. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 0.60 THF/toluene at -90 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.20 M LiHMDS.



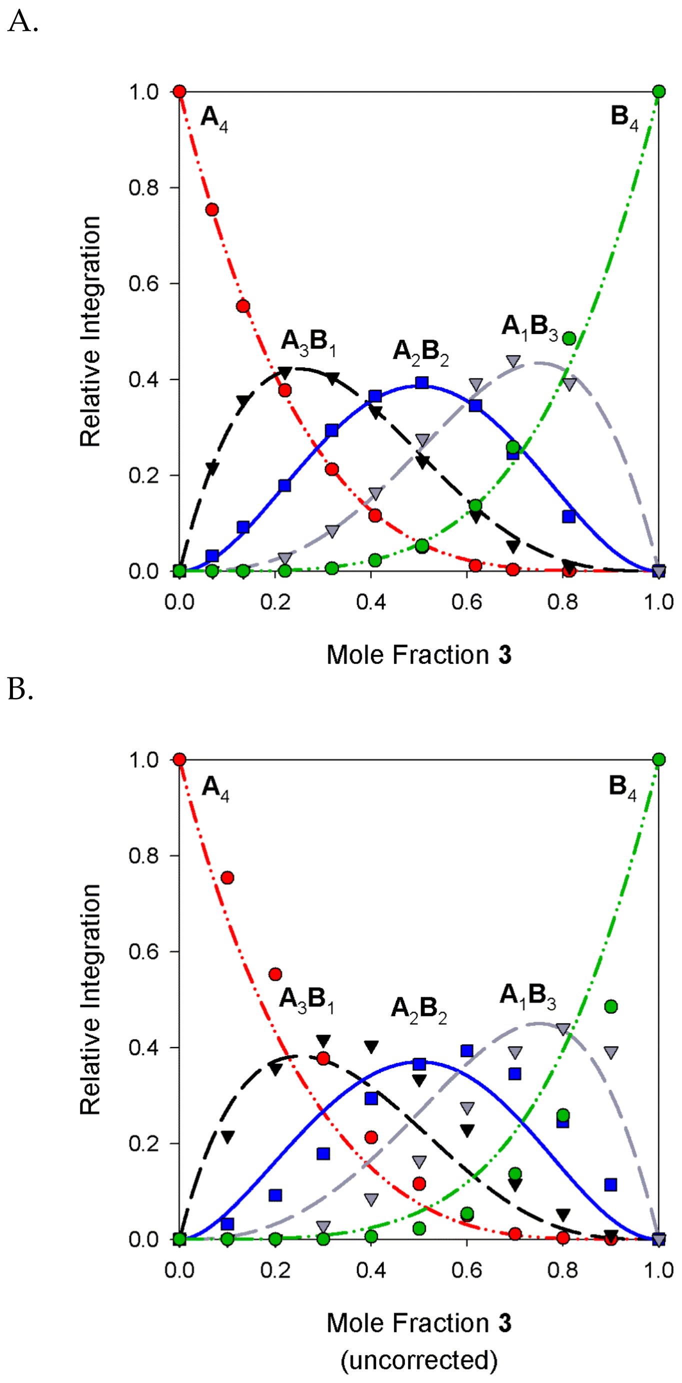
III.t. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 0.60 THF/toluene at -90 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.20 M LiHMDS.

III.u. Resonance integrations for an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions of **A** and **B**. Spectra (see **III.t**.) were recorded on a 0.20 M mixture of enolates in 0.60 M THF/toluene at -90 °C.

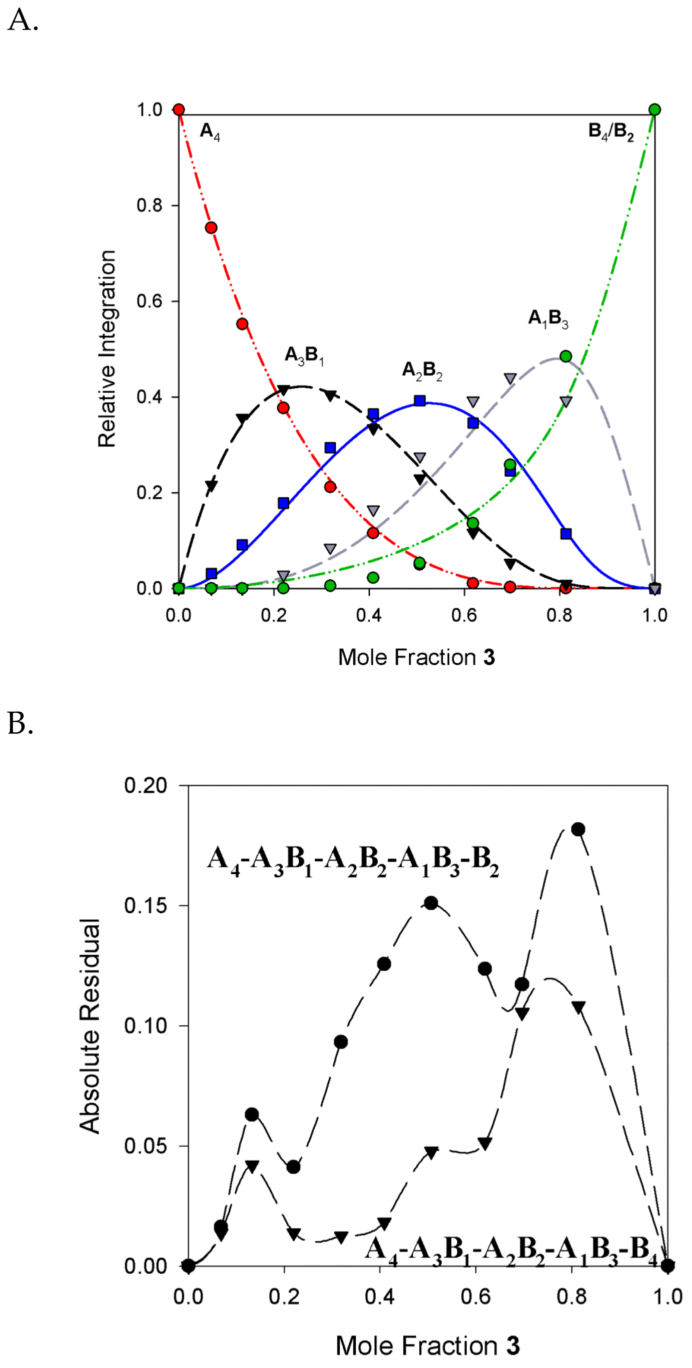
Uncorrected	Calc.	Resonance Integrations							
			$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		
X_B	X_B	$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.10	0.07	119.88	8.75	25.60	2.82	2.16	0.00	0.00	0.00
0.20	0.13	152.38	24.26	74.28	12.72	12.52	0.00	0.00	0.00
0.30	0.22	151.96	41.11	126.98	35.93	35.99	11.52	0.00	0.00
0.40	0.32	78.47	36.85	113.35	52.68	56.30	23.00	8.66	1.92
0.50	0.41	55.69	39.09	122.71	86.35	90.07	58.08	21.56	10.53
0.60	0.51	32.82	33.67	119.04	125.12	135.57	131.97	51.14	34.98
0.70	0.62	5.36	13.64	45.96	85.16	91.45	141.75	59.04	69.58
0.80	0.70	1.29	4.93	22.17	61.00	63.29	153.86	69.87	130.85
0.90	0.81	0.02	0.22	3.70	22.92	22.14	108.11	47.54	192.30
1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00

III.v. Relative integrations for aggregates in an ensemble of **1** (**A**) and **3** (**B**) at various mole fractions of **A** and **B**. Integrations were measured (see **III.r** and **III.s**) for a 0.20 M enolate ensemble in 0.60 M THF/toluene at -90 °C.

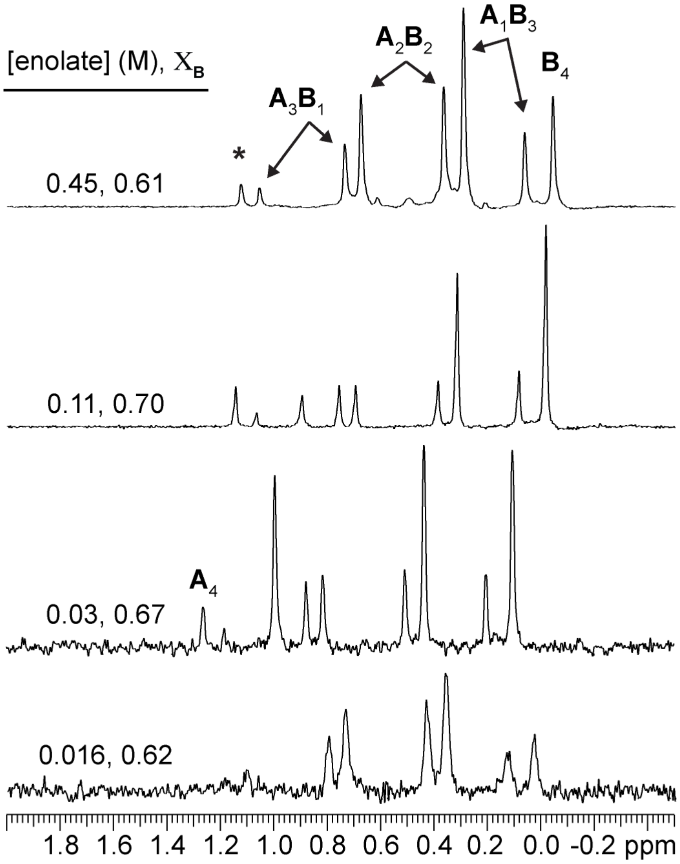
Uncorrected	Calculated	Relative Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.07	0.75	0.22	0.03	0.00	0.00
0.20	0.13	0.55	0.36	0.09	0.00	0.00
0.30	0.22	0.38	0.42	0.18	0.03	0.00
0.40	0.32	0.21	0.40	0.29	0.09	0.01
0.50	0.41	0.12	0.33	0.36	0.16	0.02
0.60	0.51	0.05	0.23	0.39	0.28	0.05
0.70	0.62	0.01	0.12	0.34	0.39	0.14
0.80	0.70	0.00	0.05	0.25	0.44	0.26
0.90	0.81	0.00	0.01	0.11	0.39	0.48
1.00	1.00	0.00	0.00	0.00	0.00	1.00



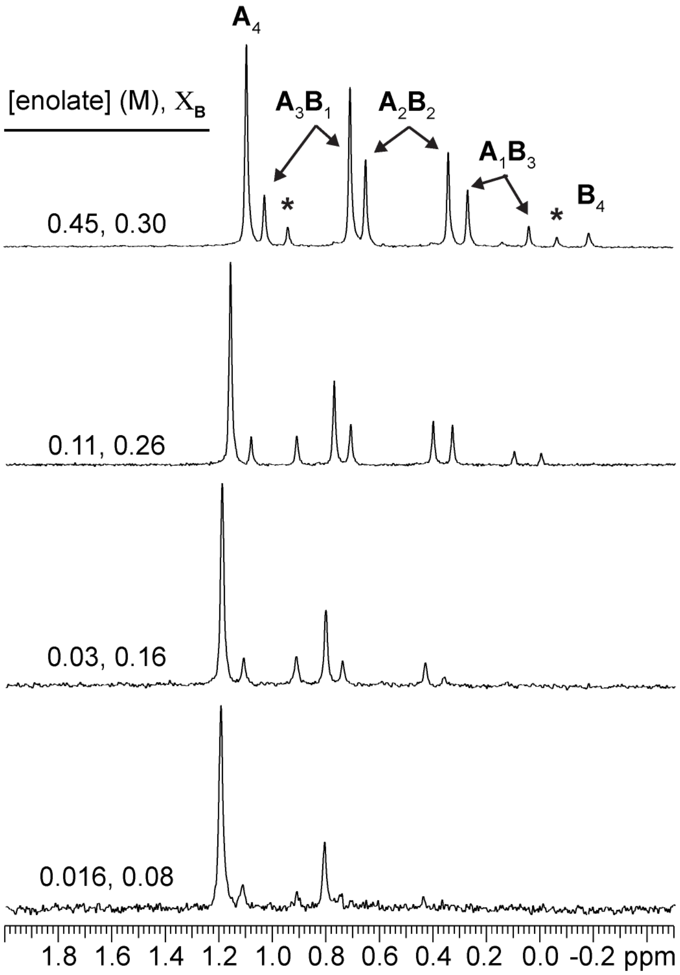
III.w. Plot of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 0.60 M THF/toluene at -90 °C (see **III.t**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 1.08$; $\phi_2 = 1.07$; $\phi_3 = 0.99$; $\phi_4 = 0.93$; rms = 0.013. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 0.87$; $\phi_2 = 1.02$; $\phi_3 = 1.21$; $\phi_4 = 1.16$; rms = 0.062.



III.x. Plots of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 3.0 equivalents of THF/toluene at -90 °C fit to an ensemble of **A_4-A_3B_1- A_2B_2- A_1B_3- B_2** (see **III.t**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3** fit to **A_4-A_3B_1- A_2B_2- A_1B_3- B_2**; ϕ_{20} = 0.21; ϕ_{21} = ϕ_{22} = 0.00; ϕ_{40} = 0.00; ϕ_{41} = 1.14; ϕ_{42} = 1.33; ϕ_{43} = 1.23; ϕ_{44} = 1.10; rms = 0.03. B) Plot of the sum of the absolute residuals for **A_4-A_3B_1- A_2B_2- A_1B_3- B_2** versus the mole fraction of **3**.



III.y. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS (*).



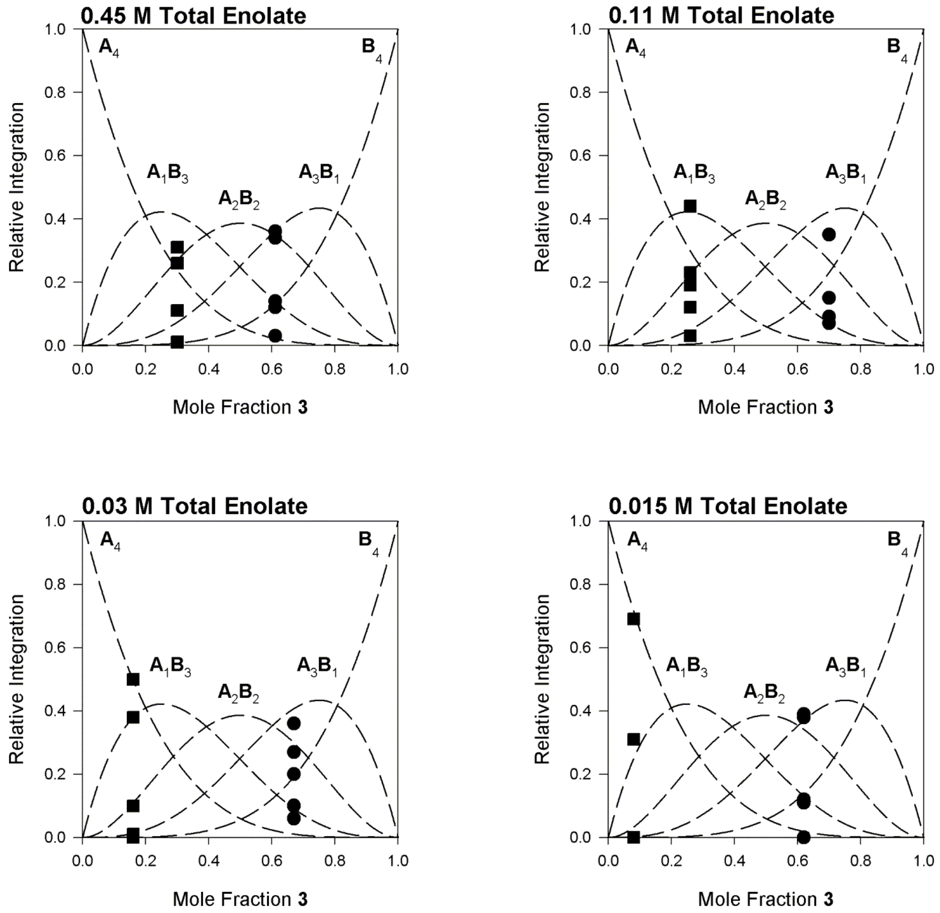
III.y (cont.). ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS (*).

III.z. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene with excess LiHMDS. Spectra (see **III.l**) were recorded at -90 °C.

		Resonance Integrations							
Calc.	[enolate]	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$
$X_\mathbf{B}$	(M)		$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	
0.30	0.45	197.05	46.05	150.44	80.62	85.94	51.68	18.70	8.93
0.26	0.11	189.53	22.74	77.33	39.31	40.89	36.50	13.88	11.33
0.16	0.03	242.23	28.88	89.30	28.05	26.88	10.41	0.00	0.00
0.08	0.015	281.98	33.28	93.55	0.00	0.00	0.00	0.00	0.00
0.61	0.45	29.78	23.87	84.12	141.04	168.04	241.84	87.15	126.38
0.70	0.11	37.74	12.96	39.62	40.28	42.92	141.97	53.59	195.27
0.67	0.03	51.68	23.38	70.15	88.95	90.18	236.96	87.99	242.32
0.62	0.015	0.00	54.63	142.99	306.17	308.13	427.39	190.65	168.42

III.aa. Relative integrations for each aggregate in ensembles of **1** (**A**) and **3** (**B**) at various absolute Li concentrations in 10 equivalents THF/toluene with excess LiHMDS. Spectra (see **III.l**) were recorded at -90 °C.

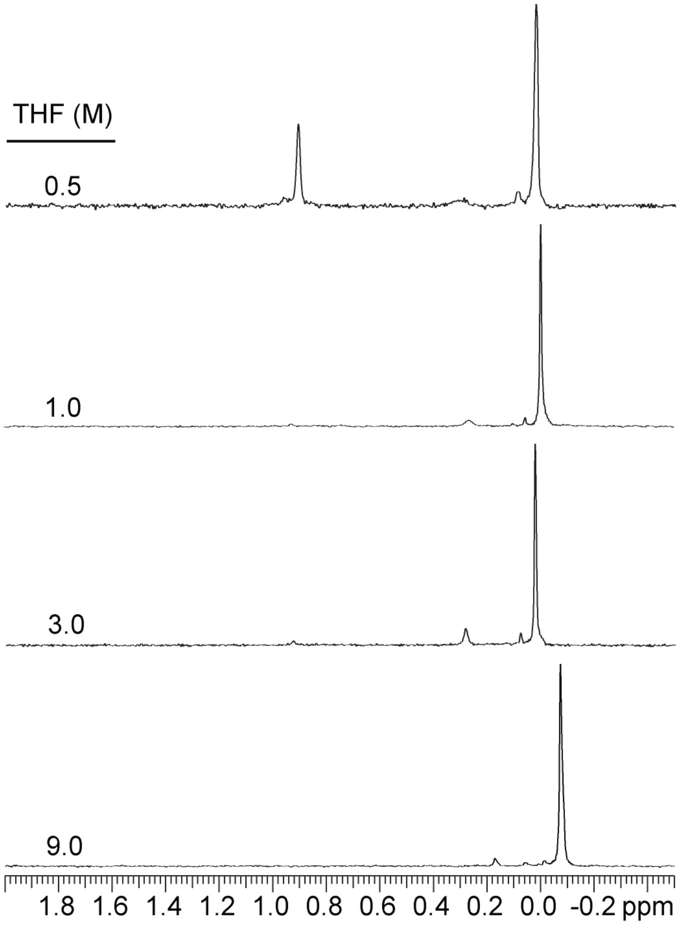
[Li]	[enolate]	Calc.	Relative Integrations				
(M)	(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.50	0.45	0.30	0.31	0.31	0.26	0.11	0.01
0.13	0.11	0.26	0.44	0.23	0.19	0.12	0.03
0.03	0.03	0.16	0.50	0.38	0.10	0.01	0.00
0.016	0.015	0.08	0.69	0.31	0.00	0.00	0.00
0.50	0.45	0.61	0.03	0.12	0.34	0.36	0.14
0.13	0.11	0.70	0.07	0.09	0.15	0.35	0.35
0.03	0.03	0.67	0.06	0.10	0.20	0.36	0.27
0.016	0.015	0.62	0.00	0.12	0.38	0.39	0.11



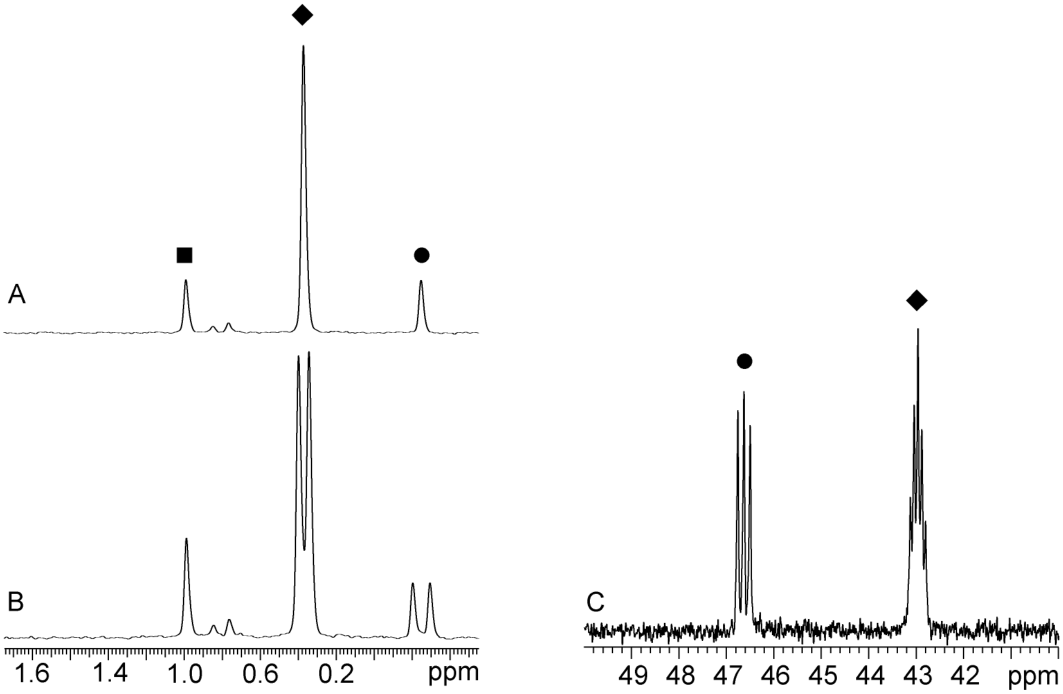
III.bb. Relative integrations of mixtures of **1** and **3** at various absolute Li concentrations in 10 equivalents of THF/toluene at -90 °C plotted on the curves for a fit to the Job plot of an ensemble of tetramers (**III.w**).

III.cc. Absolute residuals for the deviation of the relative integrations of ensembles of **1** and **2** in 10 equivalents THF/toluene at various absolute Li concentrations from the expected relative integrations based on the fit in **III.w**.

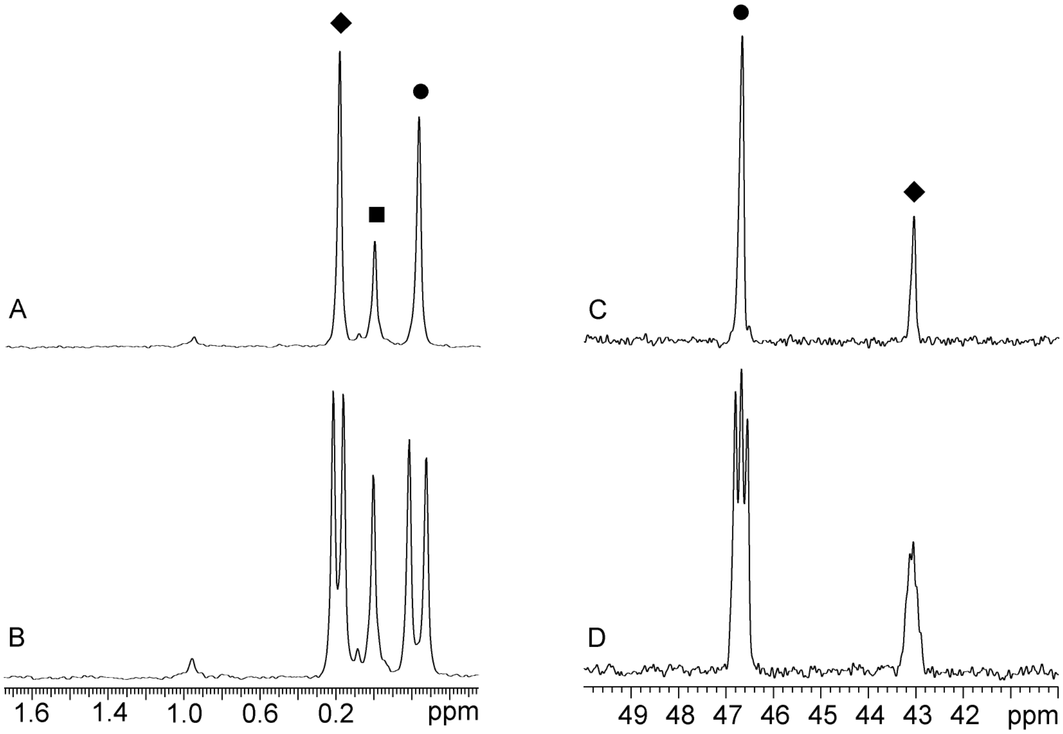
[enolate] (M)	Calc. X_B	Absolute Residuals A_4	A_3B_1	A_2B_2	A_1B_3	B_4
0.45	0.30	0.08	0.11	0.01	0.04	0.01
0.11	0.26	0.16	0.20	0.04	0.07	0.02
0.03	0.16	0.01	0.01	0.00	0.00	0.00
0.015	0.08	0.04	0.07	0.03	0.00	0.00
0.45	0.61	0.01	0.02	0.00	0.01	0.00
0.11	0.70	0.06	0.02	0.12	0.07	0.10
0.03	0.67	0.05	0.01	0.10	0.03	0.07
0.015	0.62	0.02	0.01	0.04	0.03	0.04



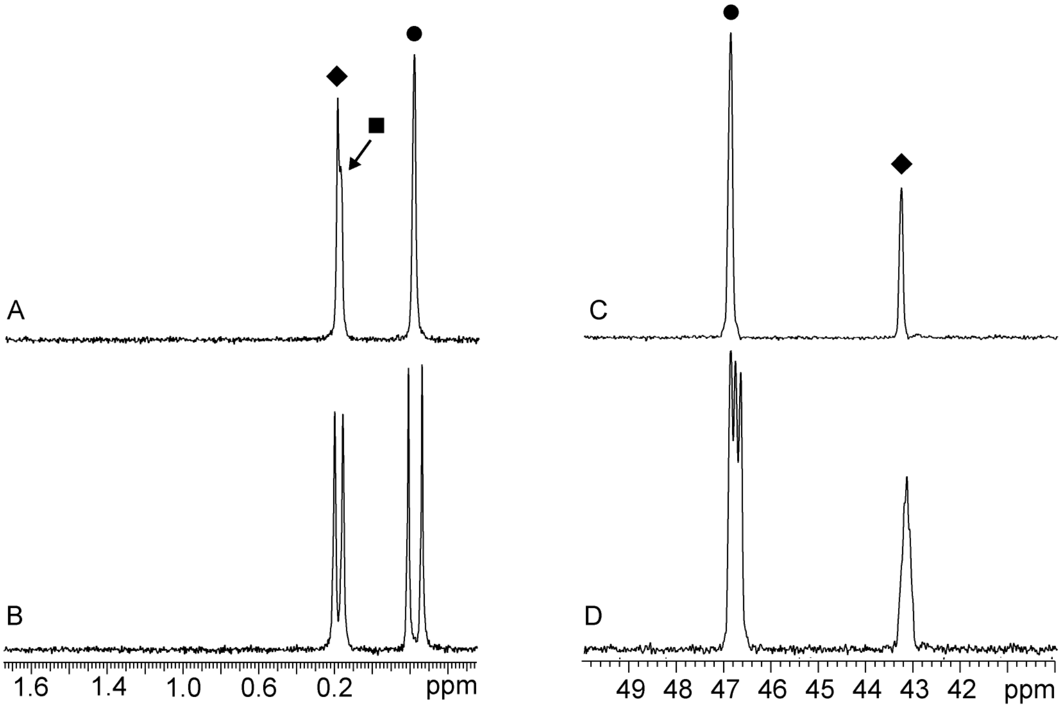
III.dd. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**3** in various THF/toluene concentrations at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone and 0.10 M [^{6}Li] LiHMDS.



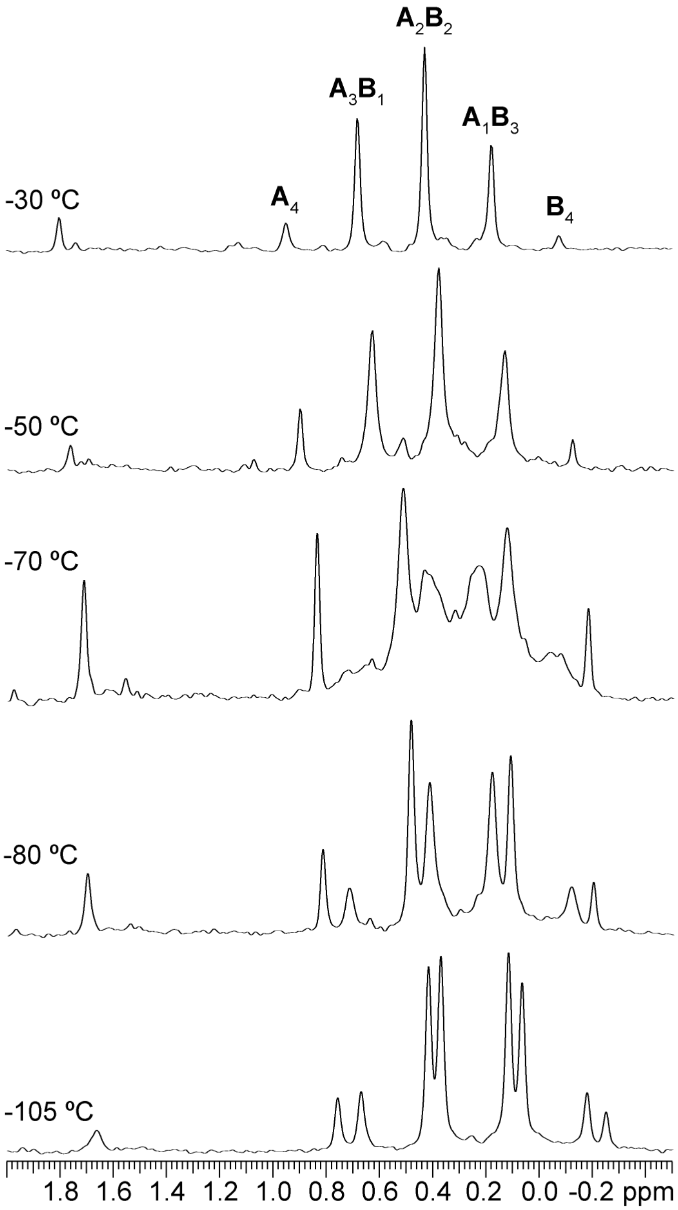
IV.a. [^{6}Li] and [^{15}N] NMR spectra of 0.10 M [^{6}Li]**1** and 0.20 M [^{15}N, ^{6}Li]LiHMDS in 2.0 M DME/toluene at -90 °C. A) {^{15}N}[^{6}Li] NMR spectrum; B) [^{6}Li] NMR spectrum; C) [^{15}N] NMR spectrum. ◆ = **1**/LiHMDS mixed aggregate; ■ = **1**; ● = LiHMDS monomer.



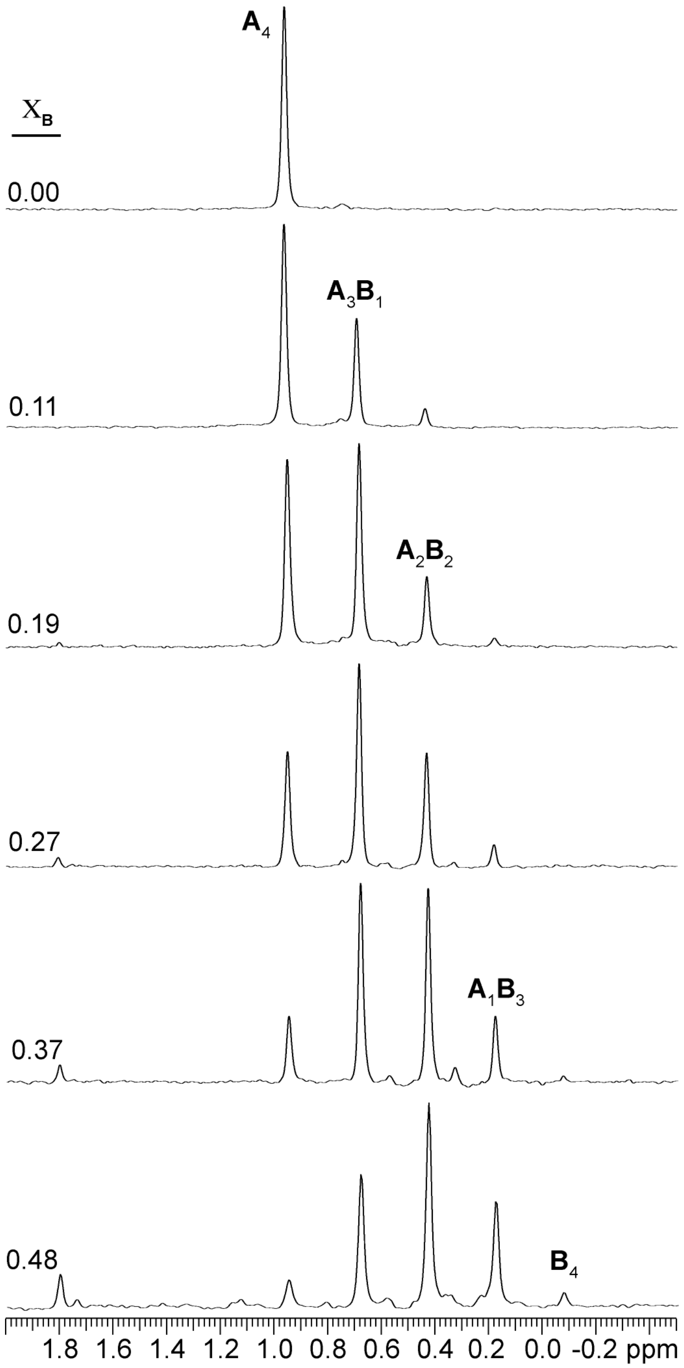
IV.b. [^{6}Li] and [^{15}N] NMR spectra of 0.10 M [^{6}Li]**2** and 0.20 M [^{15}N, ^{6}Li]LiHMDS in 2.0 M DME/toluene at -90 °C. A) {^{15}N}[^{6}Li] NMR spectrum; B) [^{6}Li] NMR spectrum; C) {^{6}Li }[^{15}N] NMR spectrum; D) [^{15}N] NMR spectrum; ◆ = **2**/LiHMDS mixed aggregate; ■ = **2**; ● = LiHMDS monomer.



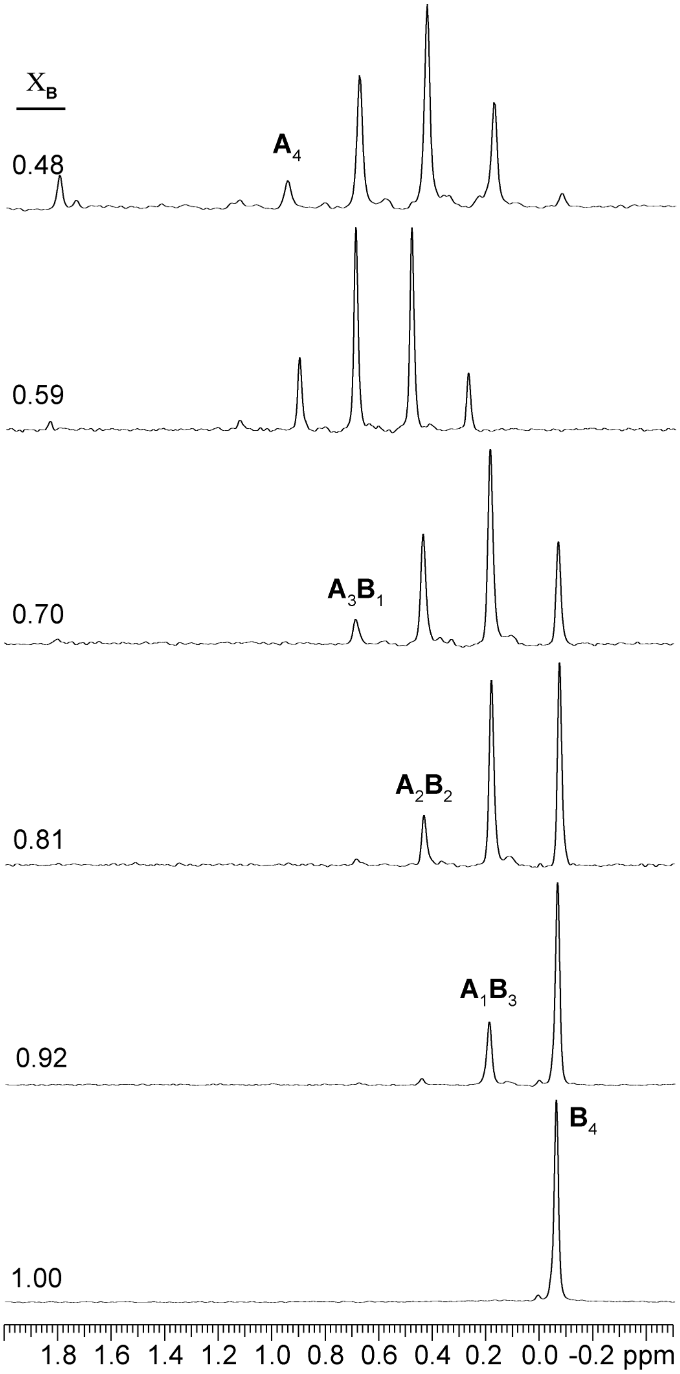
IV.c. [^{6}Li] and [^{15}N] NMR spectra of 0.10 M [^{6}Li]**3** and 0.20 M [^{15}N, ^{6}Li]LiHMDS in 2.0 M DME/toluene at -80 °C. A) {^{15}N}[^{6}Li] NMR spectrum; B) [^{6}Li] NMR spectrum; C) {^{6}Li }[^{15}N] NMR spectrum; D) [^{15}N] NMR spectrum; ◆ = **3**/LiHMDS mixed aggregate; ■ = **3**; ● = LiHMDS monomer.



IV.d. ^{6}Li NMR spectra of an equimolar mixture [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various temperatures in 2.0 M DME/toluene. Sample was prepared via in situ enolization of 0.20 M total ketone with 0.20 M LiHMDS.



IV.e. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.1 M DME/toluene at -30 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS.



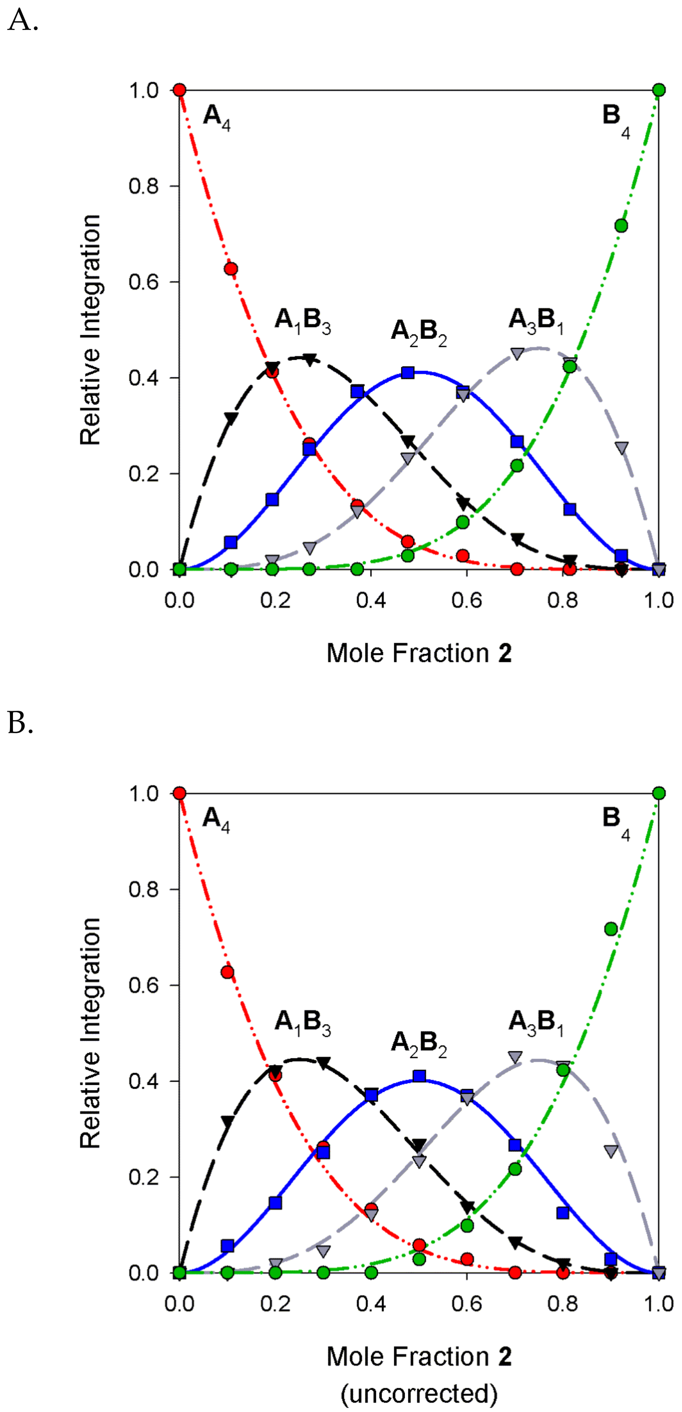
IV.e. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.1 M DME/toluene at -30 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS.

IV.f. Resonance integrations for an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -30 °C. Spectra (see **IV.e.**) were recorded on a 0.20 M mixture of enolates.

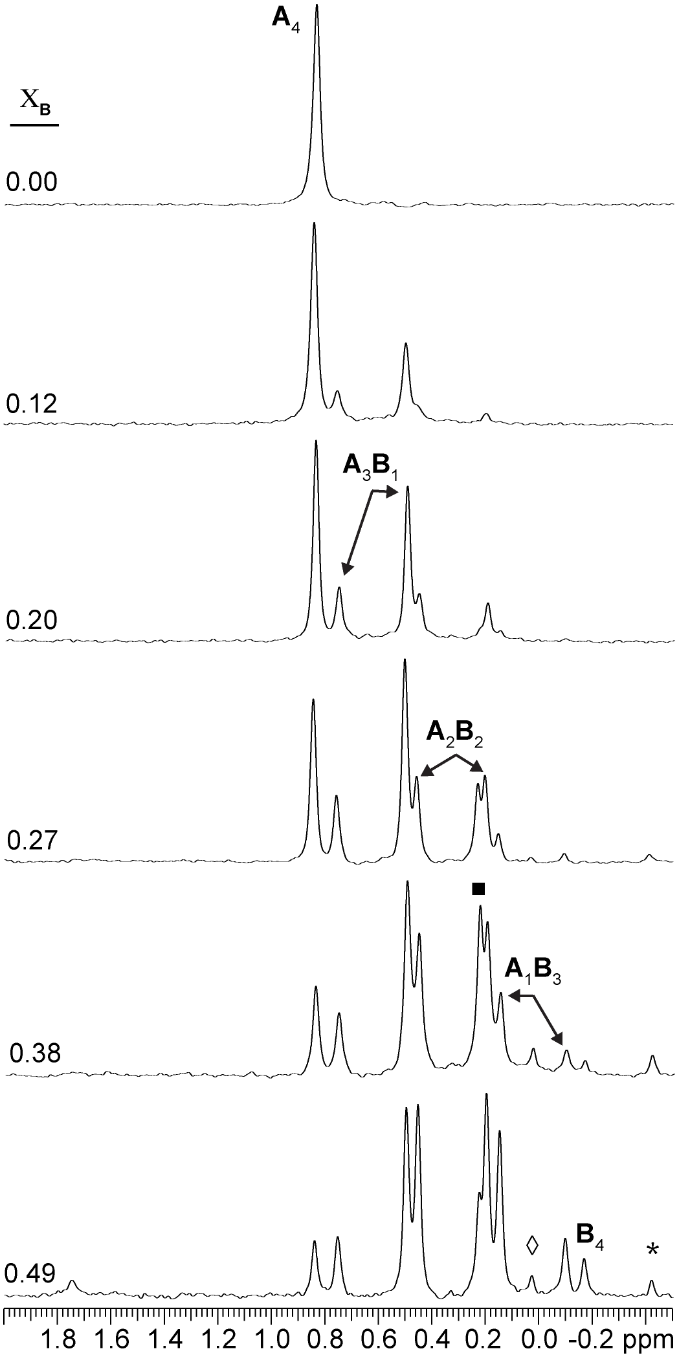
Uncorrected	Calculated	Resonance Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.11	345.18	174.98	30.72	0.00	0.00
0.20	0.19	322.92	332.00	113.98	15.64	0.00
0.30	0.27	191.06	322.58	183.86	34.72	0.00
0.40	0.37	110.93	316.68	311.90	103.40	0.00
0.50	0.48	40.19	188.97	287.18	163.98	19.44
0.60	0.59	23.97	119.49	317.75	314.45	83.95
0.70	0.70	0.00	47.16	191.02	325.08	154.59
0.80	0.81	0.00	13.02	80.44	279.56	273.09
0.90	0.92	0.00	0.00	11.27	104.33	292.39
1.00	1.00	0.00	0.00	0.00	0.00	1.00

IV.g. Relative integrations for aggregates in an ensemble of **1** (**A**) and **2** (**B**) at various mole fractions of **A** and **B**. Integrations were measured (see **IV.e** and **f**) for a 0.20 M enolate ensemble in 10 equivalents of DME/toluene at -30 °C.

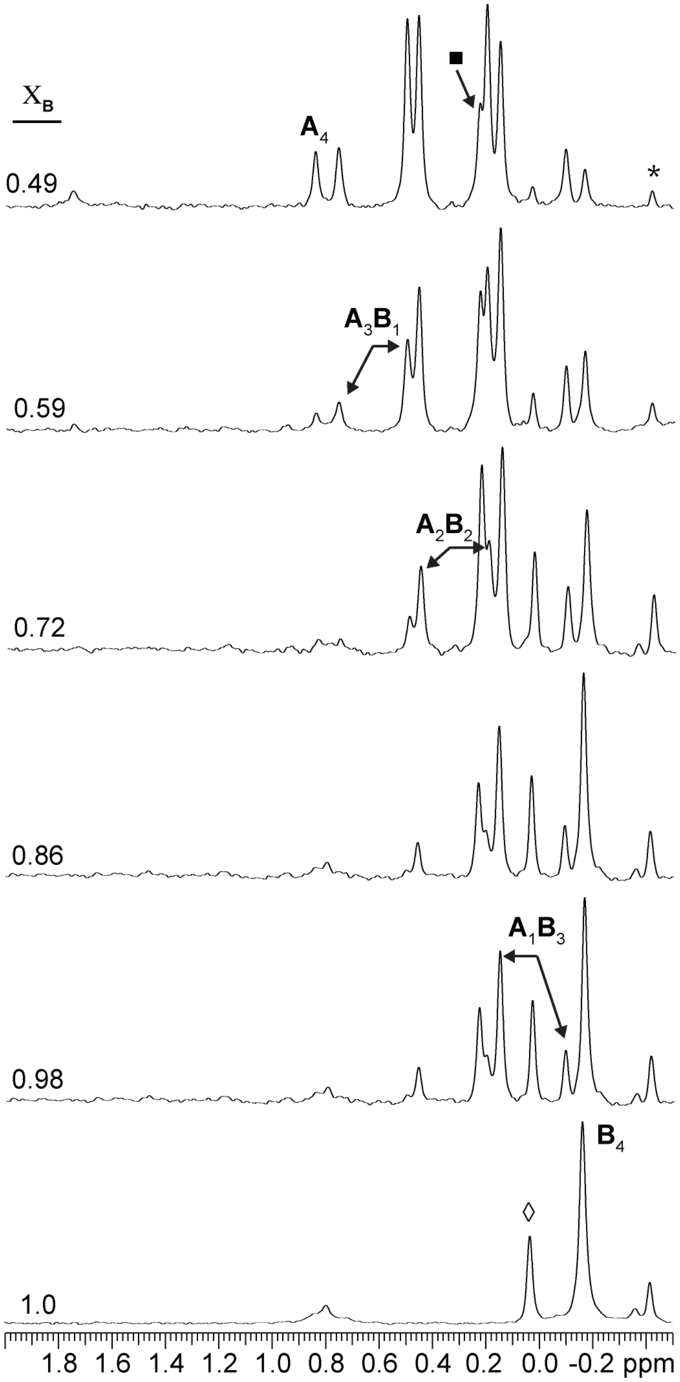
Uncorrected	Calculated	Relative Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.000	0.000	0.000	0.000	0.000
0.10	0.11	0.627	0.318	0.056	0.000	0.000
0.20	0.19	0.412	0.423	0.145	0.020	0.000
0.30	0.27	0.261	0.441	0.251	0.047	0.000
0.40	0.37	0.132	0.376	0.370	0.123	0.000
0.50	0.48	0.057	0.270	0.410	0.234	0.028
0.60	0.59	0.028	0.139	0.370	0.366	0.098
0.70	0.70	0.000	0.066	0.266	0.453	0.215
0.80	0.81	0.000	0.020	0.124	0.433	0.423
0.90	0.92	0.000	0.000	0.028	0.256	0.717
1.00	1.00	0.000	0.000	0.000	0.000	1.000



IV.h. Plot of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of DME/toluene at -30 °C (see **IV.e** and **g**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2**; ϕ_0 = 1.00; ϕ_1 = 1.22; ϕ_2 = 1.32; ϕ_3 = 1.16; ϕ_4 = 0.79; rms = 0.006. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **2**; ϕ_0 = 1.00; ϕ_1 = 1.13; ϕ_2 = 1.09 ϕ_3 = 0.91; ϕ_4 = 0.66; rms = 0.017.



IV.i. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.1 M DME/toluene at -105 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.



IV.i. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions in 2.1 M DME/toluene at -105 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.j. Resonance integrations for an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -105 °C. Spectra (see **IV.i.**) were recorded on a 0.20 M mixture of enolates.

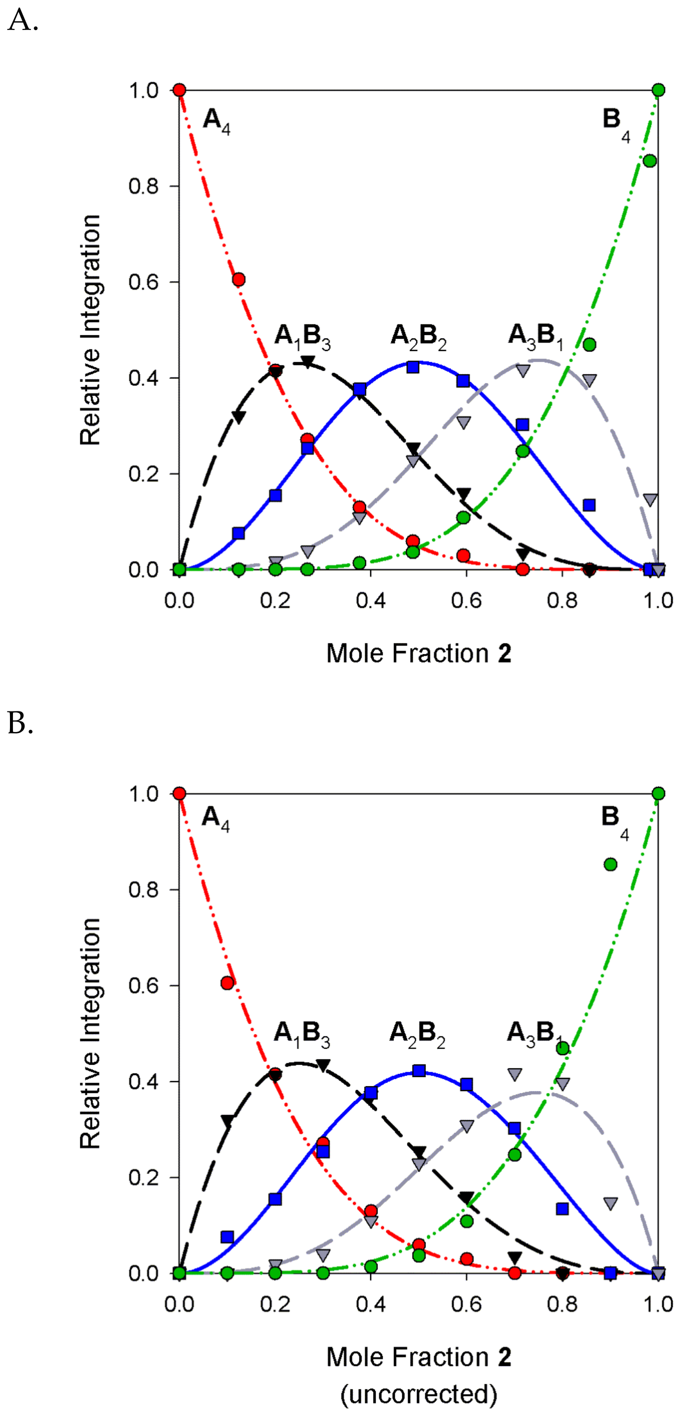
		Resonance Integrations				
Uncorrected	Calculated		**A$_3$B$_1$**		**A$_2$B$_2$**	
X_B	X_B	**A$_4$**	**B$_1$**	**A$_3$**	**A$_2$**	**B$_2$**
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.12	537.75	87.13	197.46	44.06	23.11
0.20	0.20	423.58	110.23	311.84	80.79	76.73
0.30	0.27	324.25	124.76	397.94	143.77	159.22
0.40	0.38	203.93	143.23	442.07	291.62	301.55
0.50	0.49	95.47	108.58	308.29	339.70	351.77
0.60	0.59	39.28	59.09	161.70	266.15	277.32
0.70	0.72	0.00	0.00	45.07	216.14	180.56
0.80	0.86	0.00	0.00	0.00	57.54	48.84
0.90	0.98	0.00	0.00	0.00	0.00	0.00
1.00	1.00	0.00	0.00	0.00	0.00	0.00

		Resonance Integrations				
Uncorrected	Calculated	**A$_1$B$_3$**				
X_B	X_B	**B$_3$**	**A$_1$**	**B$_4$**	■	◊
0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.10	0.12	0.00	0.00	0.00	0.00	0.00
0.20	0.20	18.55	0.00	0.00	11.44	0.00
0.30	0.27	37.00	11.08	0.00	117.23	3.28
0.40	0.38	127.50	46.08	21.16	298.05	25.38
0.50	0.49	279.29	95.71	58.98	105.49	19.76
0.60	0.59	332.57	94.76	149.03	181.14	36.98
0.70	0.72	437.91	110.58	323.13	321.80	204.54
0.80	0.86	258.76	56.38	371.78	144.35	146.93
0.90	0.98	0.00	0.00	414.40	44.33	151.62
1.00	1.00	0.00	0.00	1.00	0.00	0.00

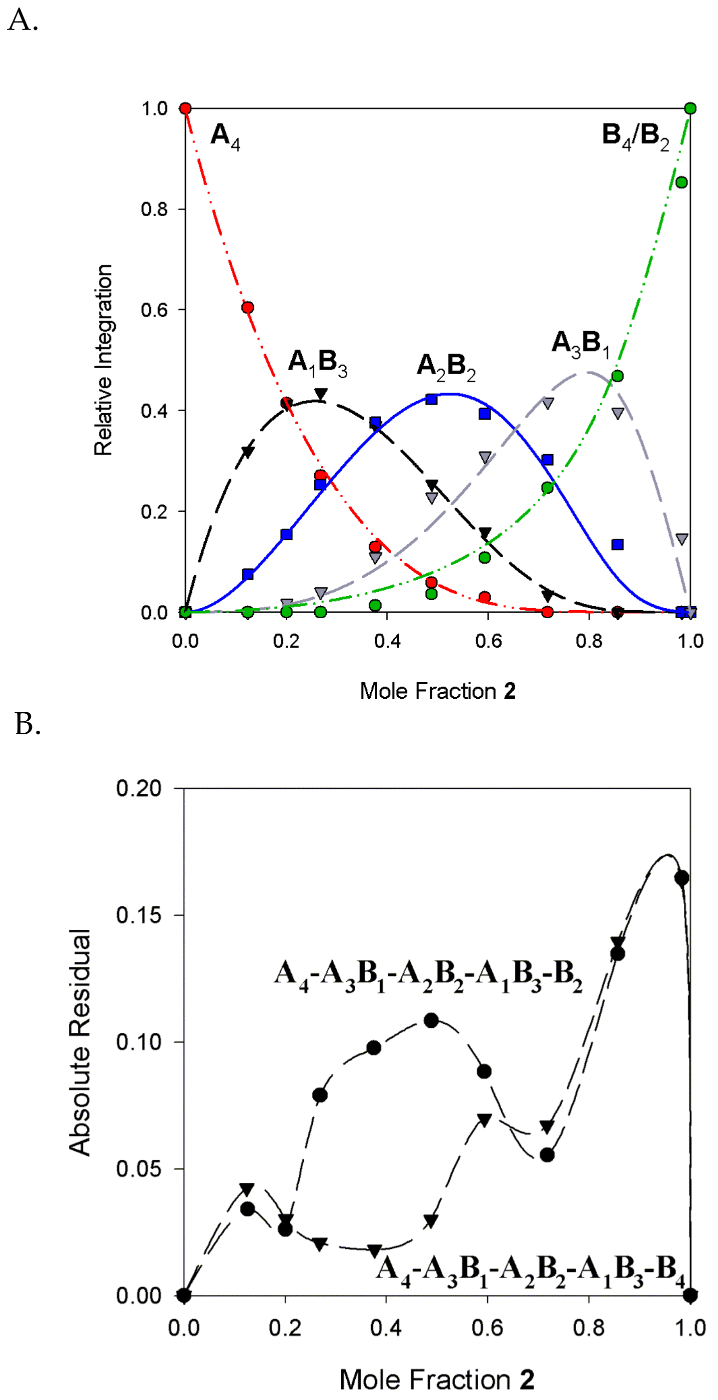
◊ denotes the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.k. Relative integrations for an ensemble of **1** (**A**) and **2** (**B**) at various mole fraction of **A** and **B** in 2.1 M DME/toluene at -105 °C. Spectra were recorded on a 0.20 M enolate ensemble.

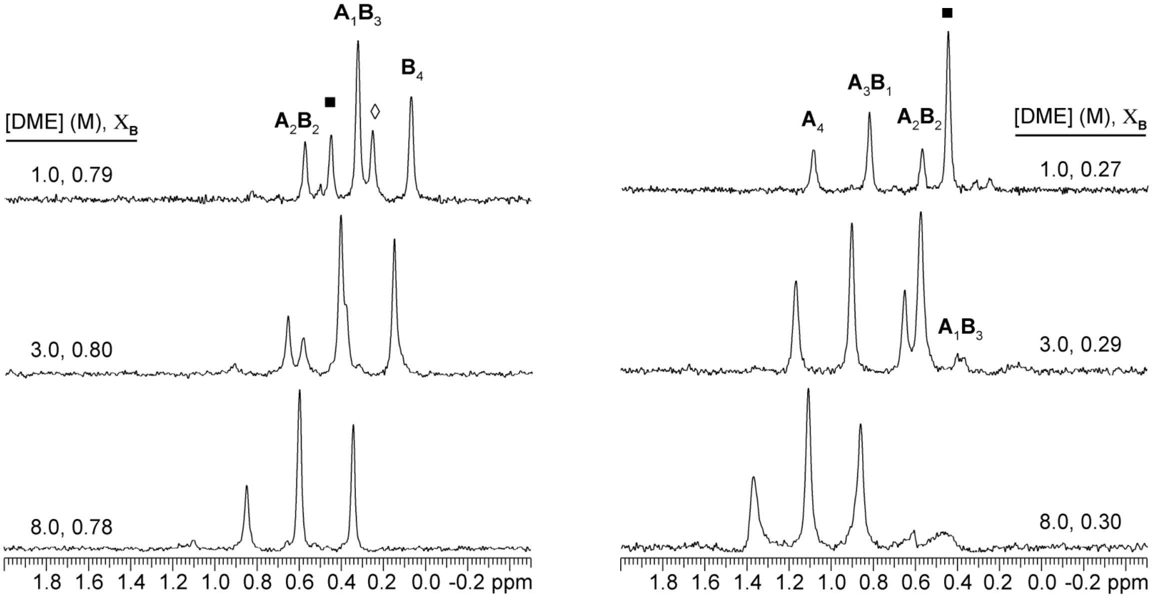
Uncorrected	Calculated	Relative Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.12	0.60	0.32	0.08	0.00	0.00
0.20	0.20	0.41	0.41	0.15	0.02	0.00
0.30	0.27	0.27	0.44	0.25	0.04	0.00
0.40	0.38	0.13	0.37	0.38	0.11	0.01
0.50	0.49	0.06	0.25	0.42	0.23	0.04
0.60	0.59	0.03	0.16	0.39	0.31	0.11
0.70	0.72	0.00	0.03	0.30	0.42	0.25
0.80	0.86	0.00	0.00	0.13	0.40	0.47
0.90	0.98	0.00	0.00	0.00	0.15	0.85
1.00	1.00	0.00	0.00	0.00	0.00	1.00



IV.l. Plot of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of DME/toluene at -105 °C (see **IV.i** and **k**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2**; $\phi_0 = 1.00$; $\phi_1 = 1.17$; $\phi_2 = 1.37$; $\phi_3 = 1.08$; $\phi_4 = 0.81$ rms = 0.020. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **2**; $\phi_0 = 1.00$; $\phi_1 = 1.15$; $\phi_2 = 1.23$; $\phi_3 = 0.92$; $\phi_4 = 1.02$ rms = 0.036.



IV.m. Plots of the relative integration versus the mole fraction of **2** (**B**) for an ensemble of **1** (**A**) and **2** (**B**) in 10 equivalents of DME/toluene at -105 °C fit to an ensemble of **A_4-A_3B_1-A_2B_2-A_1B_3-B_2** (see **IV.i** and **l**). A) Plot and fit of the relative integration versus the calculated mole fraction of **2** fit to **A_4-A_3B_1-A_2B_2-A_1B_3-B_2**; ϕ_{20} = 0.20; ϕ_{21} = ϕ_{22} = 0.00; ϕ_{40} = 0.00; ϕ_{41} = 1.06; ϕ_{42} = 1.33; ϕ_{43} = 0.91; ϕ_{44} = 0.63; rms = 0.02. B) Plot of the sum of the absolute residuals for **A_4-A_3B_1-A_2B_2-A_1B_3-B_4** and **A_4-A_3B_1-A_2B_2-A_1B_3-B_2** versus the mole fraction of **2**.



IV.n. $\{^{15}N\}^{6}Li$ NMR spectra of mixtures of $[^{6}Li]$**1** (**A**) and $[^{6}Li]$**2** (**B**) at various concentrations of DME/toluene at -30 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.15 M $[^{15}N,^{6}Li]$ LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.o. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various DME concentrations at -30 °C (see **IV.n**). Samples were prepared via in situ enolization of 0.10 M ketone with 0.15 M [^{15}N,^{6}Li] LiHMDS.

[DME]	Calc.	Resonance Integrations							
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$	■	◊	*
1.0	0.27	94.82	151.81	82.45	18.11	0.00	299.05	0.00	28.36
3.0	0.29	211.25	300.36	167.81	74.63	0.00	371.02	0.00	0.00
8.0	0.30	195.57	341.24	355.24	0.00	0.00	116.44	0.00	137.24

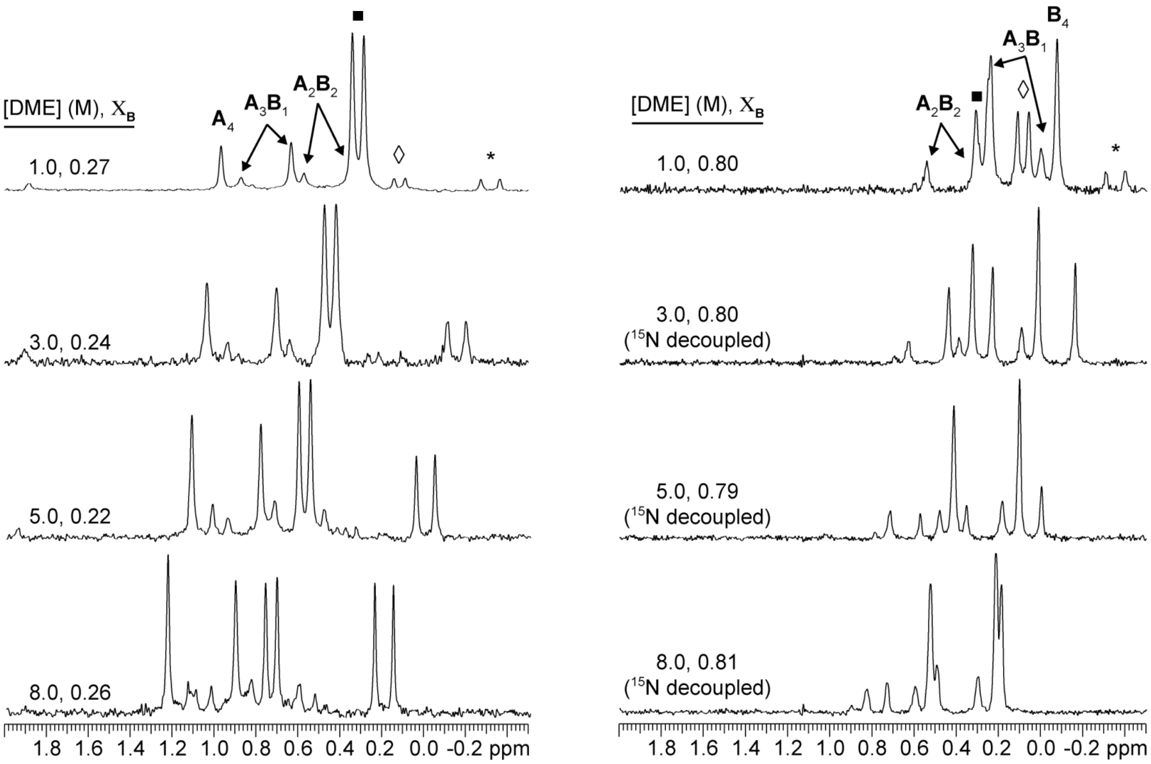
[DME]	Calc.	Resonance Integrations							
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$	■	◊	*
1.0	0.79	0.00	0.00	112.51	288.78	201.28	126.19	139.32	0.00
3.0	0.80	0.00	0.00	110.16	292.25	234.03	83.52	58.41	0.00
8.0	0.78	0.00	0.00	111.74	257.61	186.42	0.00	0.00	0.00

* denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.p. Relative integrations for each aggregate in ensembles of **1** (**A**) and **2** (**B**) at various DME concentrations at -30 °C (see **IV.n** and **o**.). Spectra were recorded on a 0.10 M mixture of **1** and **2**.

[DME]	Calc.	Relative Integrations				
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.0	0.27	0.27	0.44	0.24	0.05	0.00
3.0	0.29	0.28	0.40	0.22	0.10	0.00
8.0	0.30	0.22	0.38	0.40	0.00	0.00

[THF]	Calc.	Relative Integrations				
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.0	0.79	0.00	0.00	0.19	0.43	0.38
3.0	0.80	0.00	0.00	0.18	0.46	0.36
8.0	0.78	0.00	0.00	0.18	0.47	0.35



IV.q. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various concentrations of DME/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.15 M [^{15}N,^{6}Li] LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.r. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various DME concentrations at –90 °C (see **IV.n**). Samples were prepared via in situ enolization of 0.10 M ketone with 0.15 M [^{15}N,^{6}Li] LiHMDS.

[DME]	Calc.	Resonance Integrations								
		$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$			
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	■	◊	*
1.0	0.27	60.96	31.98	76.14	34.68	13.89	16.40	427.29	0.00	29.63
3.0	0.24	157.74	71.48	170.32	63.88	63.88	0.00	573.08	0.00	156.67
5.0	0.22	133.34	39.40	126.61	52.53	39.97	0.00	301.64	24.28	146.18
8.0	0.26	97.19	48.85	96.59	39.90	38.15	13.94	152.97	0.00	126.97

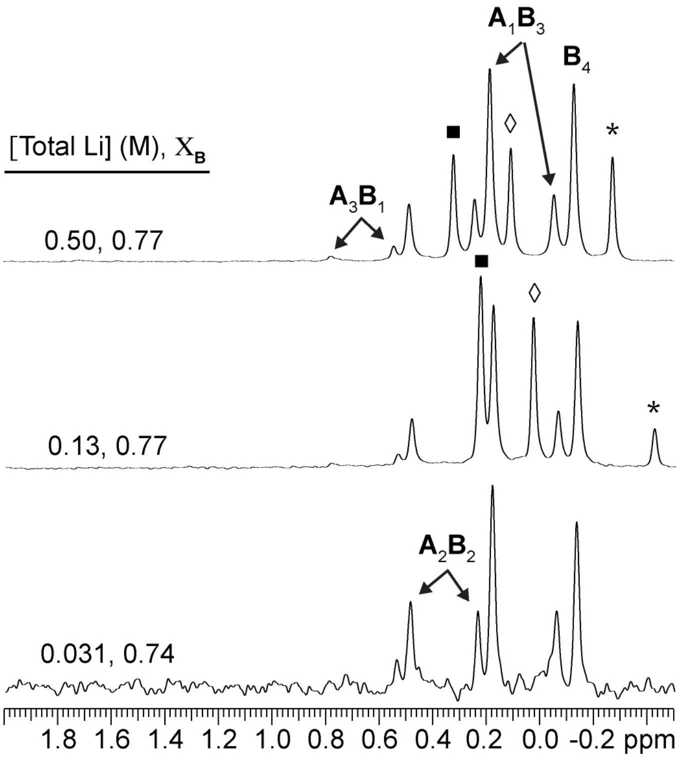
[DME]	Calc.	Resonance Integrations								
		$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$			
(M)	$X_\mathbf{B}$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$	■	◊	*
1.0	0.80	0.00	68.26	68.26	224.46	91.34	275.7	211.53	262.72	68.29
3.0	0.80	0.00	59.03	43.78	193.49	74.13	208.49	120.47	146.3	120.14
5.0	0.79	0.00	60.45	47.85	209.14	73.38	206.72	36.92	45.31	67.78
8.0	0.81	0.00	56.08	46.11	227.22	64.27	246.54	51.2	51.94	141.57

* denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

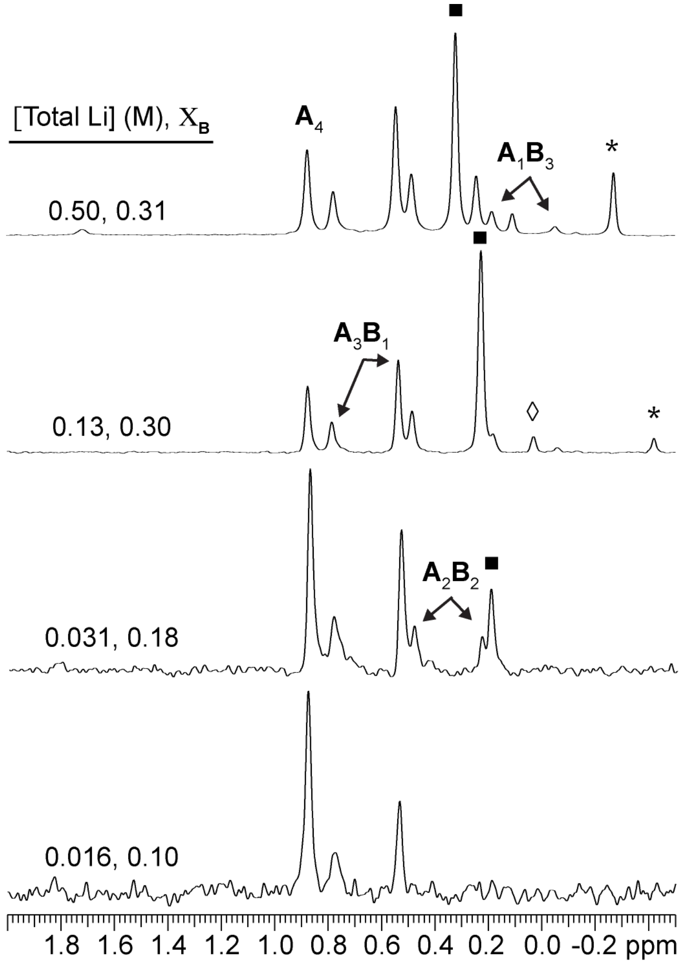
IV.s. Relative integrations for each aggregate in ensembles of **1** (**A**) and **2** (**B**) at various DME concentrations at -90 °C (see **IV.q** and **r**.). Spectra were recorded on a 0.10 M mixture of **1** and **2**.

[DME]	Calc.	Relative Integrations				
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.0	0.27	0.26	0.46	0.21	0.07	0.00
3.0	0.24	0.30	0.46	0.24	0.00	0.00
5.0	0.22	0.34	0.42	0.24	0.00	0.00
8.0	0.26	0.29	0.43	0.23	0.04	0.00

[DME]	Calc.	Relative Integrations				
(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.0	0.80	0.00	0.00	0.19	0.43	0.38
3.0	0.80	0.00	0.00	0.18	0.46	0.36
5.0	0.79	0.00	0.00	0.18	0.47	0.35
8.0	0.81	0.00	0.00	0.16	0.46	0.39



IV.t. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.



IV.**t**. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with excess LiHMDS. * denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.u. Resonance integrations for ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**2** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -100 °C (see **IV.t**).

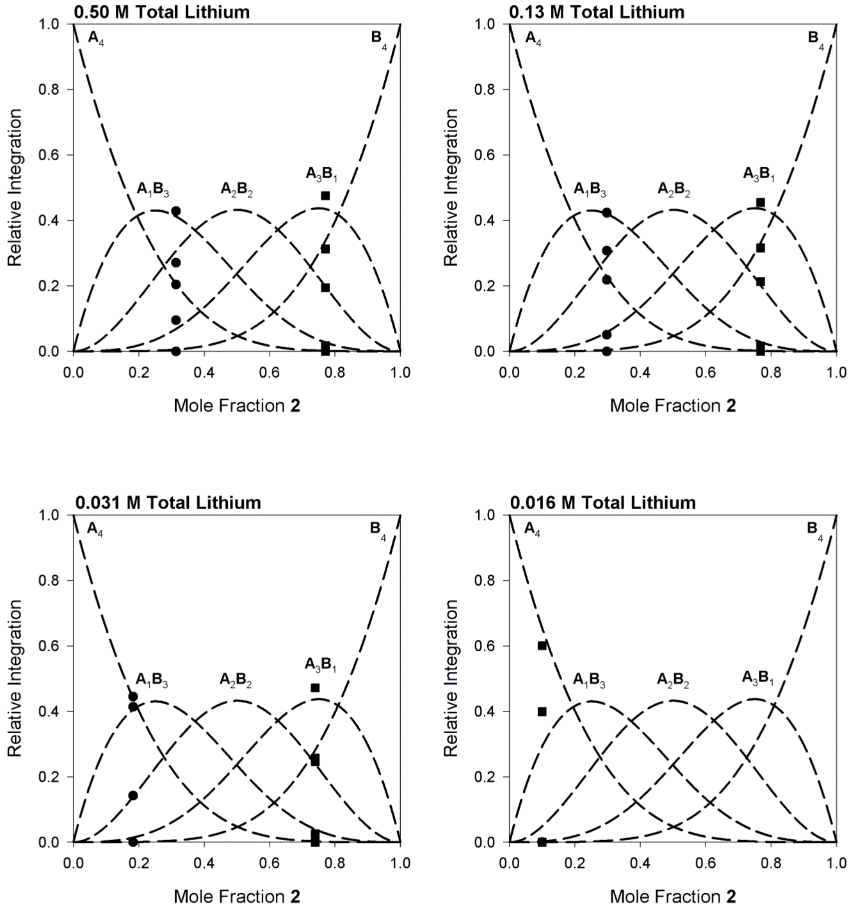
[enolate] (M)	Calc. $X_\mathbf{B}$	Resonance Integrations								
		$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$			
		$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$	■	◊	*
0.45	0.77	19.91	120.46	95.65	391.93	136.18	347.40	178.08	187.24	172.31
0.11	0.77	14.06	89.96	89.96	288.46	96.44	267.14	236.78	253.38	75.10
0.030	0.74	28.62	182.65	88.42	363.03	156.67	282.85	0.00	0.00	0.00

[enolate] (M)	Calc. $X_\mathbf{B}$	Resonance Integrations							
		$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		
		$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_1$	$\mathbf{B}_3$	$\mathbf{A}_1$	■	◊
0.45	0.31	171.26	100.93	258.23	123.11	103.83	43.73	36.08	368.19	37.23
0.11	0.30	112.46	67.21	151.12	79.35	79.35	11.56	14.44	276.78	28.86
0.030	0.18	340.11	126.76	238.99	58.27	58.87	0.00	0.00	0.00	130.17
0.015	0.10	354.66	91.38	144.06	0.00	0.00	0.00	0.00	0.00	0.00

* denotes the LiHMDS resonance, ◊ the **2**/LiHMDS mixed aggregate, and the ■ the **1**/LiHMDS mixed aggregate.

IV.v. Relative integrations ensembles of **1** (**A**) and **2** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene with excess LiHMDS at -100 °C (see **IV.t** and **u**).

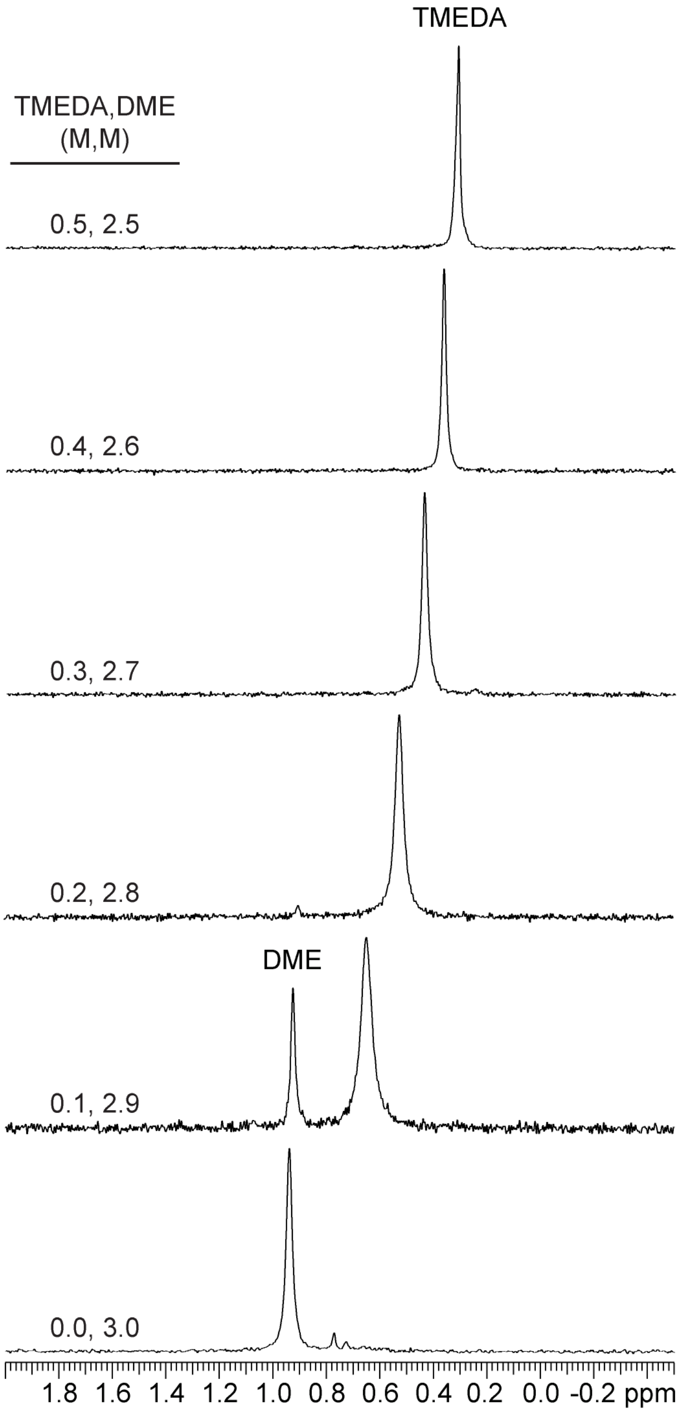
[Li] (M)	[enolate] (M)	Calc. $X_\mathbf{B}$	Relative Integrations				
			$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.50	0.45	0.77	0.00	0.02	0.19	0.48	0.31
0.13	0.11	0.77	0.00	0.02	0.21	0.45	0.32
0.031	0.030	0.74	0.00	0.03	0.25	0.47	0.26
0.50	0.45	0.31	0.20	0.43	0.27	0.10	0.00
0.13	0.11	0.30	0.22	0.42	0.31	0.05	0.00
0.031	0.030	0.18	0.41	0.44	0.14	0.00	0.00
0.016	0.015	0.10	0.60	0.40	0.00	0.00	0.00



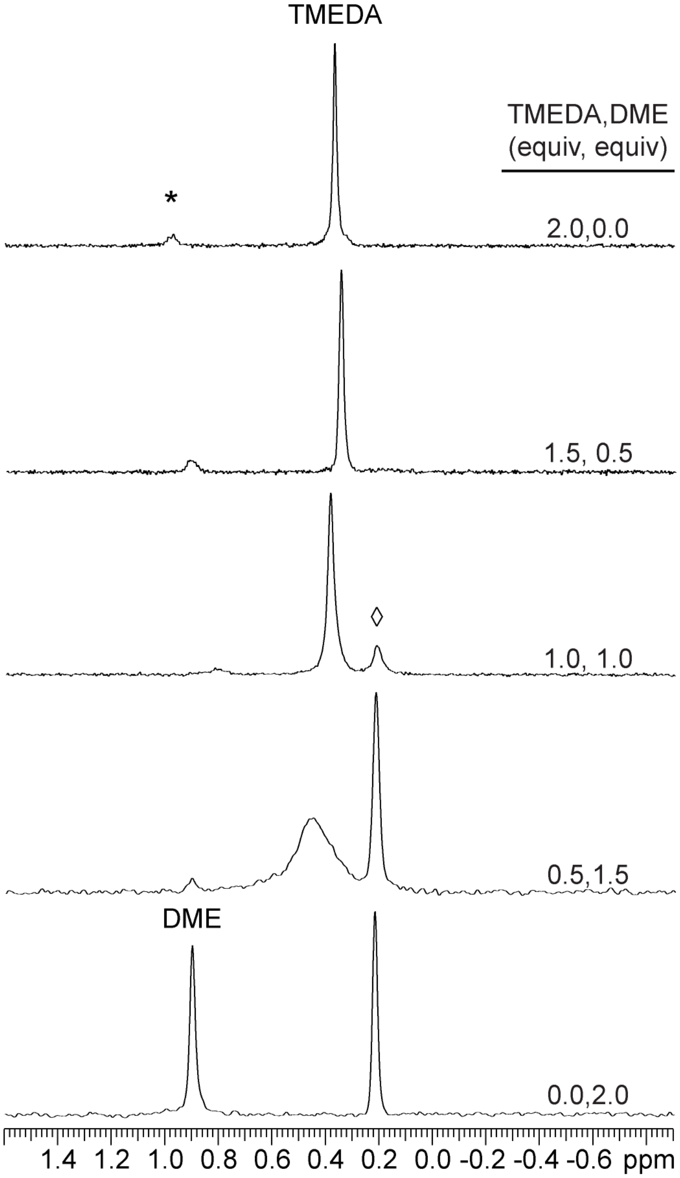
IV.w. Relative integrations of mixtures of **1** and **2** at various absolute Li concentrations in 10 equivalents of DME/toluene at -100 °C plotted on the curves for a fit to the Job plot of an ensemble of tetramers (**IV.l**).

IV.x. Absolute residuals for the deviation of the relative integrations of ensembles of **1** and **2** in 10 equivalents DME/toluene at various absolute Li concentrations from the expected relative integrations based on the fit in **IV.l**.

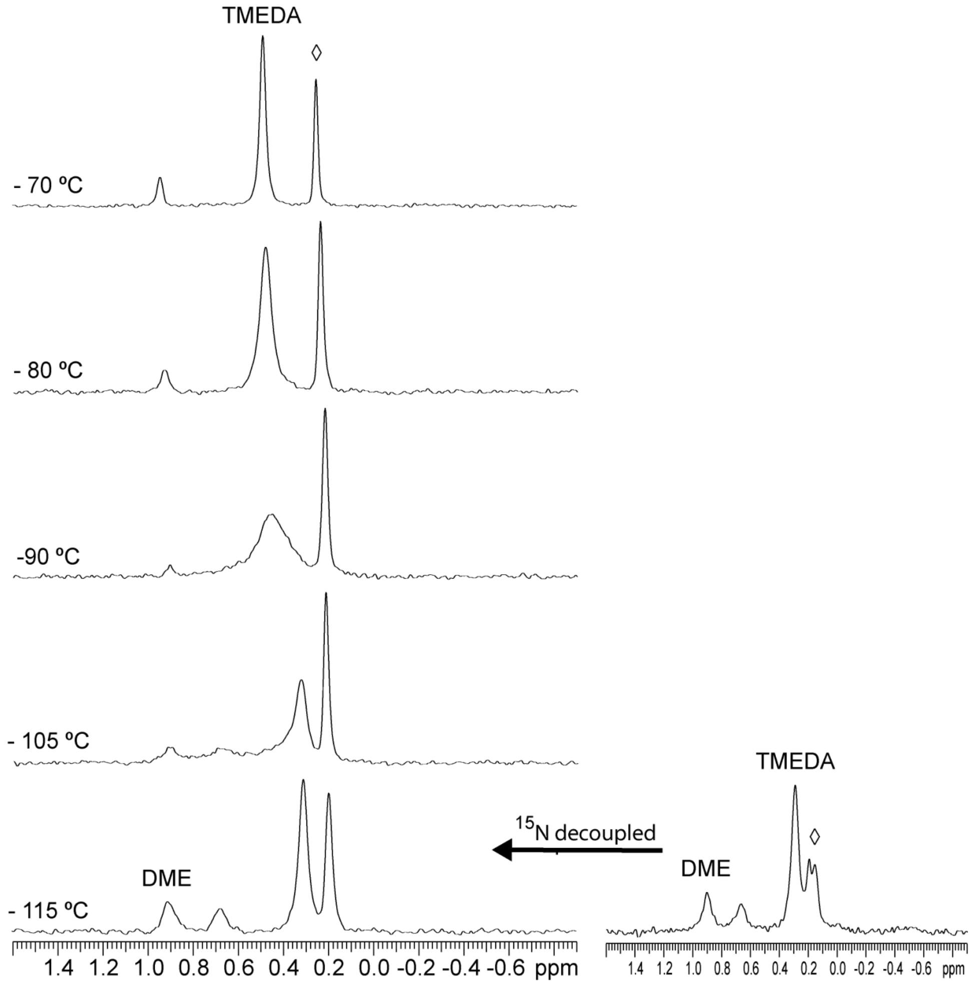
[Li]	[enolate]	Calc.	Absolute Residuals				
(M)	(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.50	0.45	0.77	0.00	0.01	0.00	0.04	0.03
0.13	0.11	0.77	0.00	0.01	0.01	0.02	0.02
0.031	0.030	0.74	0.00	0.01	0.01	0.04	0.03
0.50	0.45	0.31	0.00	0.02	0.04	0.03	0.01
0.13	0.11	0.30	0.01	0.00	0.02	0.01	0.00
0.031	0.030	0.18	0.03	0.04	0.00	0.01	0.00
0.016	0.015	0.10	0.05	0.11	0.05	0.00	0.00



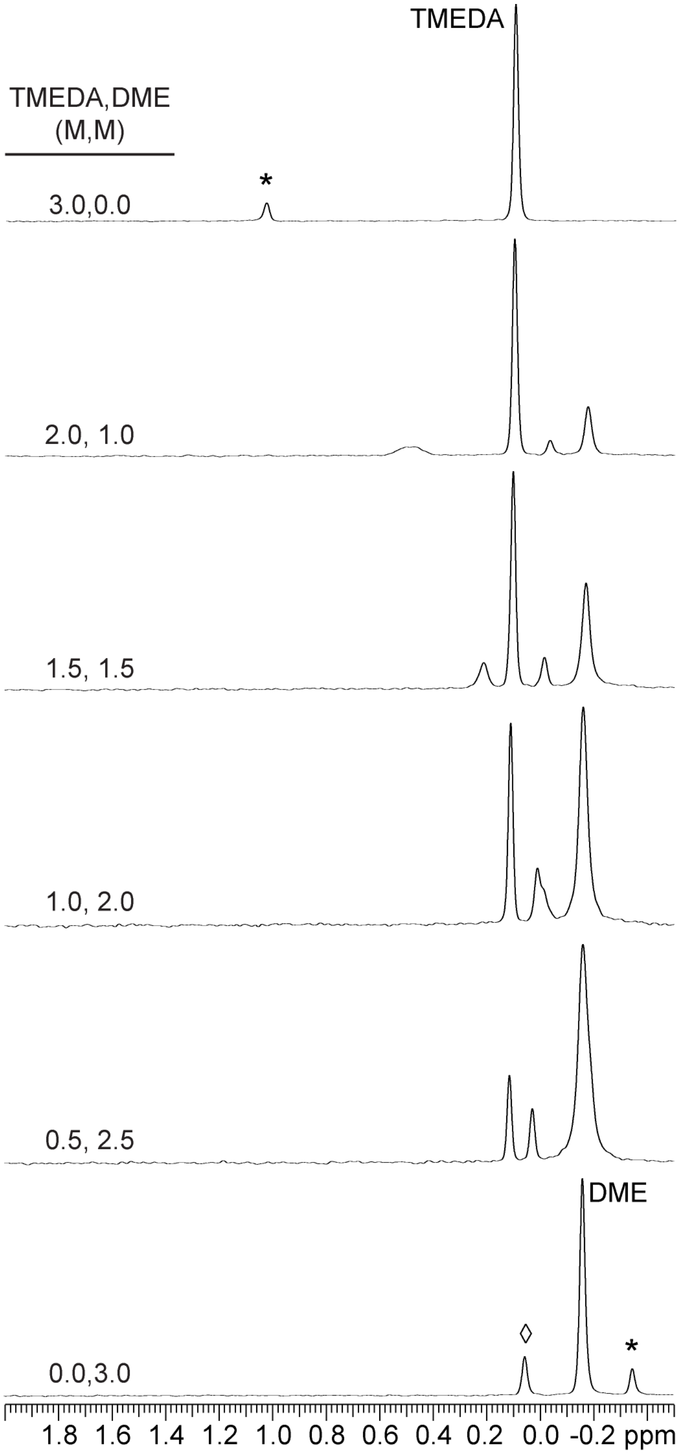
IV.y. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** at various mole fractions TMEDA and DME/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.11 M [^{6}Li] LiHMDS and 3.0 M total ligand (30 equivalents).



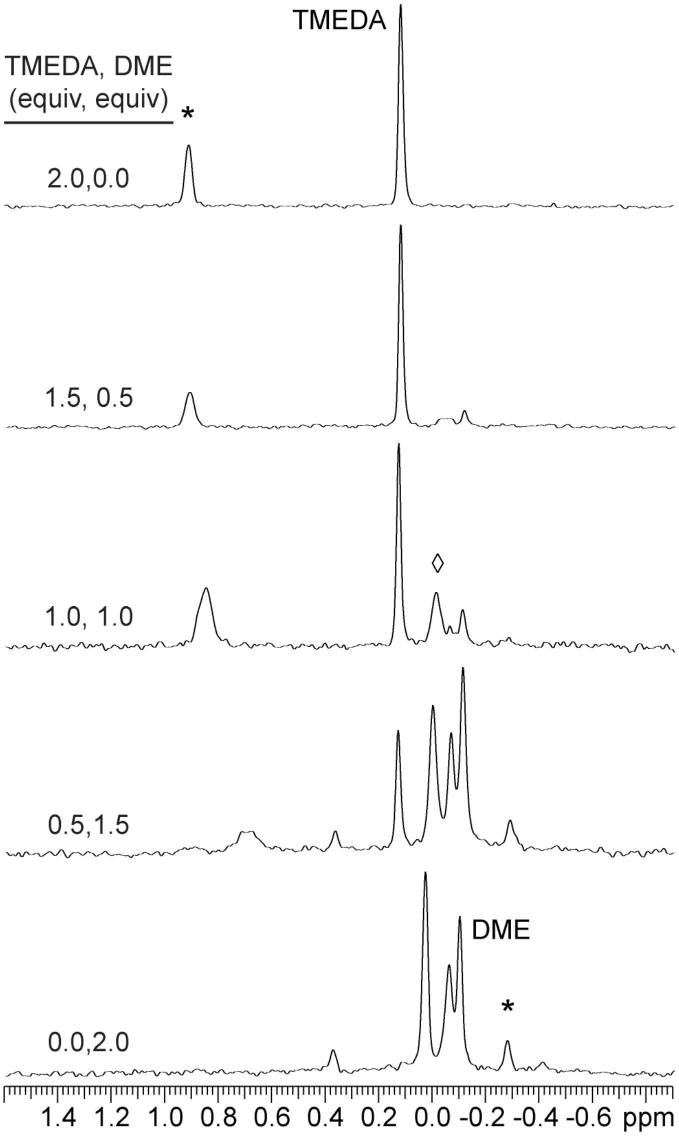
IV.z. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** at various mole fractions TMEDA and DME/toluene (2 equivalents total ligand) at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.12 M [^{6}Li] LiHMDS and 0.24 M total ligand.



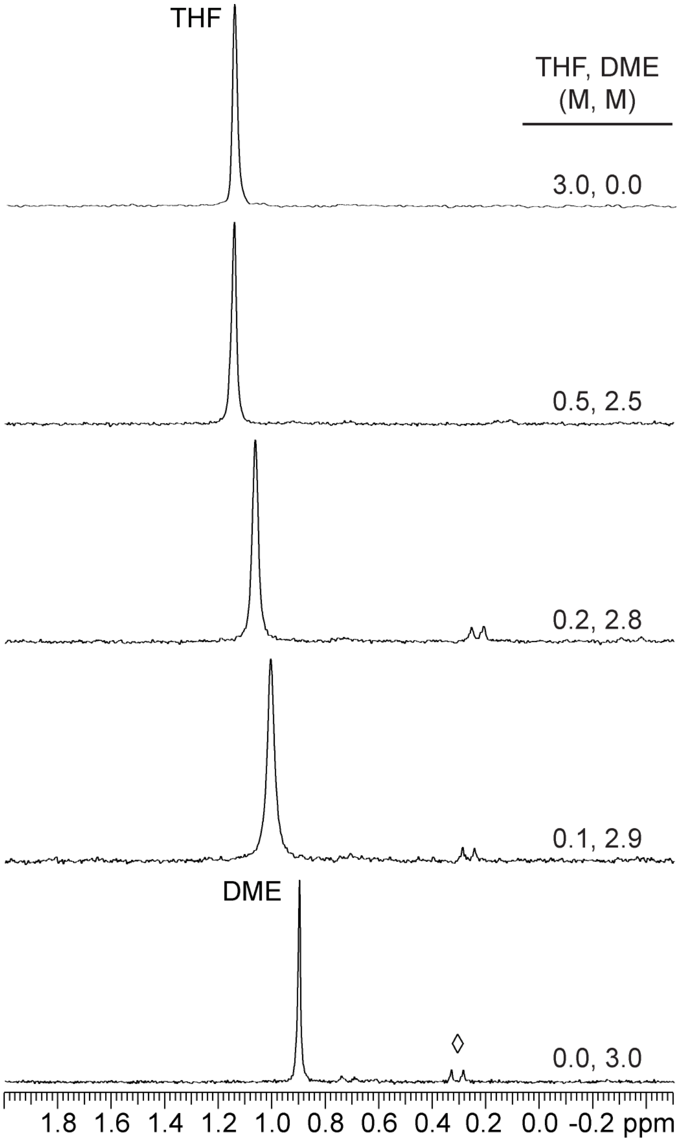
IV.aa. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** in 0.05 M TMEDA and 0.15 M DME/toluene (2 equivalents total ligand) at various temperatures. Samples were prepared via in situ enolization of 0.10 M ketone with 0.12 M [^{6}Li] LiHMDS and 0.24 M total ligand.



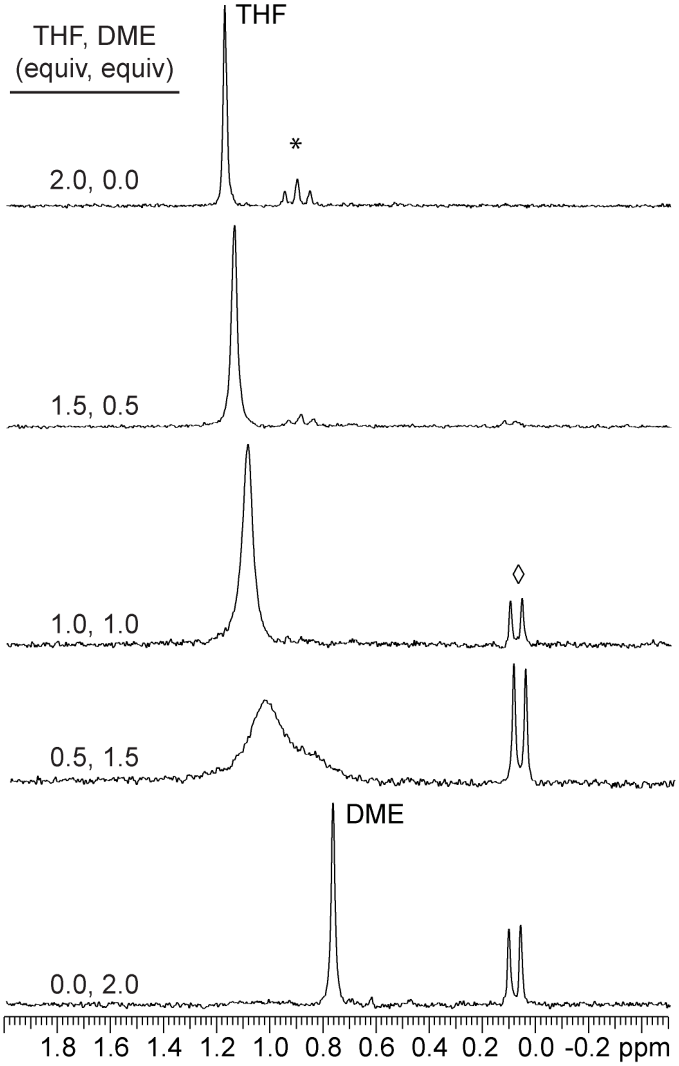
IV.bb. ^{6}Li NMR spectra of [^{6}Li]**2** at various mole fractions TMEDA and DME/toluene (30 equivalents total ligand) at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.15 M LiHMDS and 3.0 M total ligand. * and ◊ denote the LiHMDS and the **2**/LiHMDS mixed aggregate resonances, respectively.



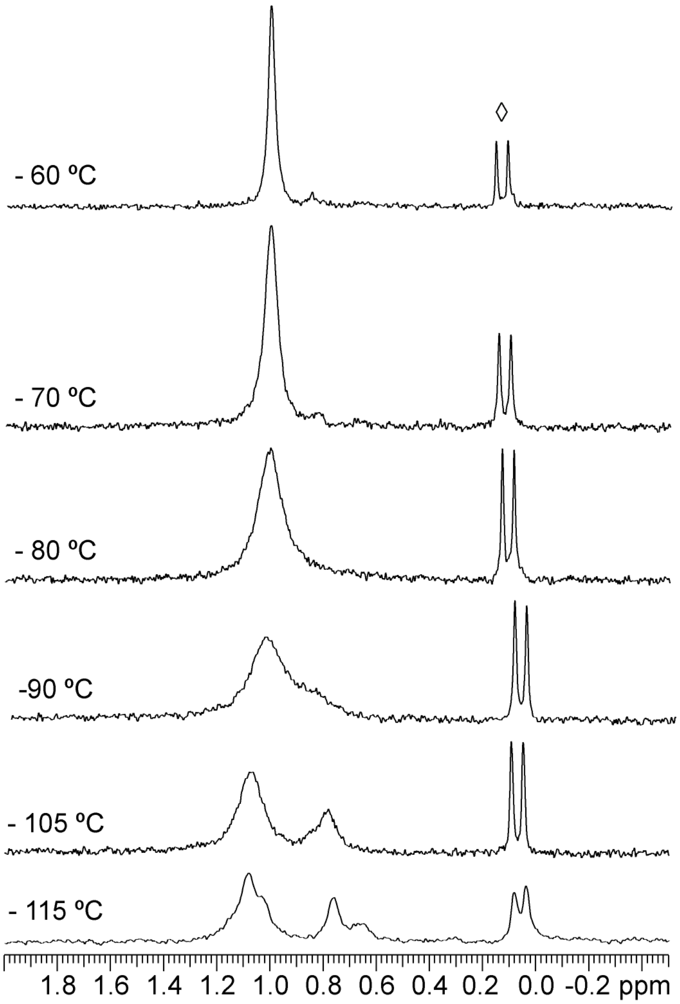
IV.cc. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**2** in various mole fractions TMEDA and DME/toluene (2 equivalents total ligand) at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.12 M [^{6}Li] LiHMDS and 0.24 M total ligand. * and ◊ denote the LiHMDS and the **2**/LiHMDS mixed aggregate resonances, respectively.



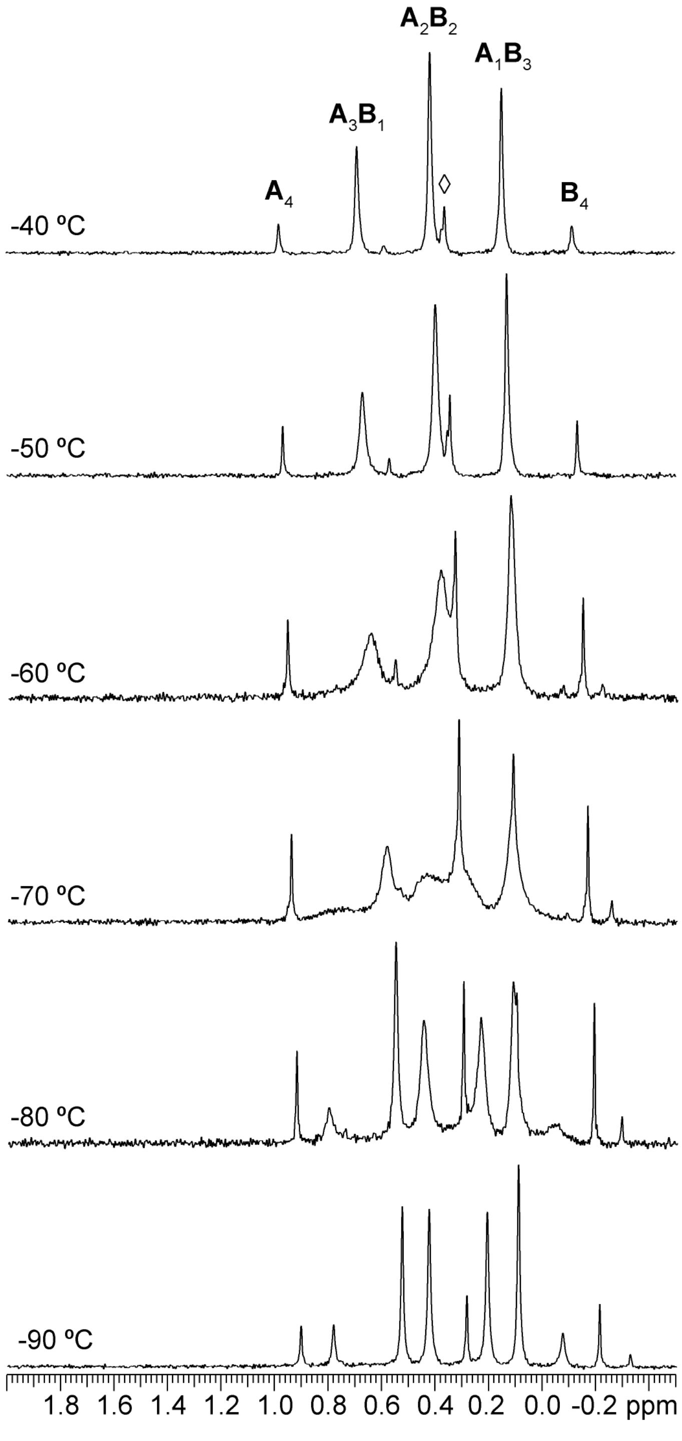
IV.dd. ^{6}Li NMR spectra of [^{6}Li]**1** at various mole fractions THF and DME/toluene (30 equivalents total ligand) at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.11 M LiHMDS and 3.0 M total ligand. ◊ denotes the **1**/LiHMDS mixed aggregate resonance.



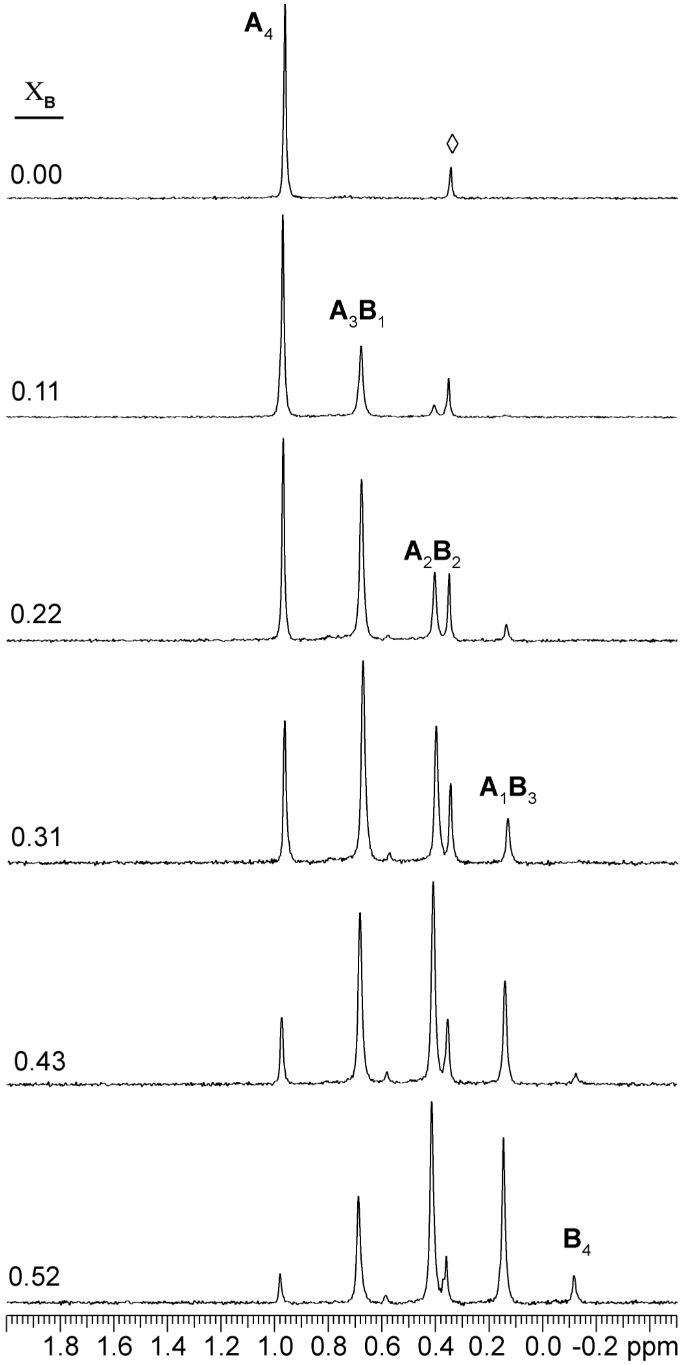
IV.ee. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** at various mole fractions THF and DME/toluene (2 equivalents total ligand) at -90 °C. Samples were prepared via in situ enolization of 0.10 M ketone with 0.11 M [^{6}Li] LiHMDS and 0.20 M total ligand. * and ◊ denote the LiHMDS and the **1**/LiHMDS mixed aggregate resonances, respectively.



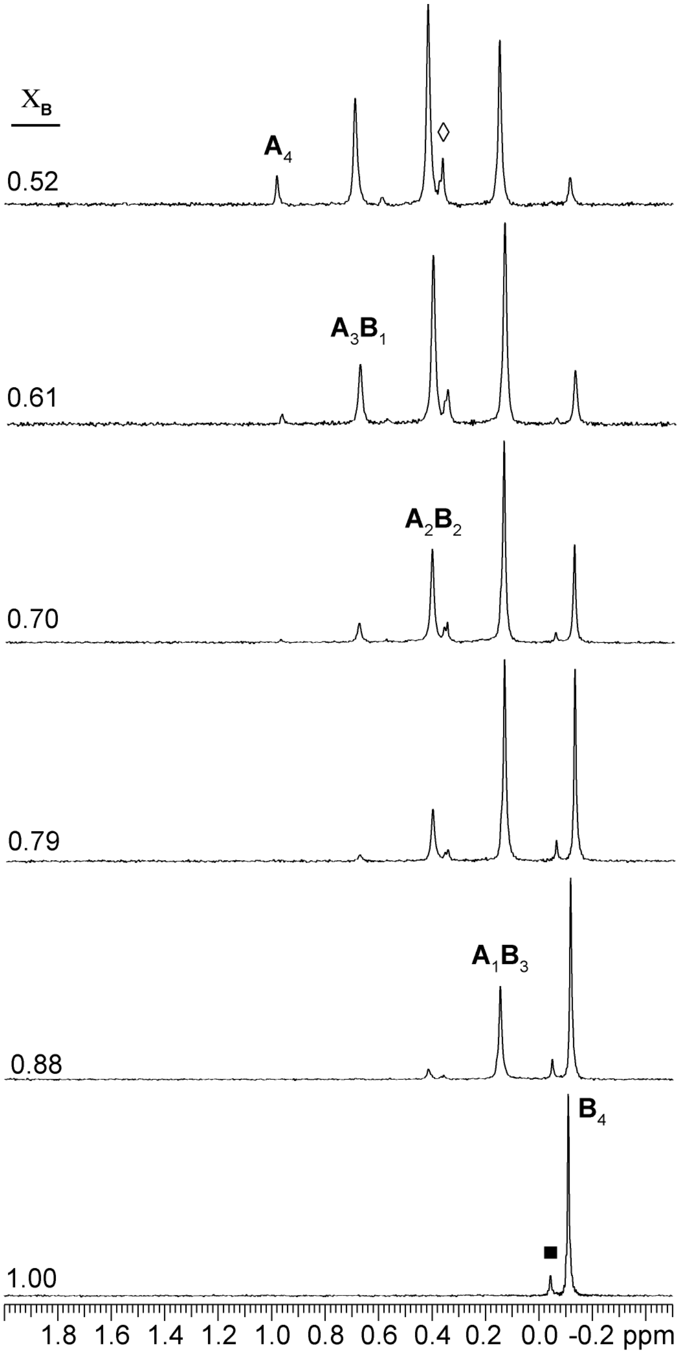
IV.ff. ^{6}Li NMR spectra of 0.10 M [^{6}Li]**1** in various temperatures in 0.10 M THF and 0.10 M DME/toluene (2 equivalents total ligand) at -90 °C (see **IV.ee**). Sample was prepared via in situ enolization of 0.10 M ketone with 0.11 M [^{6}Li] LiHMDS and 0.20 M total ligand. ◊ denotes the **1**/LiHMDS mixed aggregate resonance.



IV.gg. ^{6}Li NMR spectra of an equimolar mixture [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various temperatures in 2.1 M DME/toluene. Sample was prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS. ◊ denotes the **1**/LiHMDS mixed aggregate resonance.



IV.hh. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** and [^{6}Li]**3** at various mole fractions in 2.1 M DME/toluene at -40 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS. ◊ denotes the **1**/LiHMDS mixed aggregate.



IV.hh. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** and [^{6}Li]**3** at various mole fractions in 2.1 M DME/toluene at -40 °C. Samples were prepared via in situ enolization of 0.20 M total ketone with 0.21 M LiHMDS. ◊ denotes the **1**/LiHMDS mixed aggregate and the ■ the **3**/LiHMDS mixed aggregate.

IV.ii. Resonance integrations for an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -40 °C. Spectra (see **IV**.**hh**.) were recorded on a 0.20 M mixture of enolates.

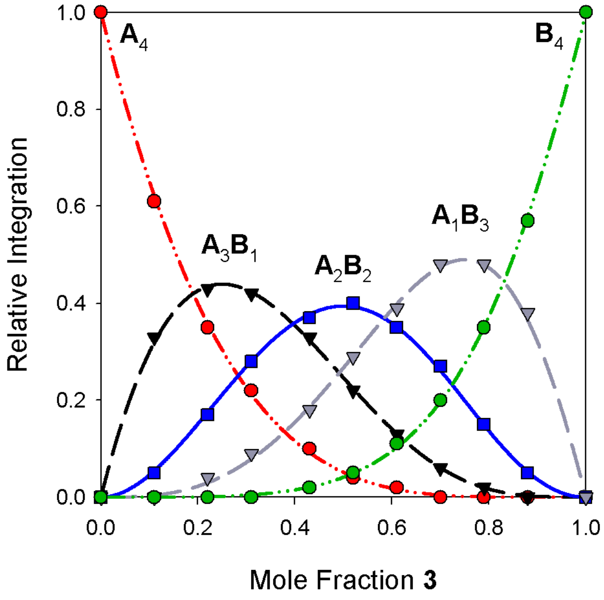
Calculated	Resonance Integrations						
X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$	◊	■
0.00	164.34	0.00	0.00	0.00	0.00	27.34	0.00
0.11	185.77	100.22	16.42	0.00	0.00	32.94	0.00
0.22	171.72	209.63	84.46	18.23	0.00	54.91	0.00
0.31	140.57	275.42	179.57	56.23	0.00	75.22	0.00
0.43	71.08	233.70	265.43	129.83	17.45	68.32	0.00
0.52	26.93	145.20	260.35	189.92	33.93	49.10	0.00
0.61	9.74	83.13	223.45	248.03	66.44	42.00	0.00
0.70	0.00	25.24	113.11	202.71	85.49	20.02	7.36
0.79	0.00	8.50	64.18	201.30	145.35	15.07	13.84
0.88	0.00	0.00	13.38	100.21	150.84	0.00	14.03
1.00	0.00	0.00	0.00	0.00	126.32	0.00	14.08

◊ denotes the **1**/LiHMDS mixed aggregate and the ■ the **3**/LiHMDS mixed aggregate.

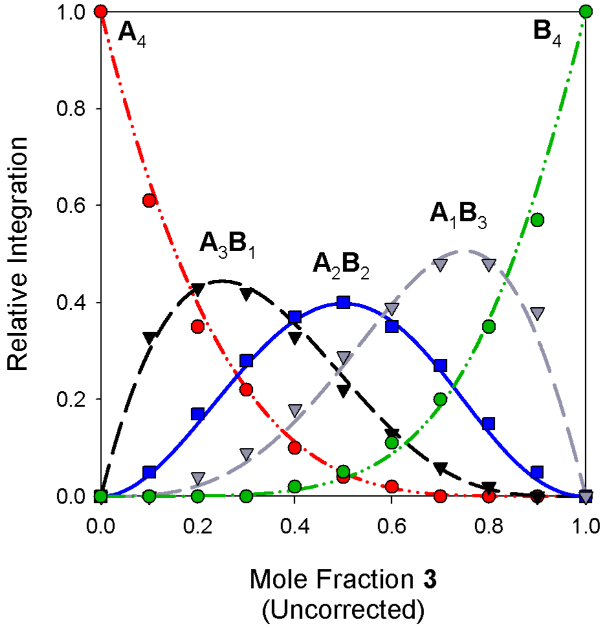
IV.**jj**. Relative integrations for aggregates in an ensemble of **1** (**A**) and **3** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -40 °C. Integrations were measured (see **IV**.**hh** and **ii**) for a 0.20 M enolate ensemble.

Uncorrected	Calculated	Relative Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.00	0.00	1.00	0.00	0.00	0.00	0.00
0.10	0.11	0.61	0.33	0.05	0.00	0.00
0.20	0.22	0.35	0.43	0.17	0.04	0.00
0.30	0.31	0.22	0.42	0.28	0.09	0.00
0.40	0.43	0.10	0.33	0.37	0.18	0.02
0.50	0.52	0.04	0.22	0.40	0.29	0.05
0.60	0.61	0.02	0.13	0.35	0.39	0.11
0.70	0.70	0.00	0.06	0.27	0.48	0.20
0.80	0.79	0.00	0.02	0.15	0.48	0.35
0.90	0.88	0.00	0.00	0.05	0.38	0.57
1.00	1.00	0.00	0.00	0.00	0.00	1.00

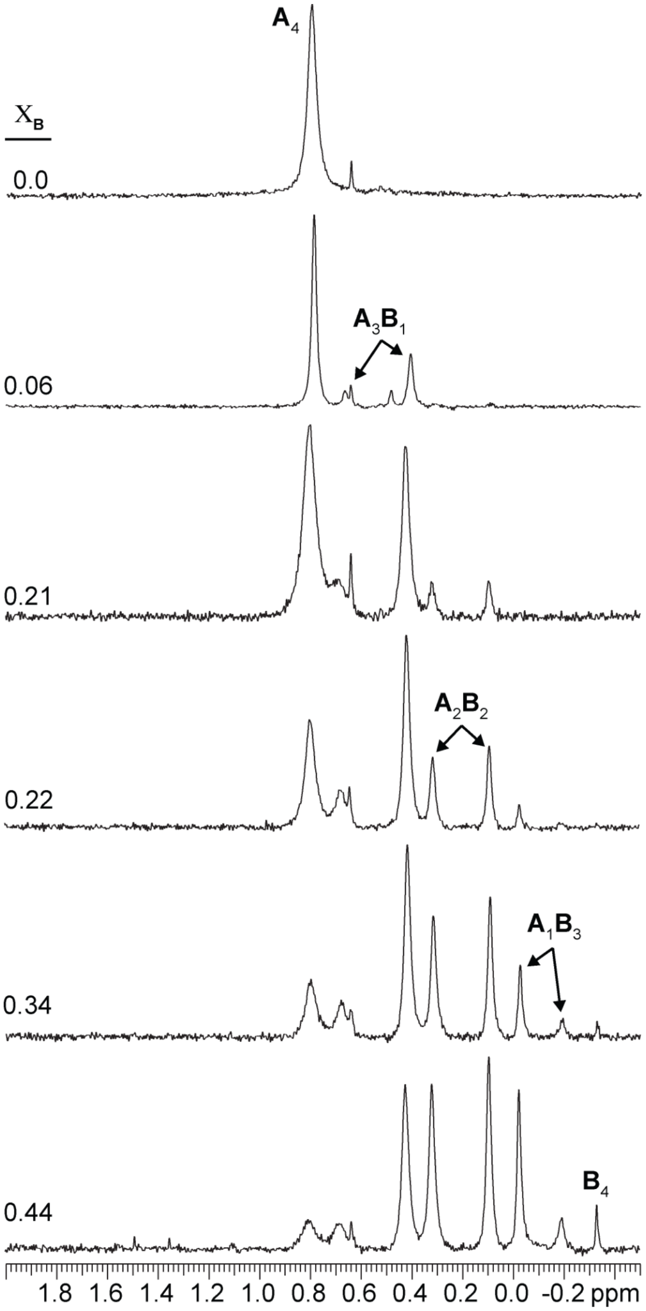
A.



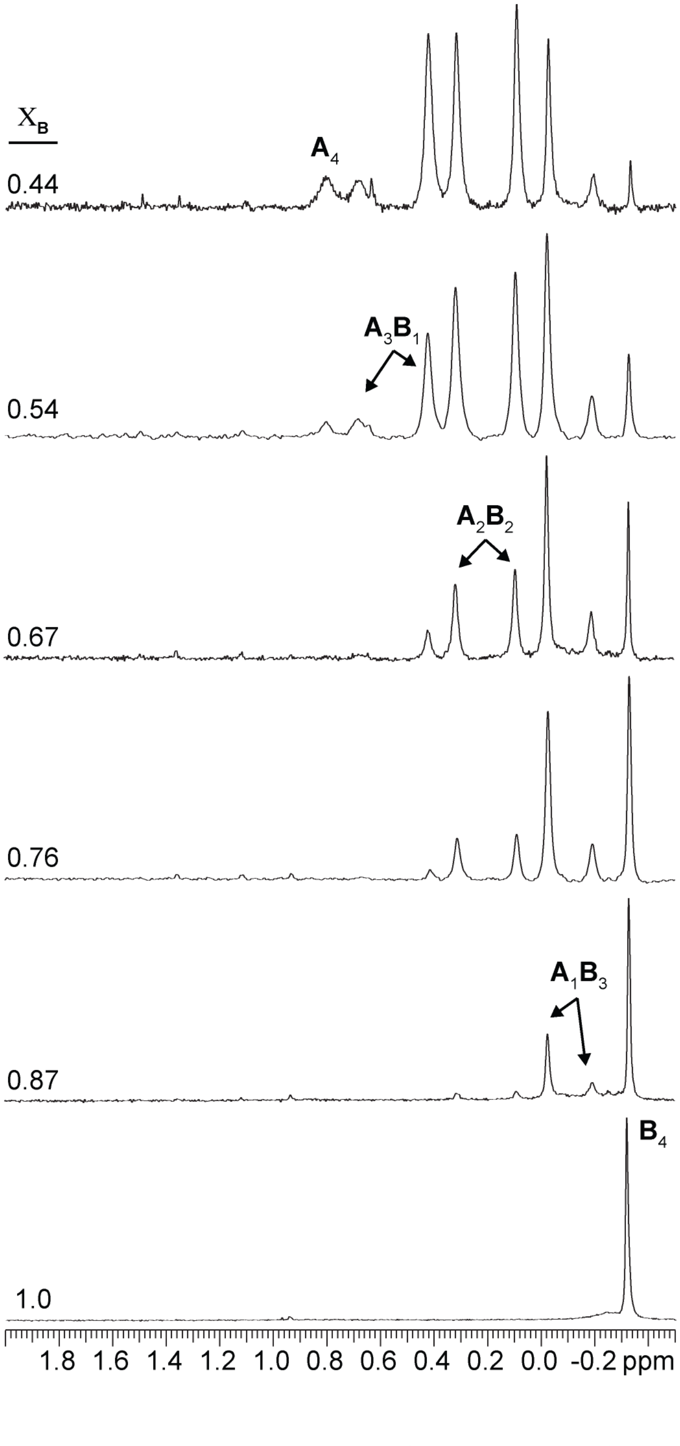
B.



IV.**kk**. Plot of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 10 equivalents of DME/toluene at -40 °C (see **IV**.**hh** and **jj**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 1.10$; $\phi_2 = 1.06$; $\phi_3 = 0.98$; $\phi_4 = 0.55$ rms = 0.004. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 1.22$; $\phi_2 = 1.28$; $\phi_3 = 1.26$; $\phi_4 = 0.67$ rms = 0.018.



IV.1l. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 10 M DME/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.10 M LiHMDS.



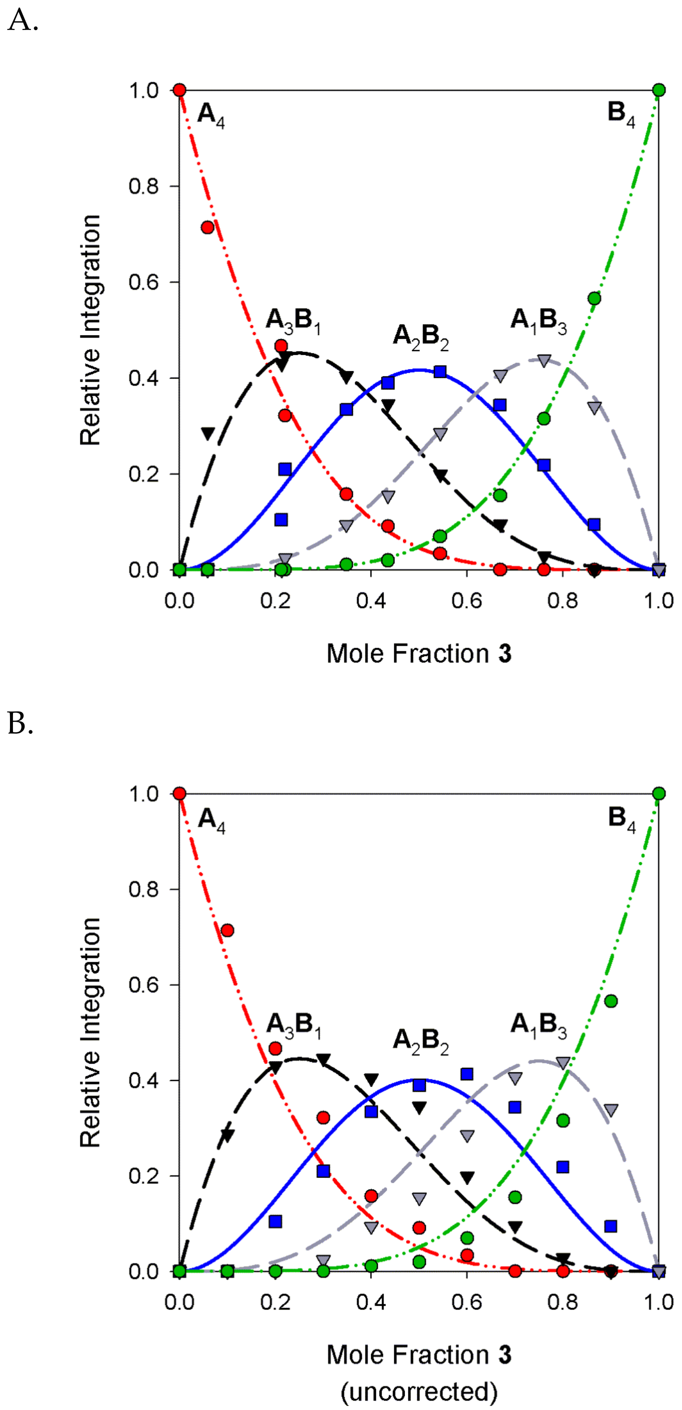
IV.1l. (cont) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions in 10 M DME/toluene at -90 °C. Samples were prepared via in situ enolization of 0.10 M total ketone with 0.10 M LiHMDS.

IV.mm. Resonance integrations for an ensemble of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -90 °C. Spectra (see **IV.ll.**) were recorded on a 0.10 M mixture of enolates.

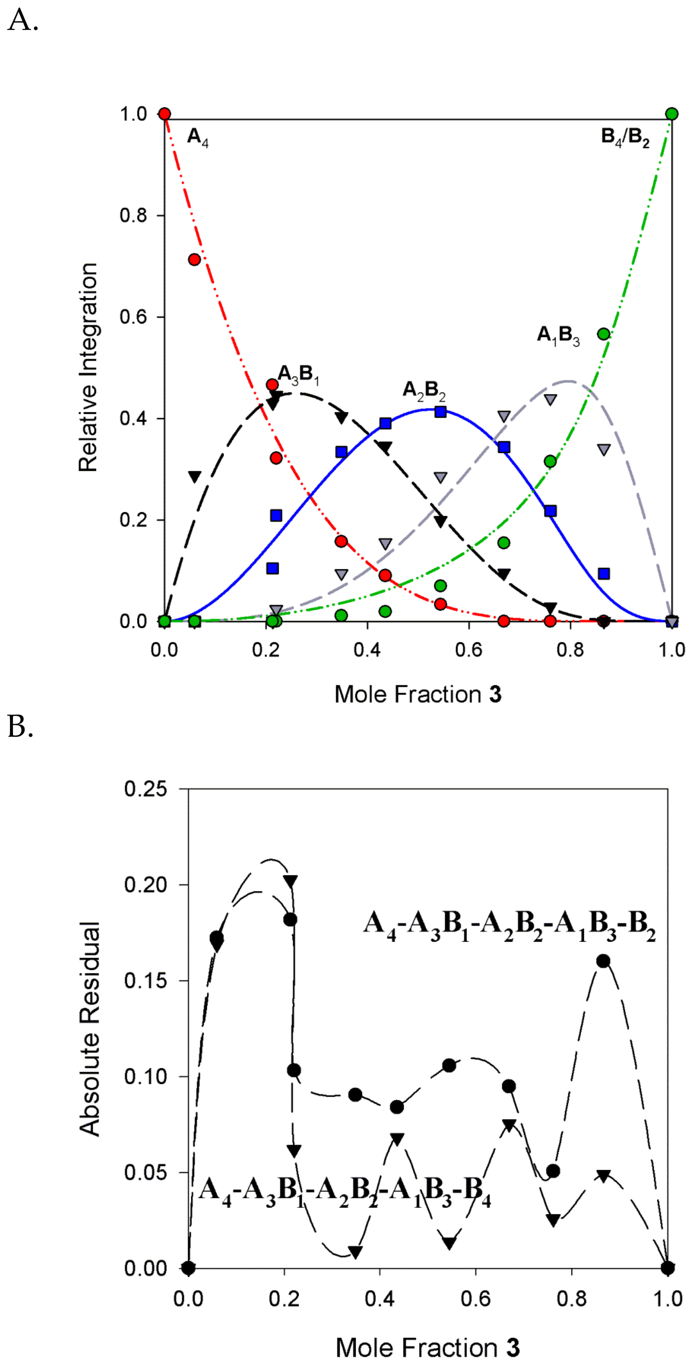
Calculated	Resonance Integrations							
		$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		
X_B	$\mathbf{A}_4$	$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	$\mathbf{B}_4$
1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
0.87	0.00	0.00	0.00	19.40	11.95	88.34	25.59	189.24
0.76	0.00	0.00	22.40	91.72	81.66	273.38	76.66	250.77
0.67	0.00	26.24	76.71	181.98	188.72	340.22	98.57	166.44
0.54	52.70	75.78	240.74	328.66	328.87	351.41	104.60	110.53
0.44	156.41	172.64	427.63	337.76	338.70	210.61	58.27	32.92
0.35	251.91	161.50	486.82	268.31	268.31	112.14	39.40	17.17
0.22	453.90	122.19	507.46	140.06	154.93	34.02	0.00	0.00
0.21	1039.88	368.65	591.23	126.49	105.96	0.00	0.00	0.00
0.06	374.74	31.11	119.86	0.00	0.00	0.00	0.00	0.00
0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

IV.nn. Relative integrations for aggregates in an ensemble of **1** (**A**) and **3** (**B**) at various mole fractions of **A** and **B** in 10 equivalents of DME/toluene at -90 °C. Integrations were measured (see **IV.ll** and **mm**) for a 0.10 M enolate ensemble.

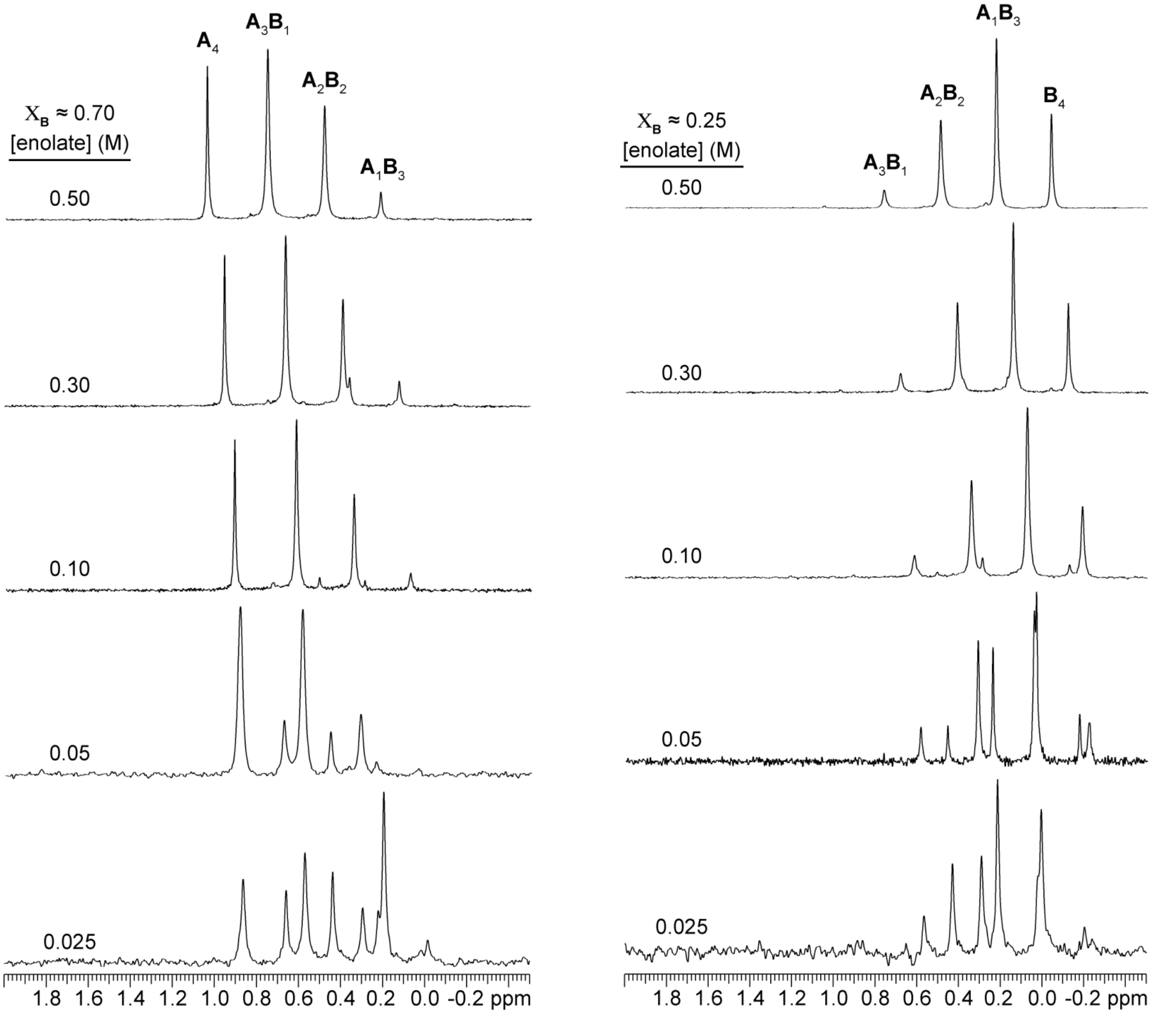
Uncorrected	Calculated	Relative Integrations				
X_B	X_B	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
1.00	1.00	0.00	0.00	0.00	0.00	1.00
0.90	0.87	0.00	0.00	0.09	0.34	0.57
0.80	0.76	0.00	0.03	0.22	0.44	0.31
0.70	0.67	0.00	0.10	0.34	0.41	0.15
0.60	0.54	0.03	0.20	0.41	0.29	0.07
0.50	0.44	0.09	0.35	0.39	0.15	0.02
0.40	0.35	0.16	0.40	0.33	0.09	0.01
0.30	0.22	0.32	0.45	0.21	0.02	0.00
0.20	0.21	0.47	0.43	0.10	0.00	0.00
0.10	0.06	0.71	0.29	0.00	0.00	0.00
0.00	0.00	1.00	0.00	0.00	0.00	0.00



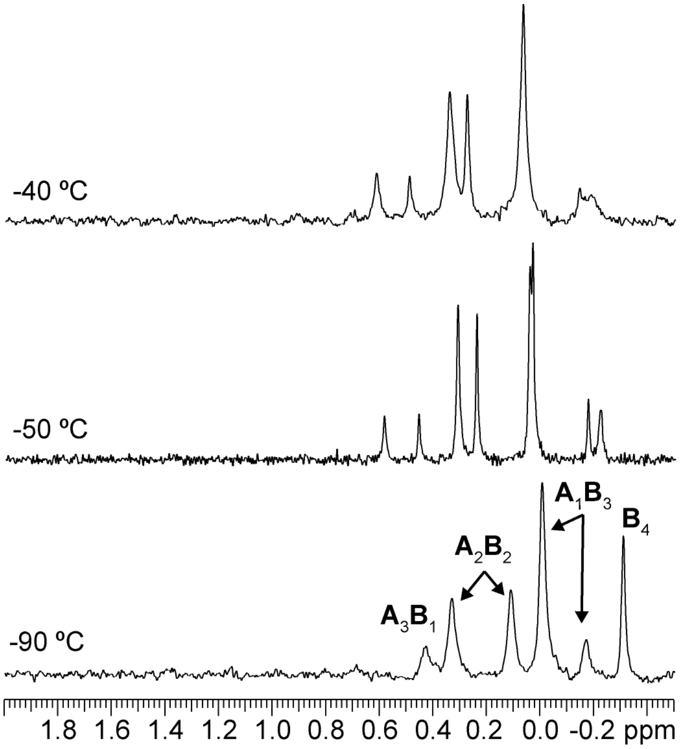
IV.oo. Plot of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 10 equivalents of DME/toluene at -90 °C (see **IV.ll** and **nn**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 1.29$; $\phi_2 = 1.38$; $\phi_3 = 1.15$; $\phi_4 = 0.88$; rms = 0.025. B) Plot and fit of the relative integration versus the uncorrected mole fraction of **3**; $\phi_0 = 1.00$; $\phi_1 = 1.16$; $\phi_2 = 1.15$; $\phi_3 = 0.99$; $\phi_4 = 0.76$; rms = 0.044.



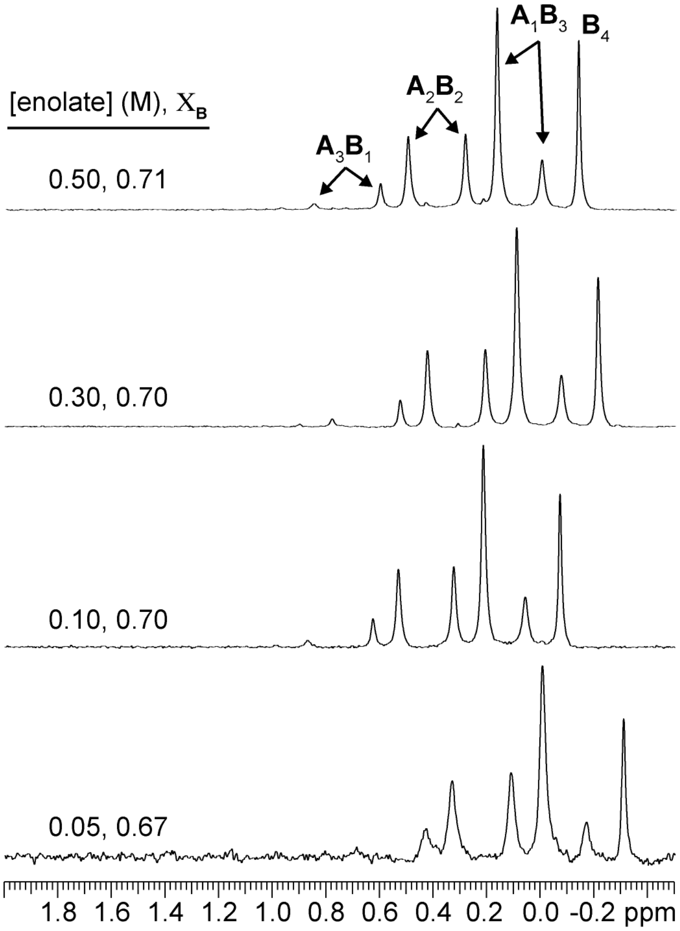
IV.pp. Plots of the relative integration versus the mole fraction of **3** (**B**) for an ensemble of **1** (**A**) and **3** (**B**) in 10 equivalents of DME/toluene at -90 °C fit to an ensemble of **A_4-A_3B_1- A_2B_2- A_1B_3- B_2** (see **IV.ll**). A) Plot and fit of the relative integration versus the calculated mole fraction of **3** fit to **A_4-A_3B_1- A_2B_2- A_1B_3- B_2**; ϕ_{20} = 0.52; ϕ_{21} = ϕ_{22} = 0.00; ϕ_{40} = 0.00; ϕ_{41} = 3.99; ϕ_{42} = 2.76; ϕ_{43} = 1.22; ϕ_{44} = 0.44; rms = 0.03. B) Plot of the sum of the absolute residuals for **A_4-A_3B_1- A_2B_2- A_1B_3- B_2** versus the mole fraction of **3**.



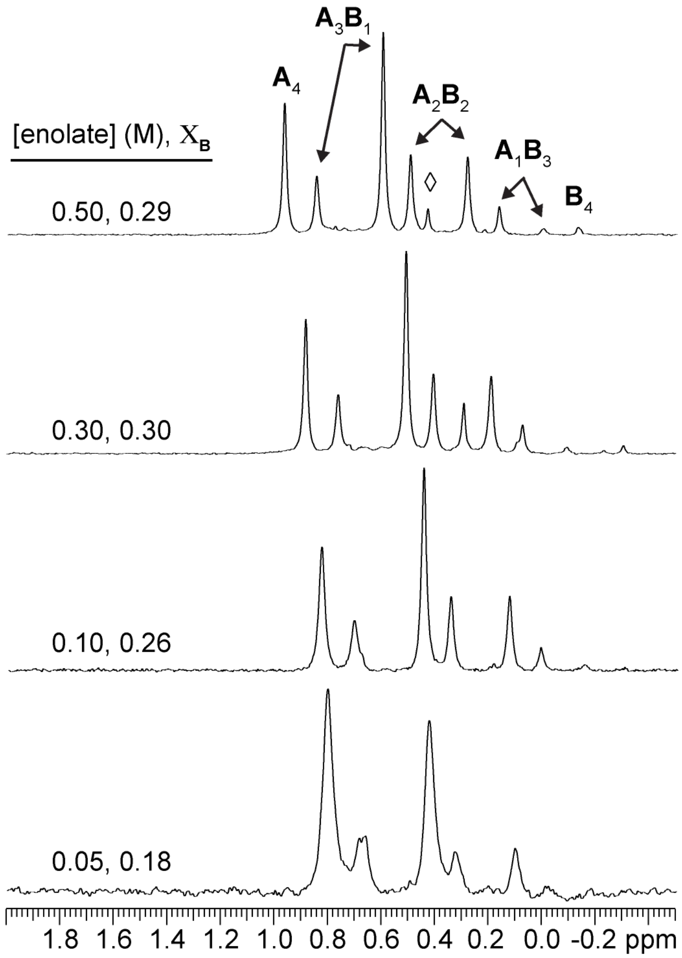
IV.qq. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -40 °C. Samples were prepared via in situ enolization of ketone with 0.05 equivalents excess LiHMDS.



IV.rr. ^{6}Li NMR spectra of a mixture of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) (X_B = 0.67) at various temperatures in 10 equivalents DME/toluene. Sample was prepared via in situ enolization of 0.050 M total ketone with 0.055 M LiHMDS.



IV.ss. ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with 0.05 equivalents excess LiHMDS.



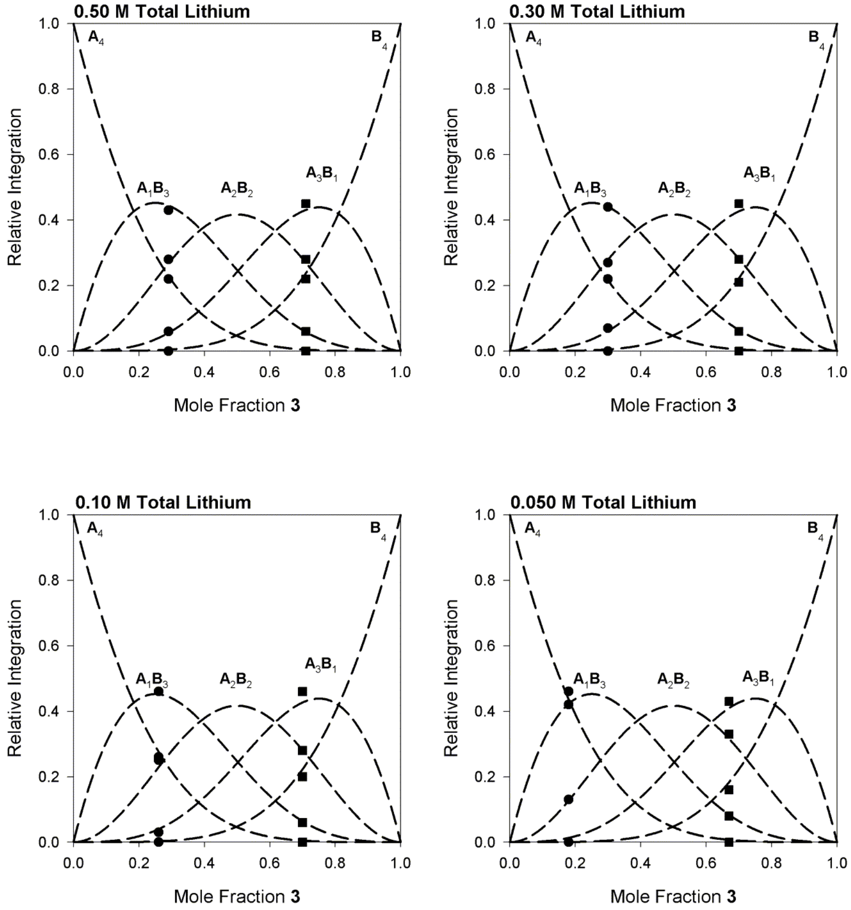
IV.ss. (cont.) ^{6}Li NMR spectra of mixtures of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -90 °C. Samples were prepared via in situ enolization of ketone with 0.05 equivalents excess LiHMDS.

IV.tt. Resonance integrations for each aggregate in ensembles of [^{6}Li]**1** (**A**) and [^{6}Li]**3** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene at -90 °C (see **IV.rr**).

[enolate]	Calc.	Resonance Integrations							
		$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$		$\mathbf{A}_2\mathbf{B}_2$		$\mathbf{A}_1\mathbf{B}_3$		$\mathbf{B}_4$
(M)	$X_\mathbf{B}$		$\mathbf{B}_1$	$\mathbf{A}_3$	$\mathbf{A}_2$	$\mathbf{B}_2$	$\mathbf{B}_3$	$\mathbf{A}_1$	
0.50	0.29	184.00	84.06	272.79	111.84	118.38	37.63	13.23	0.00
0.30	0.30	191.66	89.69	289.10	114.70	122.49	47.18	12.70	0.00
0.10	0.26	261.03	114.43	349.45	122.43	129.75	30.65	0.00	0.00
0.05	0.18	634.55	203.72	497.00	94.16	99.29	0.00	0.00	0.00
0.50	0.71	0.00	12.40	37.58	115.19	120.02	282.32	99.40	183.10
0.30	0.70	0.00	12.06	41.27	131.05	134.31	315.50	108.53	192.85
0.10	0.70	0.00	15.37	41.62	129.76	136.02	318.11	113.23	188.24
0.05	0.67	0.00	19.04	59.78	176.45	163.46	365.39	71.07	162.02

IV.uu. Relative integrations for ensembles of **1** (**A**) and **3** (**B**) at various absolute Li concentrations in 10 equivalents DME/toluene with excess LiHMDS at -90 °C (see **IV.rr**).

[Li]	[enolate]	Calc.	Relative Integrations				
(M)	(M)	$X_\mathbf{B}$	$\mathbf{A}_4$	$\mathbf{A}_3\mathbf{B}_1$	$\mathbf{A}_2\mathbf{B}_2$	$\mathbf{A}_1\mathbf{B}_3$	$\mathbf{B}_4$
0.50	0.50	0.29	0.00	0.06	0.28	0.45	0.22
0.13	0.30	0.30	0.00	0.06	0.28	0.45	0.21
0.031	0.10	0.26	0.00	0.06	0.28	0.46	0.20
0.016	0.05	0.18	0.00	0.08	0.33	0.43	0.16
0.50	0.50	0.71	0.22	0.43	0.28	0.06	0.00
0.13	0.30	0.70	0.22	0.44	0.27	0.07	0.00
0.031	0.10	0.70	0.26	0.46	0.25	0.03	0.00
0.016	0.05	0.67	0.42	0.46	0.13	0.00	0.00

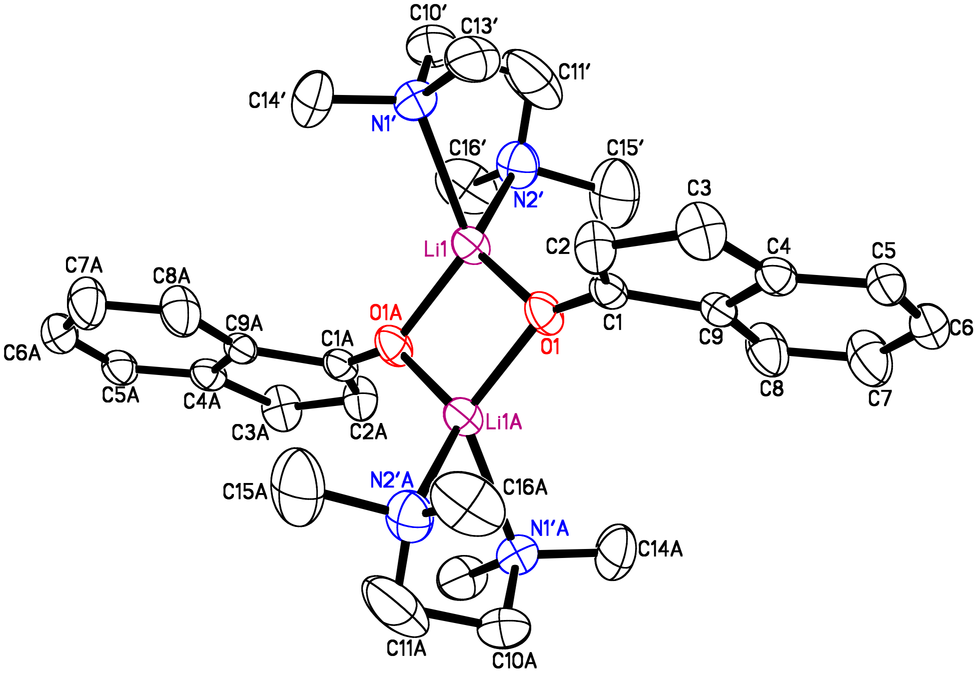


IV.vv. Relative integrations of mixtures of **1** and **3** at various absolute Li concentrations in 10 equivalents of DME/toluene at -90 °C plotted on the curves for a fit to the Job plot of an ensemble of tetramers (**IV.oo**).

IV.ww. Absolute residuals for the deviation of the relative integrations of ensembles of **1** and **3** in 10 equivalents DME/toluene at various absolute Li concentrations from the expected relative integrations based on the fit in **IV.oo**.

[Li] (M)	[enolate] (M)	Calc. X_B	Absolute Residuals $\mathbf{A_4}$	$\mathbf{A_3B_1}$	$\mathbf{A_2B_2}$	$\mathbf{A_1B_3}$	$\mathbf{B_4}$
0.50	0.45	0.71	0.00	0.00	0.00	0.02	0.02
0.13	0.11	0.70	0.00	0.01	0.00	0.03	0.02
0.031	0.030	0.70	0.00	0.00	0.00	0.03	0.02
0.016	0.015	0.67	0.01	0.01	0.02	0.02	0.02
0.50	0.45	0.29	0.00	0.01	0.01	0.00	0.00
0.13	0.11	0.30	0.00	0.00	0.00	0.01	0.00
0.031	0.030	0.26	0.01	0.01	0.02	0.01	0.00
0.016	0.015	0.18	0.03	0.04	0.00	0.01	0.00

V. Crystal Structures



V.a. ORTEP of dimeric aggregate of **1** *bis*-chelated by TMEDA (ll1). The crystal was obtained upon cooling 0.10 M **1** with 0.11 M LiHMDS in 1.1 M TMEDA/hexanes.

V.b. Crystal data and structure refinement for ll1 (see **V.a.**).

Identification code	ll1	
Empirical formula	C30 H46 Li2 N4 O2	
Formula weight	508.59	
Temperature	173(2) K	
Wavelength	0.71073 Å	
Crystal system	Monoclinic	
Space group	P2(1)/c	
Unit cell dimensions	a = 10.0495(18) Å	a= 90°.
	b = 11.7842(13) Å	b= 104.277(5)°.
	c = 13.737(2) Å	g = 90°.
Volume	1576.6(4) Å^3	
Z	2	
Density (calculated)	1.071 Mg/m^3	
Absorption coefficient	0.066 mm^{-1}	
F(000)	552	
Crystal size	0.50 x 0.40 x 0.30 mm^3	
Theta range for data collection	2.09 to 23.29°.	
Index ranges	-11<=h<=11, -12<=k<=12, -15<=l<=15	
Reflections collected	10238	
Independent reflections	2259 [R(int) = 0.0364]	
Completeness to theta = 23.29°	99.2 %	
Absorption correction	Semi-empirical from equivalents	
Max. and min. transmission	0.9804 and 0.9677	
Refinement method	Full-matrix least-squares on F^2	
Data / restraints / parameters	2259 / 0 / 247	
Goodness-of-fit on F^2	1.086	
Final R indices [I>2sigma(I)]	R1 = 0.0520, wR2 = 0.1525	
R indices (all data)	R1 = 0.0814, wR2 = 0.1719	
Largest diff. peak and hole	0.220 and -0.203 e.Å^{-3}	

V.c. Atomic coordinates (x 10^4) and equivalent isotropic displacement parameters (Å^{2}x 10^3) for ll1. U(eq) is defined as one third of the trace of the orthogonalized U^{ij} tensor (see **V.a.**).

	x	y	z	U(eq)
O(1)	1062(1)	678(1)	5515(1)	55(1)
N(1)	-1578(4)	231(3)	6691(3)	66(1)
C(13)	-2859(6)	-480(5)	6301(5)	124(2)
C(14)	-690(8)	-393(9)	7540(5)	201(4)
N(1')	-1197(3)	131(2)	7001(2)	54(1)
C(13')	-101(3)	598(3)	7767(2)	86(1)
C(14')	-1457(5)	-1027(3)	7197(3)	110(2)
C(1)	2116(1)	1163(1)	6136(1)	44(1)
C(2)	2875(2)	836(1)	7033(1)	62(1)
C(3)	3982(2)	1677(1)	7483(1)	68(1)
C(4)	3780(1)	2566(1)	6694(1)	47(1)
C(5)	4472(2)	3575(1)	6664(1)	57(1)
C(6)	4074(2)	4257(2)	5847(1)	72(1)
C(7)	3009(2)	3953(2)	5050(1)	93(1)
C(8)	2291(2)	2958(2)	5076(1)	77(1)
C(9)	2682(1)	2262(1)	5902(1)	42(1)
C(10)	-1943(6)	1284(5)	6937(3)	103(2)
C(11)	-2659(6)	1765(6)	6208(5)	160(3)
C(10')	-2487(4)	782(4)	6937(3)	85(1)
C(11')	-2508(6)	1979(4)	6284(4)	114(2)
N(2)	-1998(3)	1943(2)	5257(2)	60(1)
C(15)	-1044(4)	2902(3)	5324(4)	106(2)
C(16)	-2976(5)	2041(5)	4278(4)	144(2)
N(2')	-2411(4)	1639(3)	5380(3)	68(1)
C(15')	-1969(7)	2733(5)	4970(6)	142(3)
C(16')	-3608(4)	1219(5)	4719(4)	109(2)
Li(1)	-783(3)	418(2)	5492(2)	50(1)

V.d. Bond lengths [Å] and angles [°] for ll1. Symmetry transformations used to generate equivalent atoms: #1 -x,-y,-z+1.

O(1)-C(1)	1.3156(15)	Li(1)-Li(1)#1	2.514(5)
O(1)-Li(1)#1	1.862(3)	C(1)-O(1)-Li(1)#1	137.13(12)
O(1)-Li(1)	1.871(3)	C(1)-O(1)-Li(1)	135.89(12)
N(1)-C(10)	1.361(7)	Li(1)#1-O(1)-Li(1)	84.64(13)
N(1)-C(14)	1.477(8)	C(10)-N(1)-C(14)	113.9(5)
N(1)-C(13)	1.519(7)	C(10)-N(1)-C(13)	109.5(4)
N(1)-Li(1)	2.012(5)	C(14)-N(1)-C(13)	107.4(5)
N(1')-C(14')	1.429(5)	C(10)-N(1)-Li(1)	106.8(3)
N(1')-C(13')	1.433(4)	C(14)-N(1)-Li(1)	114.6(4)
N(1')-C(10')	1.490(5)	C(13)-N(1)-Li(1)	104.2(3)
N(1')-Li(1)	2.238(4)	C(14')-N(1')-C(13')	111.8(3)
C(1)-C(2)	1.336(2)	C(14')-N(1')-C(10')	107.8(3)
C(1)-C(9)	1.481(2)	C(13')-N(1')-C(10')	110.2(3)
C(2)-C(3)	1.504(2)	C(14')-N(1')-Li(1)	113.8(2)
C(3)-C(4)	1.486(2)	C(13')-N(1')-Li(1)	109.8(2)
C(4)-C(5)	1.383(2)	C(10')-N(1')-Li(1)	103.1(2)
C(4)-C(9)	1.3920(18)	O(1)-C(1)-C(2)	131.13(14)
C(5)-C(6)	1.359(2)	O(1)-C(1)-C(9)	122.03(12)
C(6)-C(7)	1.376(2)	C(2)-C(1)-C(9)	106.83(12)
C(7)-C(8)	1.382(3)	C(1)-C(2)-C(3)	112.70(14)
C(8)-C(9)	1.377(2)	C(4)-C(3)-C(2)	102.13(12)
C(10)-C(11)	1.218(8)	C(5)-C(4)-C(9)	120.39(13)
C(10)-Li(1)	2.736(6)	C(5)-C(4)-C(3)	130.47(13)
C(11)-N(2)	1.620(8)	C(9)-C(4)-C(3)	109.13(13)
C(10')-C(11')	1.669(7)	C(6)-C(5)-C(4)	119.02(14)
C(11')-N(2')	1.331(7)	C(5)-C(6)-C(7)	121.11(17)
N(2)-C(16)	1.461(5)	C(6)-C(7)-C(8)	120.58(17)
N(2)-C(15)	1.470(5)	C(9)-C(8)-C(7)	118.82(16)
N(2)-Li(1)	2.152(4)	C(8)-C(9)-C(4)	120.05(14)
N(2')-C(16')	1.406(5)	C(8)-C(9)-C(1)	130.75(13)
N(2')-C(15')	1.516(7)	C(4)-C(9)-C(1)	109.20(12)
N(2')-Li(1)	2.156(4)	C(11)-C(10)-N(1)	111.1(5)
Li(1)-O(1)#1	1.862(3)	C(11)-C(10)-Li(1)	81.3(4)

V.d. (cont.) Bond lengths [Å] and angles [°] for ll1. Symmetry transformations used to generate equivalent atoms: #1 -x,-y,-z+1.

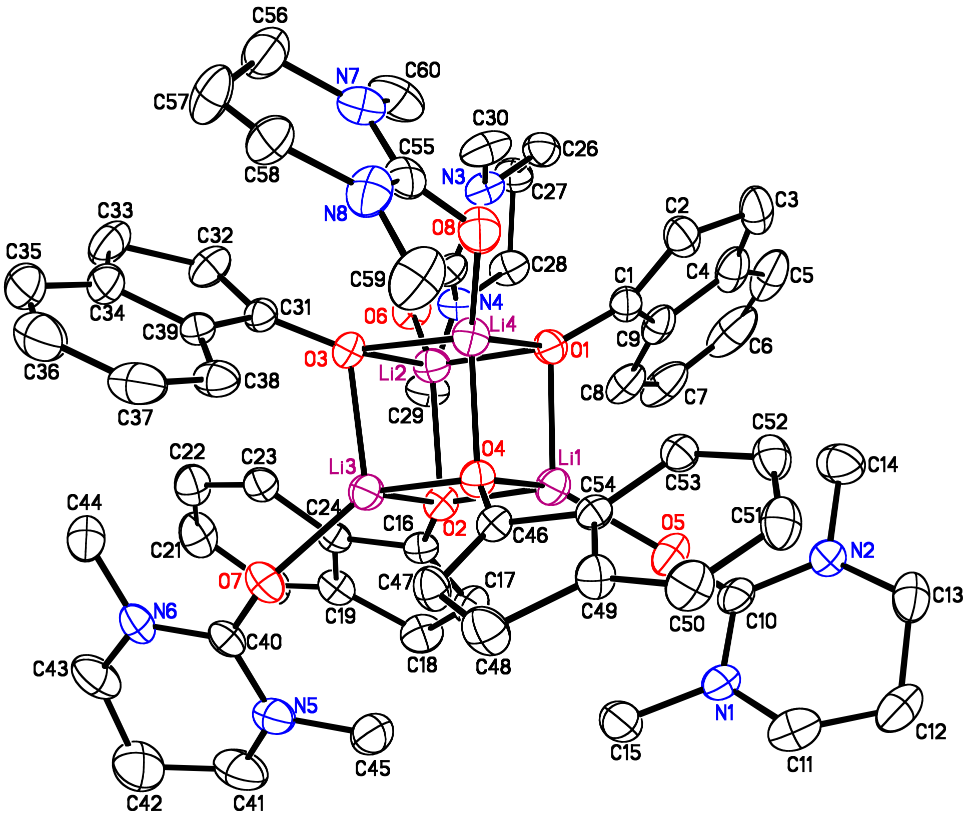
N(1)-C(10)-Li(1)	44.7(2)	O(1)#1-Li(1)-N(2')	115.92(15)
C(10)-C(11)-N(2)	116.6(5)	O(1)-Li(1)-N(2')	128.55(16)
N(1')-C(10')-C(11')	111.2(4)	N(1)-Li(1)-N(2')	71.56(17)
N(2')-C(11')-C(10')	104.6(4)	N(2)-Li(1)-N(2')	16.11(13)
C(16)-N(2)-C(15)	106.2(4)	O(1)#1-Li(1)-N(1')	123.73(15)
C(16)-N(2)-C(11)	115.8(4)	O(1)-Li(1)-N(1')	114.73(13)
C(15)-N(2)-C(11)	116.1(4)	N(1)-Li(1)-N(1')	12.40(12)
C(16)-N(2)-Li(1)	115.6(3)	N(2)-Li(1)-N(1')	92.11(14)
C(15)-N(2)-Li(1)	107.2(2)	N(2')-Li(1)-N(1')	81.68(16)
C(11)-N(2)-Li(1)	95.8(3)	O(1)#1-Li(1)-Li(1)#1	47.84(9)
C(11')-N(2')-C(16')	117.4(5)	O(1)-Li(1)-Li(1)#1	47.52(9)
C(11')-N(2')-C(15')	100.7(4)	N(1)-Li(1)-Li(1)#1	145.6(2)
C(16')-N(2')-C(15')	110.0(4)	N(2)-Li(1)-Li(1)#1	130.80(19)
C(11')-N(2')-Li(1)	111.3(3)	N(2')-Li(1)-Li(1)#1	142.0(2)
C(16')-N(2')-Li(1)	108.9(3)	N(1')-Li(1)-Li(1)#1	136.29(17)
C(15')-N(2')-Li(1)	107.9(3)	O(1)#1-Li(1)-C(10)	141.69(18)
O(1)#1-Li(1)-O(1)	95.36(12)	O(1)-Li(1)-C(10)	121.61(16)
O(1)#1-Li(1)-N(1)	120.98(17)	N(1)-Li(1)-C(10)	28.43(17)
O(1)-Li(1)-N(1)	126.55(16)	N(2)-Li(1)-C(10)	57.97(16)
O(1)#1-Li(1)-N(2)	119.43(14)	N(2')-Li(1)-C(10)	49.51(16)
O(1)-Li(1)-N(2)	112.88(14)	N(1')-Li(1)-C(10)	34.35(14)
N(1)-Li(1)-N(2)	83.64(16)	Li(1)#1-Li(1)-C(10)	166.29(19)

V.e. Anisotropic displacement parameters ($Å^2 x 10^3$) for ll1. The anisotropic displacement factor exponent takes the form: $-2\pi^2[h^2 a^{*2}U^{11} + ... + 2 h k a^* b^* U^{12}]$.

	U^{11}	U^{22}	U^{33}	U^{23}	U^{13}	U^{12}
O(1)	44(1)	50(1)	66(1)	-19(1)	7(1)	-8(1)
N(1)	60(2)	76(2)	69(2)	21(2)	31(2)	18(2)
C(13)	136(4)	122(4)	143(4)	-22(4)	92(4)	-46(4)
C(14)	176(6)	358(11)	92(4)	111(5)	77(4)	128(7)
N(1')	50(2)	62(2)	51(2)	3(1)	12(1)	2(1)
C(13')	74(2)	117(3)	65(2)	-26(2)	13(2)	-29(2)
C(14')	142(3)	80(2)	119(3)	16(2)	53(3)	-25(2)
C(1)	39(1)	43(1)	51(1)	-10(1)	13(1)	2(1)
C(2)	67(1)	50(1)	62(1)	5(1)	3(1)	-8(1)
C(3)	65(1)	63(1)	64(1)	2(1)	-3(1)	3(1)
C(4)	40(1)	51(1)	52(1)	-10(1)	14(1)	0(1)
C(5)	54(1)	55(1)	66(1)	-19(1)	20(1)	-14(1)
C(6)	99(1)	54(1)	69(1)	-14(1)	32(1)	-23(1)
C(7)	157(2)	59(1)	56(1)	5(1)	14(1)	-20(1)
C(8)	105(1)	60(1)	52(1)	-3(1)	-5(1)	-14(1)
C(9)	46(1)	39(1)	41(1)	-8(1)	13(1)	-1(1)
C(10)	107(4)	142(5)	74(3)	-24(3)	49(3)	-10(4)
C(11)	147(3)	184(5)	178(5)	8(5)	97(4)	112(4)
C(10')	70(2)	102(3)	94(3)	-4(2)	43(2)	9(2)
C(11')	109(4)	85(3)	149(4)	-59(3)	36(4)	10(3)
N(2)	51(2)	64(2)	62(2)	-8(1)	10(1)	9(1)
C(15)	107(3)	62(2)	156(4)	-15(2)	45(3)	8(2)
C(16)	126(4)	145(4)	122(4)	8(3)	-43(3)	42(3)
N(2')	67(2)	57(2)	80(2)	10(2)	18(2)	12(2)
C(15')	139(5)	74(3)	210(7)	51(4)	37(5)	23(4)
C(16')	60(3)	128(4)	118(4)	-20(3)	-17(3)	44(3)
Li(1)	46(1)	47(1)	54(1)	-8(1)	9(1)	2(1)

V.f. Hydrogen coordinates (x 10^4) and isotropic displacement parameters (Å^{2}x 10 ^{3}) for ll1.

	x	y	z	U(eq)
H(13A)	-3307	-621	6847	185
H(13B)	-2605	-1205	6047	185
H(13C)	-3493	-72	5757	185
H(14A)	-1171	-484	8075	301
H(14B)	161	34	7797	301
H(14C)	-472	-1142	7310	301
H(13D)	-292	479	8426	129
H(13E)	-23	1413	7650	129
H(13F)	763	221	7751	129
H(14D)	-1646	-1089	7862	165
H(14E)	-651	-1488	7180	165
H(14F)	-2253	-1300	6685	165
H(2A)	2732	147	7351	74
H(3A)	3855	1986	8124	81
H(3B)	4906	1330	7601	81
H(5A)	5215	3787	7207	68
H(6A)	4538	4955	5824	87
H(7A)	2764	4432	4477	111
H(8A)	1541	2758	4533	92
H(10A)	-2453	1219	7466	123
H(10D)	-1107	1740	7209	123
H(11A)	-2908	2520	6426	192
H(11B)	-3520	1327	5979	192
H(11C)	-3372	2403	6237	136
H(11D)	-1723	2472	6603	136
H(10B)	-2575	977	7605	136
H(10C)	-3274	332	6622	136
H(15A)	-1562	3615	5228	159
H(15B)	-536	2827	4803	159
H(15C)	-397	2904	5988	159
H(16A)	-3496	2749	4251	216
H(16B)	-3611	1396	4180	216
H(16C)	-2479	2044	3748	216
H(15D)	-2694	3303	4912	212
H(15E)	-1805	2592	4307	212
H(15F)	-1123	3010	5427	212
H(16D)	-4359	1762	4676	163
H(16E)	-3857	491	4970	163
H(16F)	-3442	1113	4052	163



V.g. ORTEP of a tetrameric aggregate of **1** solvated by four DMPU molecules (ar8).

V.h. Crystal data and structure refinement for ar8 (see **V.g.**).

Identification code	ar8	
Empirical formula	C60 H76 Li4 N8 O8	
Formula weight	1065.05	
Temperature	173(2) K	
Wavelength	0.71073 Å	
Crystal system	Orthorhombic	
Space group	Pbca	
Unit cell dimensions	a = 21.9709(17) Å	a= 90°.
	b = 13.8918(11) Å	b= 90°.
	c = 42.328(3) Å	g = 90°.
Volume	12919.1(17) Å^3	
Z	8	
Density (calculated)	1.095 Mg/m^3	
Absorption coefficient	0.072 mm^{-1}	
F(000)	4544	
Crystal size	0.30 x 0.20 x 0.15 mm^3	
Theta range for data collection	1.80 to 23.32°.	
Index ranges	-24<=h<=24, -13<=k<=15, -46<=l<=43	
Reflections collected	41745	
Independent reflections	9286 [R(int) = 0.0377]	
Completeness to theta = 23.32°	99.3 %	
Absorption correction	Semi-empirical from equivalents	
Max. and min. transmission	0.9893 and 0.9787	
Refinement method	Full-matrix least-squares on F^2	
Data / restraints / parameters	9286 / 0 / 734	
Goodness-of-fit on F^2	1.050	
Final R indices [I>2sigma(I)]	R1 = 0.0485, wR2 = 0.1357	
R indices (all data)	R1 = 0.0762, wR2 = 0.1467	
Largest diff. peak and hole	0.411 and -0.276 e.Å^{-3}	

V.i. Atomic coordinates (x 10^4) and equivalent isotropic displacement parameters (Å^{2}x 10^3) for ar8. U(eq) is defined as one third of the trace of the orthogonalized U^{ij} tensor (see **V.g.**).

	x	y	z	U(eq)
Li(1)	4283(2)	11345(3)	1452(1)	43(1)
Li(2)	4453(2)	9429(3)	1572(1)	43(1)
Li(3)	4863(2)	10245(3)	1039(1)	42(1)
Li(4)	5397(2)	10630(3)	1596(1)	43(1)
O(1)	4626(1)	10620(1)	1814(1)	41(1)
O(2)	4052(1)	10180(1)	1226(1)	40(1)
O(3)	5249(1)	9410(1)	1367(1)	39(1)
O(4)	5098(1)	11416(1)	1247(1)	39(1)
O(5)	3842(1)	12507(1)	1518(1)	56(1)
O(6)	4080(1)	8339(1)	1758(1)	51(1)
O(7)	4946(1)	10070(1)	599(1)	50(1)
O(8)	6167(1)	10785(1)	1795(1)	58(1)
N(1)	3914(1)	13884(2)	1238(1)	51(1)
N(2)	3821(1)	13912(2)	1785(1)	49(1)
N(3)	4090(1)	8072(1)	2287(1)	49(1)
N(4)	3220(1)	7781(1)	1987(1)	46(1)
N(5)	4096(1)	10263(2)	305(1)	55(1)
N(6)	4694(1)	8889(2)	260(1)	51(1)
N(7)	6696(1)	9403(2)	1875(1)	60(1)
N(8)	7102(1)	10653(2)	1580(1)	60(1)
C(1)	4447(1)	10827(2)	2103(1)	42(1)
C(2)	4761(1)	11166(2)	2351(1)	56(1)
C(3)	4351(2)	11259(2)	2637(1)	75(1)
C(4)	3757(2)	10900(2)	2519(1)	64(1)
C(5)	3195(2)	10774(2)	2670(1)	87(1)
C(6)	2714(2)	10390(3)	2498(1)	95(1)
C(7)	2770(1)	10178(2)	2185(1)	78(1)
C(8)	3321(1)	10317(2)	2031(1)	58(1)
C(9)	3812(1)	10661(2)	2202(1)	50(1)
C(10)	3868(1)	13401(2)	1512(1)	44(1)
C(11)	4043(1)	14899(2)	1223(1)	67(1)
C(12)	3749(1)	15421(2)	1492(1)	69(1)
C(13)	3921(1)	14950(2)	1798(1)	61(1)
C(14)	3837(1)	13405(2)	2082(1)	71(1)
C(15)	3993(1)	13344(2)	946(1)	74(1)
C(16)	3547(1)	9812(2)	1107(1)	38(1)
C(17)	2983(1)	10196(2)	1086(1)	50(1)
C(18)	2549(1)	9506(2)	934(1)	60(1)
C(19)	2938(1)	8639(2)	869(1)	49(1)
C(20)	2798(1)	7747(2)	744(1)	64(1)
C(21)	3250(2)	7062(2)	718(1)	68(1)

V.i. (cont.) Atomic coordinates (x 10^4) and equivalent isotropic displacement parameters (Å^{2}x 10^3) for ar8. U(eq) is defined as one third of the trace of the orthogonalized U^{ij} tensor (see **V.g.**).

	x	y	z	U(eq)
C(22)	3836(1)	7263(2)	815(1)	58(1)
C(23)	3983(1)	8152(2)	941(1)	44(1)
C(24)	3529(1)	8832(2)	969(1)	38(1)
C(25)	3805(1)	8086(2)	2001(1)	42(1)
C(26)	3761(1)	7952(2)	2582(1)	56(1)
C(27)	3246(1)	7276(2)	2537(1)	56(1)
C(28)	2852(1)	7619(2)	2269(1)	56(1)
C(29)	2897(1)	7861(2)	1687(1)	61(1)
C(30)	4702(1)	8467(2)	2310(1)	66(1)
C(31)	5607(1)	8712(2)	1270(1)	38(1)
C(32)	5571(1)	7756(2)	1324(1)	56(1)
C(33)	6075(1)	7232(2)	1152(1)	69(1)
C(34)	6415(1)	8018(2)	994(1)	57(1)
C(35)	6922(1)	7984(3)	798(1)	78(1)
C(36)	7139(1)	8845(4)	674(1)	88(1)
C(37)	6860(1)	9709(3)	743(1)	73(1)
C(38)	6356(1)	9741(2)	936(1)	51(1)
C(39)	6133(1)	8890(2)	1061(1)	41(1)
C(40)	4587(1)	9749(2)	398(1)	44(1)
C(41)	3609(1)	9851(3)	112(1)	86(1)
C(42)	3853(2)	9085(3)	-94(1)	95(1)
C(43)	4265(2)	8410(2)	50(1)	79(1)
C(44)	5211(1)	8327(2)	363(1)	67(1)
C(45)	3974(1)	11191(2)	453(1)	72(1)
C(46)	5378(1)	12165(2)	1123(1)	35(1)
C(47)	5593(1)	12291(2)	828(1)	47(1)
C(48)	5861(1)	13277(2)	788(1)	59(1)
C(49)	5760(1)	13723(2)	1109(1)	44(1)
C(50)	5890(1)	14633(2)	1219(1)	56(1)
C(51)	5755(1)	14857(2)	1533(1)	54(1)
C(52)	5505(1)	14169(2)	1729(1)	48(1)
C(53)	5364(1)	13255(2)	1618(1)	40(1)
C(54)	5489(1)	13043(2)	1304(1)	34(1)
C(55)	6633(1)	10285(2)	1749(1)	50(1)
C(56)	7175(2)	8735(3)	1792(1)	94(1)
C(57)	7622(3)	9205(5)	1518(3)	65(4)
C(57A)	7682(3)	9133(4)	1731(2)	60(2)
C(58)	7640(1)	10102(3)	1482(1)	69(1)
C(59)	7033(1)	11597(2)	1433(1)	79(1)
C(60)	6179(2)	8998(3)	2044(1)	86(1)

V.j. Bond lengths [Å] and angles [°] for ar8.

Li(1)-O(5)	1.903(4)	N(2)-C(14)	1.442(3)
Li(1)-O(2)	1.948(4)	N(2)-C(13)	1.459(3)
Li(1)-O(1)	1.983(4)	N(3)-C(25)	1.363(3)
Li(1)-O(4)	1.992(4)	N(3)-C(26)	1.453(3)
Li(1)-Li(3)	2.652(5)	N(3)-C(30)	1.456(3)
Li(1)-Li(4)	2.711(5)	N(4)-C(25)	1.355(3)
Li(1)-Li(2)	2.736(6)	N(4)-C(29)	1.459(3)
Li(2)-O(6)	1.893(4)	N(4)-C(28)	1.459(3)
Li(2)-O(3)	1.953(4)	N(5)-C(40)	1.353(3)
Li(2)-O(1)	1.984(4)	N(5)-C(45)	1.459(3)
Li(2)-O(2)	2.002(4)	N(5)-C(41)	1.461(4)
Li(2)-Li(4)	2.664(5)	N(6)-C(40)	1.349(3)
Li(2)-Li(3)	2.683(5)	N(6)-C(44)	1.446(3)
Li(3)-O(7)	1.884(4)	N(6)-C(43)	1.456(3)
Li(3)-O(4)	1.922(4)	N(7)-C(55)	1.343(3)
Li(3)-O(2)	1.954(4)	N(7)-C(56)	1.447(4)
Li(3)-O(3)	2.000(4)	N(7)-C(60)	1.456(4)
Li(3)-Li(4)	2.689(5)	N(8)-C(55)	1.354(3)
Li(4)-O(8)	1.901(4)	N(8)-C(59)	1.459(4)
Li(4)-O(1)	1.928(4)	N(8)-C(58)	1.468(3)
Li(4)-O(4)	1.951(4)	C(1)-C(2)	1.338(3)
Li(4)-O(3)	1.979(4)	C(1)-C(9)	1.474(3)
O(1)-C(1)	1.317(3)	C(2)-C(3)	1.515(4)
O(2)-C(16)	1.322(2)	C(3)-C(4)	1.485(4)
O(3)-C(31)	1.314(3)	C(4)-C(9)	1.387(4)
O(4)-C(46)	1.320(2)	C(4)-C(5)	1.402(4)
O(5)-C(10)	1.244(3)	C(5)-C(6)	1.389(5)
O(6)-C(25)	1.243(3)	C(6)-C(7)	1.365(5)
O(7)-C(40)	1.243(3)	C(7)-C(8)	1.386(4)
O(8)-C(55)	1.253(3)	C(8)-C(9)	1.384(4)
N(1)-C(10)	1.343(3)	C(11)-C(12)	1.495(4)
N(1)-C(11)	1.440(3)	C(12)-C(13)	1.501(4)
N(1)-C(15)	1.454(3)	C(16)-C(17)	1.351(3)
N(2)-C(10)	1.360(3)	C(16)-C(24)	1.481(3)

V.j. (cont.) Bond lengths [Å] and angles [°] for ar8.

C(17)-C(18)	1.498(3)	C(56)-C(57)	1.652(9)
C(18)-C(19)	1.504(4)	C(57)-C(58)	1.257(7)
C(19)-C(20)	1.381(4)	C(57A)-C(58)	1.712(9)
C(19)-C(24)	1.392(3)	O(5)-Li(1)-O(2)	130.1(2)
C(20)-C(21)	1.380(4)	O(5)-Li(1)-O(1)	120.8(2)
C(21)-C(22)	1.380(4)	O(2)-Li(1)-O(1)	93.26(18)
C(22)-C(23)	1.384(3)	O(5)-Li(1)-O(4)	118.7(2)
C(23)-C(24)	1.380(3)	O(2)-Li(1)-O(4)	93.51(17)
C(26)-C(27)	1.482(3)	O(1)-Li(1)-O(4)	91.13(16)
C(27)-C(28)	1.505(3)	O(5)-Li(1)-Li(3)	146.2(2)
C(31)-C(32)	1.349(3)	O(2)-Li(1)-Li(3)	47.29(12)
C(31)-C(39)	1.477(3)	O(1)-Li(1)-Li(3)	91.97(17)
C(32)-C(33)	1.511(4)	O(4)-Li(1)-Li(3)	46.25(12)
C(33)-C(34)	1.482(4)	O(5)-Li(1)-Li(4)	137.5(2)
C(34)-C(39)	1.390(3)	O(2)-Li(1)-Li(4)	92.35(17)
C(34)-C(35)	1.391(4)	O(1)-Li(1)-Li(4)	45.30(12)
C(35)-C(36)	1.390(5)	O(4)-Li(1)-Li(4)	45.94(12)
C(36)-C(37)	1.380(5)	Li(3)-Li(1)-Li(4)	60.18(14)
C(37)-C(38)	1.376(4)	O(5)-Li(1)-Li(2)	150.2(2)
C(38)-C(39)	1.385(3)	O(2)-Li(1)-Li(2)	46.99(12)
C(41)-C(42)	1.477(4)	O(1)-Li(1)-Li(2)	46.41(12)
C(42)-C(43)	1.440(4)	O(4)-Li(1)-Li(2)	90.36(16)
C(46)-C(47)	1.346(3)	Li(3)-Li(1)-Li(2)	59.71(14)
C(46)-C(54)	1.463(3)	Li(4)-Li(1)-Li(2)	58.56(13)
C(47)-C(48)	1.500(3)	O(6)-Li(2)-O(3)	124.1(2)
C(48)-C(49)	1.509(3)	O(6)-Li(2)-O(1)	122.3(2)
C(49)-C(50)	1.377(3)	O(3)-Li(2)-O(1)	93.93(17)
C(49)-C(54)	1.390(3)	O(6)-Li(2)-O(2)	122.1(2)
C(50)-C(51)	1.395(3)	O(3)-Li(2)-O(2)	94.42(17)
C(51)-C(52)	1.378(4)	O(1)-Li(2)-O(2)	91.59(18)
C(52)-C(53)	1.389(3)	O(6)-Li(2)-Li(4)	145.2(2)
C(53)-C(54)	1.385(3)	O(3)-Li(2)-Li(4)	47.77(12)
C(56)-C(57A)	1.270(7)	O(1)-Li(2)-Li(4)	46.21(12)

V.j. (cont.) Bond lengths [Å] and angles [°] for ar8.

O(2)-Li(2)-Li(4)	92.54(17)	O(8)-Li(4)-O(1)	124.8(2)
O(6)-Li(2)-Li(3)	146.5(2)	O(8)-Li(4)-O(4)	124.8(2)
O(3)-Li(2)-Li(3)	48.01(12)	O(1)-Li(4)-O(4)	94.04(17)
O(1)-Li(2)-Li(3)	91.03(17)	O(8)-Li(4)-O(3)	117.4(2)
O(2)-Li(2)-Li(3)	46.56(12)	O(1)-Li(4)-O(3)	94.86(17)
Li(4)-Li(2)-Li(3)	60.39(14)	O(4)-Li(4)-O(3)	93.09(17)
O(6)-Li(2)-Li(1)	142.8(2)	O(8)-Li(4)-Li(2)	141.3(2)
O(3)-Li(2)-Li(1)	93.06(17)	O(1)-Li(4)-Li(2)	47.97(13)
O(1)-Li(2)-Li(1)	46.38(12)	O(4)-Li(4)-Li(2)	93.40(17)
O(2)-Li(2)-Li(1)	45.36(12)	O(3)-Li(4)-Li(2)	46.95(12)
Li(4)-Li(2)-Li(1)	60.26(14)	O(8)-Li(4)-Li(3)	143.0(2)
Li(3)-Li(2)-Li(1)	58.59(14)	O(1)-Li(4)-Li(3)	92.08(16)
O(7)-Li(3)-O(4)	122.5(2)	O(4)-Li(4)-Li(3)	45.59(12)
O(7)-Li(3)-O(2)	118.9(2)	O(3)-Li(4)-Li(3)	47.82(12)
O(4)-Li(3)-O(2)	95.54(18)	Li(2)-Li(4)-Li(3)	60.16(14)
O(7)-Li(3)-O(3)	124.8(2)	O(8)-Li(4)-Li(1)	149.4(2)
O(4)-Li(3)-O(3)	93.32(17)	O(1)-Li(4)-Li(1)	46.95(12)
O(2)-Li(3)-O(3)	94.45(17)	O(4)-Li(4)-Li(1)	47.19(12)
O(7)-Li(3)-Li(1)	140.6(2)	O(3)-Li(4)-Li(1)	93.23(16)
O(4)-Li(3)-Li(1)	48.47(12)	Li(2)-Li(4)-Li(1)	61.18(14)
O(2)-Li(3)-Li(1)	47.10(12)	Li(3)-Li(4)-Li(1)	58.82(14)
O(3)-Li(3)-Li(1)	94.52(17)	C(1)-O(1)-Li(4)	134.85(18)
O(7)-Li(3)-Li(2)	143.9(2)	C(1)-O(1)-Li(1)	119.56(17)
O(4)-Li(3)-Li(2)	93.49(17)	Li(4)-O(1)-Li(1)	87.75(17)
O(2)-Li(3)-Li(2)	48.06(12)	C(1)-O(1)-Li(2)	127.24(17)
O(3)-Li(3)-Li(2)	46.53(12)	Li(4)-O(1)-Li(2)	85.82(17)
Li(1)-Li(3)-Li(2)	61.70(15)	Li(1)-O(1)-Li(2)	87.21(17)
O(7)-Li(3)-Li(4)	148.2(2)	C(16)-O(2)-Li(1)	136.74(18)
O(4)-Li(3)-Li(4)	46.48(12)	C(16)-O(2)-Li(3)	128.96(18)
O(2)-Li(3)-Li(4)	92.88(16)	Li(1)-O(2)-Li(3)	85.61(17)
O(3)-Li(3)-Li(4)	47.16(12)	C(16)-O(2)-Li(2)	116.50(17)
Li(1)-Li(3)-Li(4)	61.00(14)	Li(1)-O(2)-Li(2)	87.64(17)
Li(2)-Li(3)-Li(4)	59.46(14)	Li(3)-O(2)-Li(2)	85.38(16)

V.j. (cont.) Bond lengths [Å] and angles [°] for ar8.

C(31)-O(3)-Li(2)	133.20(18)	C(44)-N(6)-C(43)	116.5(2)
C(31)-O(3)-Li(4)	133.46(17)	C(55)-N(7)-C(56)	124.3(3)
Li(2)-O(3)-Li(4)	85.28(17)	C(55)-N(7)-C(60)	117.9(2)
C(31)-O(3)-Li(3)	117.60(17)	C(56)-N(7)-C(60)	116.0(3)
Li(2)-O(3)-Li(3)	85.46(16)	C(55)-N(8)-C(59)	119.1(2)
Li(4)-O(3)-Li(3)	85.02(17)	C(55)-N(8)-C(58)	124.4(3)
C(46)-O(4)-Li(3)	127.46(17)	C(59)-N(8)-C(58)	115.5(2)
C(46)-O(4)-Li(4)	125.96(17)	O(1)-C(1)-C(2)	130.6(2)
Li(3)-O(4)-Li(4)	87.94(17)	O(1)-C(1)-C(9)	120.7(2)
C(46)-O(4)-Li(1)	129.31(17)	C(2)-C(1)-C(9)	108.7(2)
Li(3)-O(4)-Li(1)	85.28(17)	C(1)-C(2)-C(3)	110.5(3)
Li(4)-O(4)-Li(1)	86.86(16)	C(4)-C(3)-C(2)	102.9(2)
C(10)-O(5)-Li(1)	145.06(19)	C(9)-C(4)-C(5)	119.4(3)
C(25)-O(6)-Li(2)	141.3(2)	C(9)-C(4)-C(3)	109.2(2)
C(40)-O(7)-Li(3)	131.45(19)	C(5)-C(4)-C(3)	131.4(3)
C(55)-O(8)-Li(4)	126.5(2)	C(6)-C(5)-C(4)	118.6(3)
C(10)-N(1)-C(11)	122.7(2)	C(7)-C(6)-C(5)	121.5(3)
C(10)-N(1)-C(15)	119.0(2)	C(6)-C(7)-C(8)	120.3(4)
C(11)-N(1)-C(15)	116.4(2)	C(9)-C(8)-C(7)	119.0(3)
C(10)-N(2)-C(14)	119.0(2)	C(8)-C(9)-C(4)	121.1(3)
C(10)-N(2)-C(13)	122.5(2)	C(8)-C(9)-C(1)	130.3(2)
C(14)-N(2)-C(13)	116.4(2)	C(4)-C(9)-C(1)	108.6(3)
C(25)-N(3)-C(26)	122.5(2)	O(5)-C(10)-N(1)	121.4(2)
C(25)-N(3)-C(30)	118.4(2)	O(5)-C(10)-N(2)	119.9(2)
C(26)-N(3)-C(30)	116.5(2)	N(1)-C(10)-N(2)	118.6(2)
C(25)-N(4)-C(29)	118.4(2)	N(1)-C(11)-C(12)	110.9(2)
C(25)-N(4)-C(28)	122.6(2)	C(11)-C(12)-C(13)	109.7(2)
C(29)-N(4)-C(28)	117.04(19)	N(2)-C(13)-C(12)	111.1(2)
C(40)-N(5)-C(45)	119.2(2)	O(2)-C(16)-C(17)	129.8(2)
C(40)-N(5)-C(41)	122.7(3)	O(2)-C(16)-C(24)	121.90(19)
C(45)-N(5)-C(41)	116.8(2)	C(17)-C(16)-C(24)	108.3(2)
C(40)-N(6)-C(44)	118.9(2)	C(16)-C(17)-C(18)	111.1(2)
C(40)-N(6)-C(43)	123.8(2)	C(17)-C(18)-C(19)	103.2(2)

V.j. (cont.) Bond lengths [Å] and angles [°] for ar8.

C(20)-C(19)-C(24)	119.8(3)
C(20)-C(19)-C(18)	131.5(2)
C(24)-C(19)-C(18)	108.7(2)
C(21)-C(20)-C(19)	119.3(3)
C(20)-C(21)-C(22)	120.5(3)
C(21)-C(22)-C(23)	121.0(3)
C(24)-C(23)-C(22)	118.3(2)
C(23)-C(24)-C(19)	121.1(2)
C(23)-C(24)-C(16)	130.1(2)
C(19)-C(24)-C(16)	108.8(2)
O(6)-C(25)-N(4)	120.9(2)
O(6)-C(25)-N(3)	121.1(2)
N(4)-C(25)-N(3)	118.0(2)
N(3)-C(26)-C(27)	109.9(2)
C(26)-C(27)-C(28)	109.5(2)
N(4)-C(28)-C(27)	110.35(19)
O(3)-C(31)-C(32)	129.7(2)
O(3)-C(31)-C(39)	122.1(2)
C(32)-C(31)-C(39)	108.1(2)
C(31)-C(32)-C(33)	110.6(2)
C(34)-C(33)-C(32)	103.3(2)
C(39)-C(34)-C(35)	120.6(3)
C(39)-C(34)-C(33)	109.0(2)
C(35)-C(34)-C(33)	130.4(3)
C(34)-C(35)-C(36)	118.1(3)
C(37)-C(36)-C(35)	121.1(3)
C(38)-C(37)-C(36)	120.8(3)
C(37)-C(38)-C(39)	118.9(3)
C(38)-C(39)-C(34)	120.6(2)
C(38)-C(39)-C(31)	130.4(2)
C(34)-C(39)-C(31)	109.0(2)
O(7)-C(40)-N(6)	120.3(2)
O(7)-C(40)-N(5)	121.0(2)
N(6)-C(40)-N(5)	118.6(2)
N(5)-C(41)-C(42)	110.2(3)
C(43)-C(42)-C(41)	116.5(3)
C(42)-C(43)-N(6)	111.5(3)
O(4)-C(46)-C(47)	129.6(2)
O(4)-C(46)-C(54)	121.63(19)
C(47)-C(46)-C(54)	108.7(2)
C(46)-C(47)-C(48)	111.1(2)
C(47)-C(48)-C(49)	102.5(2)
C(50)-C(49)-C(54)	120.7(2)
C(50)-C(49)-C(48)	130.7(2)
C(54)-C(49)-C(48)	108.6(2)
C(49)-C(50)-C(51)	118.9(2)
C(52)-C(51)-C(50)	120.1(2)
C(51)-C(52)-C(53)	121.3(2)
C(54)-C(53)-C(52)	118.3(2)
C(53)-C(54)-C(49)	120.7(2)
C(53)-C(54)-C(46)	130.4(2)
C(49)-C(54)-C(46)	108.96(19)
O(8)-C(55)-N(7)	121.9(2)
O(8)-C(55)-N(8)	119.6(3)
N(7)-C(55)-N(8)	118.4(2)
C(57A)-C(56)-N(7)	114.1(4)
C(57A)-C(56)-C(57)	33.4(3)
N(7)-C(56)-C(57)	110.4(3)
C(58)-C(57)-C(56)	119.7(6)
C(56)-C(57A)-C(58)	114.8(5)
C(57)-C(58)-N(8)	117.2(4)
C(57)-C(58)-C(57A)	31.4(5)
N(8)-C(58)-C(57A)	106.3(3)

V.l. Anisotropic displacement parameters ($Å^2 x 10^3$) for ar8. The anisotropic displacement factor exponent takes the form: $-2\pi^2[h^2 a^{*2}U^{11} + ... + 2 h k a^* b^* U^{12}]$.

	U^{11}	U^{22}	U^{33}	U^{23}	U^{13}	U^{12}
Li(1)	44(2)	34(2)	50(2)	1(2)	2(2)	-2(2)
Li(2)	40(2)	47(3)	43(2)	6(2)	3(2)	-2(2)
Li(3)	44(2)	40(2)	42(2)	0(2)	-1(2)	-1(2)
Li(4)	38(2)	43(2)	47(2)	-2(2)	0(2)	-4(2)
O(1)	41(1)	45(1)	36(1)	1(1)	5(1)	2(1)
O(2)	34(1)	38(1)	49(1)	-1(1)	-2(1)	-4(1)
O(3)	36(1)	36(1)	45(1)	-2(1)	3(1)	4(1)
O(4)	42(1)	33(1)	41(1)	2(1)	5(1)	-5(1)
O(5)	50(1)	42(1)	76(1)	-3(1)	-2(1)	9(1)
O(6)	48(1)	46(1)	58(1)	11(1)	12(1)	-4(1)
O(7)	53(1)	59(1)	39(1)	-8(1)	-2(1)	-7(1)
O(8)	38(1)	69(1)	68(1)	-17(1)	-7(1)	-1(1)
N(1)	54(1)	49(2)	49(1)	4(1)	-3(1)	16(1)
N(2)	52(1)	49(2)	47(1)	-3(1)	-4(1)	10(1)
N(3)	41(1)	44(1)	61(2)	10(1)	-4(1)	-3(1)
N(4)	41(1)	49(1)	49(1)	11(1)	0(1)	-9(1)
N(5)	54(1)	66(2)	45(1)	5(1)	-5(1)	1(1)
N(6)	62(1)	56(2)	37(1)	-9(1)	0(1)	-4(1)
N(7)	61(1)	70(2)	50(1)	3(1)	-13(1)	0(1)
N(8)	37(1)	61(2)	80(2)	-11(1)	-3(1)	-3(1)
C(1)	57(2)	33(1)	36(2)	4(1)	9(1)	2(1)
C(2)	86(2)	38(2)	44(2)	1(1)	2(2)	-4(1)
C(3)	147(3)	34(2)	45(2)	4(1)	20(2)	5(2)
C(4)	98(2)	35(2)	59(2)	11(1)	32(2)	12(2)
C(5)	131(3)	53(2)	75(2)	26(2)	64(2)	32(2)
C(6)	79(3)	73(3)	134(4)	47(3)	57(3)	29(2)
C(7)	59(2)	63(2)	113(3)	35(2)	35(2)	20(2)
C(8)	50(2)	46(2)	77(2)	17(2)	20(2)	12(1)
C(9)	63(2)	33(2)	55(2)	12(1)	22(1)	9(1)
C(10)	32(1)	46(2)	54(2)	1(2)	-3(1)	10(1)
C(11)	57(2)	65(2)	78(2)	19(2)	-1(2)	5(2)
C(12)	61(2)	44(2)	101(3)	4(2)	-10(2)	8(1)
C(13)	49(2)	58(2)	75(2)	-22(2)	-2(1)	6(1)
C(14)	65(2)	96(2)	53(2)	8(2)	5(1)	19(2)
C(15)	74(2)	99(3)	50(2)	-7(2)	-5(2)	38(2)
C(16)	35(1)	40(2)	39(1)	6(1)	2(1)	-4(1)
C(17)	41(1)	45(2)	63(2)	-2(1)	-1(1)	0(1)
C(18)	40(1)	68(2)	73(2)	2(2)	-9(1)	-8(1)
C(19)	48(2)	54(2)	44(2)	1(1)	0(1)	-12(1)
C(20)	63(2)	65(2)	63(2)	-3(2)	-7(1)	-26(2)
C(21)	87(2)	49(2)	67(2)	-9(2)	9(2)	-22(2)

V.l. (cont.) Anisotropic displacement parameters ($Å^2$x 10^3) for ar8. The anisotropic displacement factor exponent takes the form: $-2\pi^2$[h^2 $a^{*2}U^{11}$ + ... + 2 h k a* b* U^{12}].

	U^{11}	U^{22}	U^{33}	U^{23}	U^{13}	U^{12}
C(22)	73(2)	44(2)	58(2)	1(1)	12(2)	-7(1)
C(23)	53(2)	38(2)	42(1)	5(1)	4(1)	-6(1)
C(24)	39(1)	41(2)	34(1)	4(1)	2(1)	-8(1)
C(25)	42(1)	31(1)	52(2)	6(1)	2(1)	-1(1)
C(26)	63(2)	53(2)	51(2)	5(1)	-4(1)	-2(1)
C(27)	61(2)	61(2)	47(2)	12(1)	5(1)	-4(1)
C(28)	47(1)	58(2)	62(2)	17(1)	9(1)	-5(1)
C(29)	58(2)	66(2)	60(2)	13(2)	-10(1)	-12(1)
C(30)	51(2)	51(2)	97(2)	23(2)	-21(2)	-6(1)
C(31)	36(1)	37(2)	42(1)	-3(1)	-4(1)	2(1)
C(32)	49(2)	39(2)	78(2)	5(1)	-2(1)	3(1)
C(33)	68(2)	44(2)	95(2)	-12(2)	-17(2)	16(2)
C(34)	49(2)	66(2)	56(2)	-12(2)	-7(1)	15(2)
C(35)	57(2)	114(3)	64(2)	-20(2)	-6(2)	35(2)
C(36)	51(2)	159(4)	54(2)	4(2)	9(2)	22(2)
C(37)	44(2)	117(3)	56(2)	26(2)	3(1)	4(2)
C(38)	37(1)	69(2)	48(2)	10(1)	-4(1)	2(1)
C(39)	38(1)	46(2)	38(1)	-3(1)	-7(1)	9(1)
C(40)	49(2)	53(2)	31(1)	3(1)	6(1)	-7(1)
C(41)	66(2)	132(3)	59(2)	12(2)	-14(2)	3(2)
C(42)	80(2)	120(3)	84(3)	-21(2)	-29(2)	2(2)
C(43)	108(3)	81(2)	48(2)	-7(2)	-15(2)	-22(2)
C(44)	74(2)	63(2)	63(2)	-8(2)	9(2)	11(2)
C(45)	84(2)	66(2)	65(2)	12(2)	13(2)	22(2)
C(46)	31(1)	34(1)	40(1)	2(1)	2(1)	-1(1)
C(47)	59(2)	40(2)	42(2)	-5(1)	8(1)	-9(1)
C(48)	73(2)	57(2)	47(2)	6(1)	12(1)	-15(1)
C(49)	44(1)	38(2)	49(2)	-1(1)	5(1)	-8(1)
C(50)	55(2)	44(2)	68(2)	5(2)	5(1)	-12(1)
C(51)	48(2)	46(2)	67(2)	-15(2)	0(1)	-8(1)
C(52)	42(1)	51(2)	50(2)	-12(1)	-1(1)	-3(1)
C(53)	37(1)	42(2)	41(2)	0(1)	0(1)	0(1)
C(54)	29(1)	35(1)	40(1)	2(1)	-2(1)	0(1)
C(55)	37(2)	63(2)	50(2)	-15(2)	-11(1)	-6(1)
C(56)	107(3)	96(3)	78(2)	12(2)	16(2)	51(2)
C(57)	57(4)	51(5)	88(9)	14(4)	42(4)	11(3)
C(58)	50(2)	79(3)	78(2)	-6(2)	-2(1)	20(2)
C(59)	60(2)	54(2)	121(3)	-2(2)	4(2)	-12(2)
C(60)	110(3)	101(3)	47(2)	19(2)	-1(2)	-13(2)

V.m. Hydrogen coordinates (x 10^4) and isotropic displacement parameters ($Å^2$x 10^3) for ar8.

	x	y	z	U(eq)
H(2A)	5181	11326	2347	67
H(3A)	4501	10860	2814	90
H(3B)	4321	11937	2707	90
H(5A)	3145	10947	2886	104
H(6A)	2337	10273	2602	114
H(7A)	2431	9933	2072	94
H(8A)	3359	10179	1813	69
H(11A)	3890	15163	1021	80
H(11B)	4488	15002	1230	80
H(12A)	3301	15409	1466	82
H(12B)	3883	16101	1493	82
H(13A)	4355	15080	1844	73
H(13B)	3674	15228	1971	73
H(14A)	3736	12726	2047	107
H(14B)	3541	13691	2227	107
H(14C)	4246	13453	2173	107
H(15A)	4428	13306	895	112
H(15B)	3776	13670	774	112
H(15C)	3830	12693	973	112
H(17A)	2877	10822	1158	59
H(18A)	2380	9776	736	72
H(18B)	2209	9344	1079	72
H(20A)	2395	7607	678	77
H(21A)	3156	6447	633	81
H(22A)	4142	6785	795	70
H(23A)	4387	8290	1007	53
H(26A)	3604	8584	2654	67
H(26B)	4039	7700	2747	67
H(27A)	3002	7239	2734	67
H(27B)	3404	6625	2490	67
H(28A)	2535	7132	2223	67
H(28B)	2647	8225	2330	67
H(29A)	2694	8488	1675	92
H(29B)	2593	7347	1672	92
H(29C)	3188	7802	1512	92
H(30A)	4908	8398	2106	99
H(30B)	4931	8119	2472	99
H(30C)	4679	9150	2366	99
H(32A)	5271	7455	1451	67
H(33A)	6339	6879	1302	83
H(33B)	5908	6772	996	83
H(35A)	7115	7389	750	94

V.m. (cont.) Hydrogen coordinates (x 10^4) and isotropic displacement parameters ($Å^2$x 10^3) for ar8.

	x	y	z	U(eq)
H(36A)	7486	8838	540	105
H(37A)	7017	10289	656	87
H(38A)	6164	10337	983	62
H(41A)	3422	10361	-18	103
H(41B)	3290	9580	252	103
H(42A)	3505	8721	-182	114
H(42B)	4066	9396	-273	114
H(43A)	4493	8065	-117	95
H(43B)	4029	7928	171	95
H(44A)	5503	8748	471	100
H(44B)	5406	8028	180	100
H(44C)	5073	7825	509	100
H(45A)	3682	11106	625	108
H(45B)	3804	11634	296	108
H(45C)	4354	11458	537	108
H(47A)	5578	11817	666	57
H(48A)	5647	13642	621	70
H(48B)	6300	13242	736	70
H(50A)	6067	15101	1084	67
H(51A)	5836	15484	1612	64
H(52A)	5428	14324	1943	57
H(53A)	5187	12787	1753	48
H(57A)	8042	8986	1563	78
H(57B)	7502	8920	1313	78
H(57C)	7956	8647	1635	72
H(57D)	7869	9345	1932	72
H(59A)	6891	11518	1215	118
H(59B)	7426	11930	1433	118
H(59C)	6736	11977	1552	118
H(60A)	5953	9516	2149	129
H(60B)	6325	8539	2203	129
H(60C)	5911	8666	1894	129

VI. Mathematical Descriptions of Ensembles

Note: The following mathematical descriptions of enolate ensembles are based on an ensemble of hexamers composed of two enantiomers, *R* and *S*, which is archived in the supporting information for McNeil, A. J.; Toombes, G. E. S.; Chandramouli, S. V.; Vanasse, B. J.; Ayers, T. A.; O'Brien, M. K.; Lobkovsky, E.; Gruner, S. M.; Marohn, J. A.; Collum, D. B. *J. Am. Chem. Soc.* **2004**, *126*, 5938. Here *R* and *S* will be replaced with the more general definition *A* and *B*. In addition, X_n that defined the mole fraction of the aggregate with *n* subunits of type *A* will be replaced with relative integration, I_n.

a. Ensembles of Aggregates of the Same Aggregation Number

a.1. General Description

A mixture of two lithium enolates, *A* and *B*, of the same aggregation number, *N*, form an ensemble of aggregates generally described as

$$A_n + B_n \rightarrow A_n + A_{n-1}B_1 + A_{n-2}B_2 + A_{n-3}B_3 + \ldots B_n \qquad (1)$$

where *n* is the number of *A* subunits in the aggregate. The following ensembles are most likely:

$$A_2 + B_2 \rightarrow A_2 + A_1B_1 + B_2$$

$$A_4 + B_4 \rightarrow A_4 + A_3B_1 + A_2B_2 + A_1B_3 + B_4$$

$$A_6 + B_6 \rightarrow A_6 + A_5B_1 + A_4B_2 + A_3B_3 + A_2B_4 + A_1B_5 + B_6$$

In the continuous variation experiment, the ratio of *A* and *B* are varied while keeping the total concentration of the two constant. The relative integrations of each aggregate in the ensemble are measured through integration of the corresponding NMR resonances. The independent variable is the mole fraction of subunits *A*, X_A, and the dependent variables are the relative integrations of each aggregated species, I_n. Thus, I_n is predicted as a function of X_A for a given model.

The mathematical description of the equilibria in the above ensembles begins by considering that each aggregate with *n* subunits of *A* and *N-n* subunits of *B* has a discrete number of permutations or statistically unequal combinations. For example, a tetrameric aggregate A_2B_2 derives from six statistically discrete combinations (Chart 1). Rather than consider each permutation, ρ, individually, a linear combination of the permutations with the same number of *A* subunits, n_ρ, are treated as a single species, A_nB_{N-n} (Chart 1).

Chart 1. A description of the linear combinations of permutations for ensembles of dimers, tetramers or hexamers.

Dimers	**Tetramers**
$A_2 \Rightarrow AA$	$A_4 \Rightarrow AAAA$
$A_1B_1 \Rightarrow AB + BA$	$A_3B_1 \Rightarrow AAAB + AABA + ABAA + BAAA$
$B_2 \Rightarrow BB$	$A_2B_2 \Rightarrow AABB + ABAB + BAAB + BBAA + BABA + ABBA$
	$A_1B_3 \Rightarrow ABBB + BABB + BBAB + BBBA$
	$B_4 \Rightarrow BBBB$

Hexamers
$A_6 \Rightarrow AAAAAA$
$A_5B_1 \Rightarrow AAAAAB + AAAABA + AAABAA + 3\text{ more}$
$A_4B_2 \Rightarrow AAAABB + AAABAB + AABAAB + 12\text{ more}$
$A_3B_3 \Rightarrow AAABBB + AABABB + ABAABB + 17\text{ more}$
$A_2B_4 \Rightarrow AABBBB + ABABBB + BAABBB + 12\text{ more}$
$A_1B_5 \Rightarrow ABBBBB + BABBBB + BBABBB + 3\text{ more}$
$B_6 \Rightarrow BBBBBB$

The concentrations of each group of permutations, $[A_nB_{N-n}]$, are described by the Boltzmann distribution. The concentrations will depend on

1. Multiplicity (M_n) : The number of permutations, ρ, for which $n_\rho = n$ is the number of ways an aggregate of stoichiometry A_nB_{N-n} can be arranged. The numerical value of M_n is determined with Pascal's triangle or binomial theory to achieve the general result

$$M_n = \frac{N!}{(N-n)! \times n!}$$

2. Free Energy (g_ρ) : Each permutation may have a different energy of assembly. In theory, *AABB* may be a less stable permutation than *ABAB*. In practice, positional isomers occur in only hexamers.

3. Chemical Potential (μ_A and μ_B) : The total concentration of *A*, $[A]_{total}$, and of *B*, $[B]_{total}$, will set the chemical potentials and shift the

likelihood of various species. If $[A]_{total}$ increases relative to $[B]_{total}$, for instance, then $[A_3B_1]$ will increase relative to $[A_1B_3]$.

a.2. Mathematical Description

Consider a given permutation, ρ, with n_ρ subunits of type A and N-n_ρ of type B. The Boltzmann distribution gives its equilibrium concentration as

$$[\rho] = C \times \exp\left(\frac{-g_\rho + n_p\mu_A + (N - n_p)\mu_B}{kT}\right)$$

where C is a constant that relates the concentration of the solution to the activity, g_p is the free energy of assembly of ρ, μ_A is the chemical potential of A, and μ_B is the chemical potential of B. For the proposed experiments, all states for which $n_p = n$ are indistinguishable. The linear combination of concentrations of ρ for which $n_p = n$ is given by

$$[A_nB_{N-n}] = \sum_{\rho;n_\rho = n} [\rho] = C \times \exp\left(\frac{n\mu_A + (N - n)\mu_B}{kT}\right) \times \sum_{\rho;n_\rho = n} \exp\left(\frac{-g_\rho}{kT}\right)$$

$$= C \times \exp\left(\frac{n\mu_A + (N - n)\mu_B}{kT}\right) \times M_n \times \left\langle \exp\left(\frac{-g_\rho}{kT}\right)\right\rangle_{\rho;n_\rho = n}$$

where the average free energy is taken over all states for which $n_\rho = n$. For the remainder of the discussion, the effective variables will be defined as

$$a = \exp\left(\frac{\mu_A}{kT}\right) \qquad b = \exp\left(\frac{\mu_B}{kT}\right) \qquad \phi_n = \left\langle \exp\left(\frac{-g_\rho}{kT}\right)\right\rangle_{\rho;n_\rho = n}$$

where $kT\ln\phi_n$ describes the mean free energy of permutations in $[A_nB_{N-n}]$. ϕ_n can be thought of as a measure of the relative stability among the aggregates. Increasing ϕ_n favors $[A_nB_{N-n}]$ as would be expected if those states have a low free energy.[1] Free energies can only be measured relative to the free energy of a reference state; only the relative energies of the aggregates can be measured, not the absolute values.

Substituting the effective variables into the expression for $[A_nB_{N-n}]$ gives

$$[A_nB_{N-n}] = C \times M_n \times \phi_n \times a^n \times b^{N-n} \qquad (2)$$

---

[1] Though this statement may seem counter intuitive at first glance, one should note that the relationship between ϕ_n and g_ρ is exponential.

Using eq 2 to compute [$A_nB_{N\text{-}n}$], the relative integration, I_n is given by

$$I_n = \frac{\left[A_nB_{N-n}\right]}{\sum_{j=0}^{N}\left[A_jB_{N-j}\right]} = \frac{C \times M_n \times \phi_n \times a^n \times b^{N-n}}{\sum_{j=0}^{N} C \times M_j \times \phi_j \times a^j \times b^{N-j}}$$

$$= \frac{C \times M_n \times \phi_n \times \left(\frac{a}{b}\right)^n \times b^N}{\sum_{j=0}^{N} C \times M_j \times \phi_j \times \left(\frac{a}{b}\right)^j \times b^N} = \frac{M_n \times \phi_n \times \left(\frac{a}{b}\right)^n}{\sum_{j=0}^{N} M_j \times \phi_j \times \left(\frac{a}{b}\right)^j}$$

$$= \frac{M_n \times \phi_n \times \exp\left(\frac{n \times (\mu_A - \mu_B)}{kT}\right)}{\sum_{j=0}^{N} M_j \times \phi_j \times \exp\left(\frac{j \times (\mu_A - \mu_B)}{kT}\right)} \tag{3}$$

which is independent of the value C.

Summing the number of *A* subunits in the whole ensemble gives the total number of *A* subunits. Thus, the mole fraction of *A*, X_A, is given by

$$X_A = \frac{[A]_{total}}{[A]_{total} + [B]_{total}} = \frac{\sum_{n=0}^{N} n \times [A_nB_{N-n}]}{\sum_{n=0}^{N} N \times [A_nB_{N-n}]} = \frac{\sum_{n=0}^{N} n \times M_n \times \phi_n \times a^n \times b^{N-n}}{\sum_{n=0}^{N} N \times M_n \times \phi_n \times a^n \times b^{N-n}}$$

$$= \frac{\sum_{n=0}^{N} n \times M_n \times \phi_n \times a^n \times \frac{b^N}{b^n}}{\sum_{n=0}^{N} N \times M_n \times \phi_n \times a^n \times \frac{b^N}{b^n}} = \frac{\sum_{n=0}^{N} n \times M_n \times \phi_n \times \left(\frac{a}{b}\right)^n}{\sum_{n=0}^{N} N \times M_n \times \phi_n \times \left(\frac{a}{b}\right)^n} \tag{4}$$

In general, no simple analytic expression for I_n as a function of X_A and ϕ_n exists. However, the values of X_A and all I_n depend only on the ratio a/b and ϕ_n. Thus, for a given set of ϕ_n and value of X_A, eq 4 uniquely determines a/b because X_A is a strictly monotonic function of a/b and permits I_n and X_A to be evaluated as functions of a/b. This value of a/b can be substituted into eq 3 to calculate the value of any I_n. Functions describing the specific cases of ensembles of dimers, tetramers, or hexamers follow.

The equilibrium mole fractions of different species depends only on the difference in chemical potential between *A* and *B* parameterized by the ratio a/b.

For the purposes of calculation, the average chemical potential of A and B is such that

$$a + b = 1 \leftrightarrow \frac{a}{b} = \frac{a}{1 - a}$$

This assumption restricts the values of a and b to between 0 and 1 and has no effect on any calculated quantity because eqs 3 and 4 depend only on the ratio of a/b.

a.3. Equations for Dimers

Consider an ensemble of dimers

$$A_2,\ AB, \text{ and } B_2$$

where $N = 2$. The total mole fraction of A for an ensemble of dimers is

$$X_A = \frac{\sum_{n=0}^{N} nM_n\phi_n a^n b^{N-n}}{\sum_{n=0}^{N} NM_n\phi_n a^n b^{N-n}} = \frac{2\phi_1 a^1 b^1 + 2\phi_2 a^2}{2\phi_0 b^2 + 4\phi_1 a^1 b^1 + 2\phi_2 a^2}$$

$$= \frac{\phi_1 a^1 b^1 + \phi_2 a^2}{\phi_0 b^2 + 2\phi_1 a^1 b^1 + \phi_2 a^2}$$

where $M_0 = 1$, $M_1 = 2$, and $M_2 = 1$. The experimentally measured I_n are

$$I_0 = \frac{C \times M_n \times \phi_n \times a^n \times b^{N-n}}{\sum_{j=0}^{N} C \times M_j \times \phi_j \times a^j \times b^{N-j}} = \frac{\phi_0 b^2}{\phi_0 b^2 + 2\phi_1 a^1 b^1 + \phi_2 a^2}$$

$$I_1 = \frac{2\phi_1 a^1 b^1}{\phi_0 b^2 + 2\phi_1 a^1 b^1 + \phi_2 a^2}$$

$$I_2 = \frac{\phi_2 a^2}{\phi_0 b^2 + 2\phi_1 a^1 b^1 + \phi_2 a^2}$$

a.4. Equations for Tetramers

For an ensemble of tetramers ($N = 4$)

$$A_4,\ A_3B_1,\ A_2B_2,\ A_1B_3,\ \text{and}\ B_4$$

the total mole fraction of A is

$$X_A = \frac{\sum_{n=0}^{N} nM_n\phi_n a^n b^{N-n}}{\sum_{n=0}^{N} NM_n\phi_n a^n b^{N-n}} = \frac{4\phi_1 a^1 b^3 + 12\phi_2 a^2 b^2 + 12\phi_3 a^3 b^1 + 4\phi_4 a^4}{4\phi_0 b^4 + 16\phi_1 a^1 b^3 + 24\phi_2 a^2 b^2 + 16\phi_3 a^3 b^1 + 4\phi_4 a^4}$$

$$= \frac{\phi_1 a^1 b^3 + 3\phi_2 a^2 b^2 + 3\phi_3 a^3 b^1 + \phi_4 a^4}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

where $M_0 = 1$, $M_1 = 4$, $M_2 = 6$, $M_3 = 4$, $M_4 = 1$. The experimentally measured relative integrations, I_n, are

$$I_0 = \frac{C \times M_n \times \phi_n \times a^n \times b^{N-n}}{\sum_{j=0}^{N} C \times M_j \times \phi_j \times a^j \times b^{N-j}} = \frac{\phi_0 b^4}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

$$I_1 = \frac{4\phi_1 a^1 b^3}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

$$I_2 = \frac{6\phi_2 a^2 b^2}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

$$I_3 = \frac{4\phi_3 a^3 b^1}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

$$I_4 = \frac{\phi_4 a^4}{\phi_0 b^4 + 4\phi_1 a^1 b^3 + 6\phi_2 a^2 b^2 + 4\phi_3 a^3 b^1 + \phi_4 a^4}$$

a.5. Equations for Hexamers

When $N = 6$ as in the case for an ensemble of hexamers

$$A_6, A_5B_1, A_4B_2, A_3B_3, A_2B_4, A_1B_5, \text{ and } B_6$$

the total mole fraction of A is defined as

$$X_A = \frac{\sum_{n=0}^{N} nM_n\phi_n a^n b^{N-n}}{\sum_{n=0}^{N} NM_n\phi_n a^n b^{N-n}}$$

$$X_A = \frac{6\phi_1 a^1 b^5 + 30\phi_2 a^2 b^4 + 60\phi_3 a^3 b^3 + 60\phi_4 a^4 b^2 + 30\phi_5 a^5 b^1 + 6\phi_6 a^6}{6\phi_0 b^6 + 36\phi_1 a^1 b^5 + 90\phi_2 a^2 b^4 + 120\phi_3 a^3 b^3 + 90\phi_4 a^4 b^2 + 36\phi_5 a^5 b^1 + 6\phi_6 a^6}$$

$$= \frac{\phi_1 a^1 b^5 + 5\phi_2 a^2 b^4 + 10\phi_3 a^3 b^3 + 10\phi_4 a^4 b^2 + 5\phi_5 a^5 b^1 + \phi_6 a^6}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

where $M_0 = 1$, $M_1 = 6$, $M_2 = 15$, $M_3 = 20$, $M_4 = 15$, $M_5 = 6$, and $M_6 = 1$. The experimentally measured relative integrations, I_n, are

$$I_0 = \frac{\phi_0 b^6}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_1 = \frac{6\phi_1 a^1 b^5}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_2 = \frac{15\phi_2 a^2 b^4}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_3 = \frac{20\phi_3 a^3 b^3}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_4 = \frac{15\phi_4 a^4 b^2}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_5 = \frac{6\phi_5 a^5 b^1}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

$$I_6 = \frac{\phi_6 a^6}{\phi_0 b^6 + 6\phi_1 a^1 b^5 + 15\phi_2 a^2 b^4 + 20\phi_3 a^3 b^3 + 15\phi_4 a^4 b^2 + 6\phi_5 a^5 b^1 + \phi_6 a^6}$$

a.6. Maximum of I_n as a function of X_A

I_n depends on X_A and has a maximum at a particular value of X_A. When all aggregates in the ensemble have the same aggregation number, the maximum occurs when $X_A = n/N$ as shown by examining eq 3. The maximum value of I_n occurs when the derivative of eq 3 with respect to a/b is zero. The derivative is given by

$$\frac{d(I_n)}{d\left(\frac{a}{b}\right)} = \frac{M_n \times \phi_n \times n \times \left(\frac{a}{b}\right)^{n-1}}{\sum_{j=0}^{N} M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}} - \frac{\left(M_n \times \phi_n \times \left(\frac{a}{b}\right)^{n}\right) \times \sum_{j=0}^{N} M_j \times \phi_j \times j \times \left(\frac{a}{b}\right)^{j-1}}{\left(\sum_{j=0}^{N} M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}\right)^{2}}$$

$$= n \times \left(\frac{a}{b}\right)^{-1} \times \frac{M_n \times \phi_n \times \left(\frac{a}{b}\right)^{n}}{\sum_{j=0}^{N} M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}} - \frac{M_n \times \phi_n \times \left(\frac{a}{b}\right)^{n}}{\sum_{j=0}^{N} M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}} \times N \times \left(\frac{a}{b}\right)^{-1} \times \frac{\sum_{j=0}^{N} j \times M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}}{\sum_{j=0}^{N} N \times M_j \times \phi_j \times \left(\frac{a}{b}\right)^{j}}$$

$$= n \times \left(\frac{a}{b}\right)^{-1} \times I_n - I_n \times N \times \left(\frac{a}{b}\right)^{-1} \times X_A$$

$$= N \times I_n \times \left(\frac{a}{b}\right)^{-1} \times \left(\frac{n}{N} - X_A\right)$$

Setting the derivative equal to zero

$$0 = \frac{d(I_n)}{d\left(\frac{a}{b}\right)} = N \times I_n \times \left(\frac{a}{b}\right)^{-1} \times \left(\frac{n}{N} - X_A\right)$$

the maximum value of I_n occurs when $X_A = n/N$. This derivation requires that all aggregates have the same aggregation number.

b. Ensembles of Aggregates with Different Aggregation Numbers

b.1. General Description

Until this point, ensembles in which all aggregates are of the same aggregation number have been discussed. However, ensembles in which the homoaggregates are of different aggregation numbers could exist. For example, a mixture of subunits A and B could yield an ensemble of monomers and dimers

$$A, B, A_2, AB, \text{ and } B_2$$

or an ensemble of dimers and tetramers

$$A_2, AB, B_2, A_4, A_3B_1, A_2B_2, A_1B_3, \text{ and } B_4$$

Ensembles of these types have yet to be experimentally observed or explored, but they are plausible.

For ensembles of more than one aggregation number, the absolute concentration of the subunits impacts the equilibrium concentration of the various aggregates as a direct result of the equilibrium between the two aggregation states. Consequently, the maximum of the curve for a particular aggregate in the Job plot does not necessarily occur at the stoichiometry of the aggregate (Figure 1). In these ensembles, the position of the maximum depends on both the a/b ratio and the absolute subunit concentration. Conversely, for ensembles of a single aggregation number, the absolute concentration of the subunits affects all aggregates equally and, therefore, does not need to be considered in the mathematical descriptions of the ensembles.

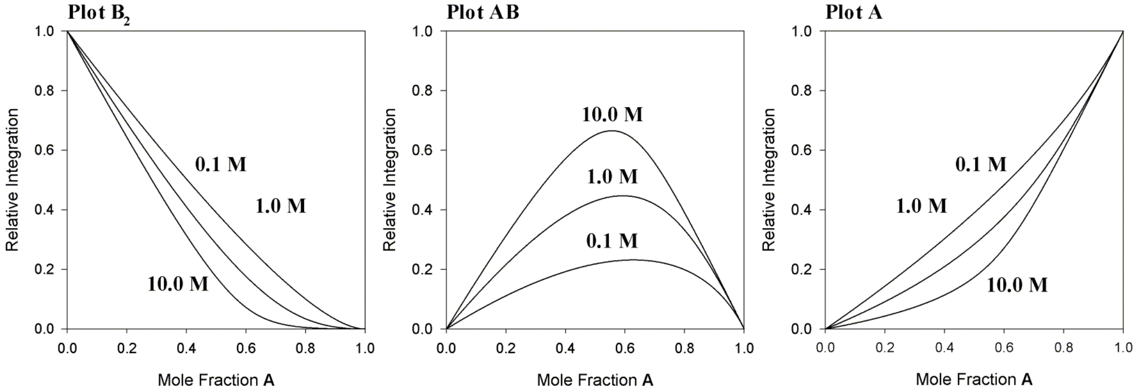


Figure 1. Job plots of a monomer/dimer ensemble of A, AB, and B_2 at different absolute total subunit concentrations.

b.2. Ensemble of Monomers and Dimers

An ensemble of monomers and dimers

$$A,\ B,\ A_2,\ AB, \text{ and } B_2$$

accounts for the simultaneous presence of all aggregates in the ensemble. A discussion of how to apply this general description to a specific ensemble follows.

The effective variables are defined as

$$a = \exp\left(\frac{\mu_A}{kT}\right) \qquad b = \exp\left(\frac{\mu_B}{kT}\right) \qquad \phi_{N_n} = \left\langle \exp\left(\frac{-g_{\rho,N}}{kT}\right)\right\rangle_{\rho;n_\rho = n}$$

where the designation N_n refers to an aggregate of N total subunits with n subunits of type A. The total subunit concentration in the ensemble is

$$[A]_{total} = [A] + 2[A_2] + [AB] \qquad\qquad [B]_{total} = [B] + 2[B_2] + [AB]$$

$$[A]_{total} + [B]_{total} = [A] + [B] + 2[A_2] + 2[AB] + 2[B_2]$$

From eq 2

$$\left[A_n B_{N-n}\right] = C \times M_{N_n} \times \phi_{N_n} \times a^n \times b^{N-n}$$

$$\left[B\right] = C \times \phi_{1_0} \times b$$

$$\left[A\right] = C \times \phi_{1_1} \times a$$

$$\left[B_2\right] = C \times \phi_{2_0} \times b^2$$

$$\left[AB\right] = 2 \times C \times \phi_{2_1} \times a \times b$$

$$\left[A_2\right] = C \times \phi_{2_2} \times a^2$$

By substitution

$$\left[A\right]_{total} + \left[B\right]_{total} = C(\phi_{1_0} b + \phi_{1_1} a) + 2C(\phi_{2_0} b^2 + 2\phi_{2_1} ab + \phi_{2_2} a^2)$$

For ensembles with only one aggregation number, X_A and I_n are uniquely determined by ϕ_n and a/b and are independent of the total subunit concentration. In contrast, the total subunit concentration is important for ensembles with more than one aggregation number, and X_A and I_{Nn} depend on ϕ_{N_n}, a, and b. For convenience, the value of a and b can be expressed as

$$\alpha = \frac{a}{a+b} \qquad \chi = a + b \qquad a = \alpha\chi \qquad b = (1-\alpha)\chi$$

where χ can be thought of as the sum of the activities of *A* and *B*, and α is the proportion of χ resulting from *a*. By substitution

$$[A]_{total} + [B]_{total} = \chi C(\phi_{1_0}(1-\alpha) + \phi_{1_1}\alpha) + \chi^2 C(2\phi_{2_0}(1-\alpha)^2 + 4\phi_{2_1}\alpha(1-\alpha) + 2\phi_{2_2}\alpha^2)$$

$$0 = 2\chi^2 C(\phi_{2_0}(1-\alpha)^2 + 2\phi_{2_1}\alpha(1-\alpha) + \phi_{2_2}\alpha^2) + \chi C(\phi_{1_0}(1-\alpha) + \phi_{1_1}\alpha) - \left([A]_{total} + [B]_{total}\right)$$

$$0 = 2\chi^2 CD_{total} + \chi CM_{total} - \left([A]_{total} + [B]_{total}\right)$$

where,

$$M_{total} = (\phi_{1_0}(1-\alpha) + \phi_{1_1}\alpha) \qquad D_{total} = (\phi_{2_0}(1-\alpha)^2 + 2\phi_{2_1}\alpha(1-\alpha) + \phi_{2_2}\alpha^2)$$

Using the quadratic equation to solve for χ,

$$\chi = \frac{-CM_{total} \pm \sqrt{C^2 M_{total}^2 + 8CD_{total}\left([A]_{total} + [B]_{total}\right)}}{4CD_{total}}$$

$$= \sqrt{\frac{C^2 M_{total}^2}{16C^2 D_{total}^2} + \frac{8CD_{total}\left([A]_{total} + [B]_{total}\right)}{16C^2 D_{total}^2}} - \frac{M_{total}}{4D_{total}}$$

$$= \sqrt{\frac{M_{total}^2}{16D_{total}^2} + \frac{\left([A]_{total} + [B]_{total}\right)}{2CD_{total}}} - \frac{M_{total}}{4D_{total}}$$

$$= \frac{M_{total}}{4D_{total}} \times \left(\sqrt{1 + \frac{8D_{total}\left([A]_{total} + [B]_{total}\right)}{CM_{total}^2}} - 1\right)$$

$$= \frac{M_{total}}{4D_{total}} \times \frac{\left(\sqrt{1 + \frac{8D_{total}\left([A]_{total} + [B]_{total}\right)}{CM_{total}^2}} - 1\right) \times \left(\sqrt{1 + \frac{8D_{total}\left([A]_{total} + [B]_{total}\right)}{CM_{total}^2}} + 1\right)}{\sqrt{1 + \frac{8D_{total}\left([A]_{total} + [B]_{total}\right)}{CM_{total}^2}} + 1}$$

$$= \frac{2\times\left(\left[A\right]_{total}+\left[B\right]_{total}\right)/C}{M_{total}+\sqrt{M_{total}^{2}+8\times D_{total}\left(\left[A\right]_{total}+\left[B\right]_{total}\right)/C}}$$

where only the positive result is accepted because a negative chemical potential is not physically possible. The above equations can be used to describe X_A such that

$$\mathrm{X}_A = \frac{\left[A\right]_{total}}{\left[A\right]_{total}+\left[B\right]_{total}} = \frac{C\left(2\phi_{2_1}\chi^2\alpha(1-\alpha)+\left(2\phi_{2_2}\chi^2\alpha^2\right)+\chi\phi_{1_1}\alpha\right)}{C\left(2\chi^2 D_{total}+\chi M_{total}\right)}$$

$$= \frac{2\phi_{2_1}\chi\alpha(1-\alpha)+\left(2\phi_{2_2}\chi\alpha^2\right)+\phi_{1_1}\alpha}{2\chi D_{total}+M_{total}}$$

The relative integrations of all possible aggregated species are defined as

$$I_{1_n} = \frac{N\left[A_n B_{N-n}\right]}{\left[A\right]_{total}+\left[B\right]_{total}} = \frac{M_n C\chi\phi_{1_n}\alpha^n(1-\alpha)^{1-n}}{2\chi^2 CD_{total}+\chi CM_{total}} = \frac{\phi_{1_n}\alpha^n(1-\alpha)^{1-n}}{2\chi D_{total}+M_{total}}$$

$$I_{1_0} = \frac{\phi_{1_0}(1-\alpha)}{2\chi D_{total}+M_{total}} \qquad I_{1_1} = \frac{\phi_{1_1}\alpha}{2\chi D_{total}+M_{total}}$$

$$I_{2_n} = \frac{N\left[A_n B_{N-n}\right]}{\left[A\right]_{total}+\left[B\right]_{total}} = \frac{2M_n C\chi^2\phi_{2_n}\alpha^n(1-\alpha)^{2-n}}{2\chi^2 CD_{total}+\chi CM_{total}} = \frac{2M_n\chi\phi_{2_n}\alpha^n(1-\alpha)^{2-n}}{2\chi D_{total}+M_{total}}$$

$$I_{2_0} = \frac{2\chi\phi_{2_0}(1-\alpha)^2}{2\chi D_{total}+M_{total}}$$

$$I_{2_1} = \frac{4\chi\phi_{2_1}\alpha(1-\alpha)}{2\chi D_{total}+M_{total}}$$

$$I_{2_2} = \frac{2\chi\phi_{2_2}\alpha^2}{2\chi D_{total}+M_{total}}$$

Although the theoretical monomer/dimer ensemble is

A, B, A_2, AB, and B_2

where all aggregation states are populated, simpler ensembles that are more probable based on known aggregation behaviors include

$$A,\ B \text{ and } AB$$

$$A,\ AB, \text{ and } B_2$$

In these systems, the general derivation above still applies. Missing aggregates are accounted for by assigning the appropriate ϕ_{Nn} as zero, indicating that the corresponding species have no free energies.

b.3. Ensembles of Dimers and Tetramers

The following ensemble of dimers and tetramers

$$A_2,\ AB,\ B_2,\ A_4,\ A_3B_1,\ A_2B_2,\ A_1B_3, \text{ and } B_4$$

includes all possible dimers and tetramers. Such a complex ensemble seems most likely if both subunits form dimer and tetramer homoaggregates when separate. Simpler, perhaps more deceptive to the experimentalist ensembles in which only one homoaggregate is of a different aggregation number are

$$A_4,\ AB, \text{ and } B_2$$

$$A_4,\ A_3B_1,\ A_2B_2,\ A_1B_3, \text{ and } B_2$$

As in the monomer/dimer examples, missing aggregates are accounted for by assigning the corresponding ϕ_{Nn} to zero.

The effective variables remain defined as

$$a = \exp\left(\frac{\mu_A}{kT}\right) \qquad b = \exp\left(\frac{\mu_B}{kT}\right) \qquad \phi_{N_n} = \left\langle \exp\left(\frac{-g_{\rho,N}}{kT}\right)\right\rangle_{\rho;n_\rho = n}$$

where the designation N_n refers to an aggregate of N total subunits with n subunits of type A. To account for the effect of total subunit concentration on the equilibrium concentration of each aggregate in the ensemble

$$[A]_{total} = 2[A_2] + [AB] + 4[A_4] + 3[A_3B_1] + 2[A_2B_2] + [A_1B_3]$$

$$[B]_{total} = 2[B_2] + [AB] + [A_3B_1] + 2[A_2B_2] + 3[A_1B_3] + 4[B_4]$$

$$[A]_{total} + [B]_{total} = 2\big([B_2] + [AB] + [B_2]\big) + 4\big([A_4] + [A_3B_1] + [A_2B_2] + [A_1B_3] + [B_4]\big)$$

From eq 2, the concentration of dimers is given by

$$\left[A_2\right] = C \times \phi_{2_2} \times a^2$$

$$\left[AB\right] = 2 \times C \times \phi_{2_1} \times a \times b$$

$$\left[B_2\right] = C \times \phi_{2_0} \times b^2$$

Similarly, the concentration of the tetramers is given by

$$\left[A_4\right] = C \times \phi_{4_4} \times a^4$$

$$\left[A_3B_1\right] = 4 \times C \times \phi_{4_3} \times a^3 \times b^1$$

$$\left[A_2B_2\right] = 6 \times C \times \phi_{4_2} \times a^2 \times b^2$$

$$\left[A_1B_3\right] = 4 \times C \times \phi_{4_1} \times a^1 \times b^3$$

$$\left[B_4\right] = C \times \phi_{4_0} \times b^4$$

By substitution,

$$\left[A\right]_{total} + \left[B\right]_{total} = 2C(\phi_{2_2}a^2 + 2\phi_{2_1}ab + \phi_{2_0}b^2) + 4C(\phi_{4_4}a^4 + 4\phi_{4_3}a^3b + 6\phi_{4_2}a^2b^2 + 4\phi_{4_1}a^1b^3 + \phi_{4_0}b^4)$$

As described above

$$\alpha = \frac{a}{a+b} \qquad \chi = a + b \qquad a = \alpha\chi \qquad b = (1-\alpha)\chi$$

By substitution

$$\begin{aligned}\left[A\right]_{total} + \left[B\right]_{total} &= 2\chi^2C(\phi_{2_2}\alpha^2 + 2\phi_{2_1}\alpha(1-\alpha) + \phi_{2_0}(1-\alpha)^2) \\ &+4\chi^4C(\phi_{4_4}\alpha^4 + 4\phi_{4_3}\alpha^3(1-\alpha) + 6\phi_{4_2}\alpha^2(1-\alpha)^2 + 4\phi_{4_1}\alpha^1(1-\alpha)^3 + \phi_{4_0}(1-\alpha)^4)\end{aligned}$$

$$\left[A\right]_{total} + \left[B\right]_{total} = 4\chi^4CT_{total} + 2\chi^2CD_{total}$$

$$0 = 4\chi^4CT_{total} + 2\chi^2CD_{total} - \left(\left[A\right]_{total} + \left[B\right]_{total}\right)$$

where

$$D_{total} = \phi_{2_2}\alpha^2 + 2\phi_{2_1}\alpha(1-\alpha) + \phi_{2_0}(1-\alpha)^2$$

$$T_{total} = \phi_{4_4}\alpha^4 + 4\phi_{4_3}\alpha^3(1-\alpha) + 6\phi_{4_2}\alpha^2(1-\alpha)^2 + 4\phi_{4_1}\alpha^1(1-\alpha)^3 + \phi_{4_0}(1-\alpha)^4$$

As the total concentration of subunits increases, χ^2 increases changing the relative concentrations of dimers and tetramers. The relationship is quadratic. Solving for χ^2 by using the quadratic equation gives

$$\chi^2 = \frac{-2CD_{total} \pm \sqrt{4C^2D_{total}^2 + 16CT_{total}\left([A]_{total} + [B]_{total}\right)}}{8CT_{total}}$$

$$= -\frac{D_{total}}{4T_{total}} \pm \sqrt{\frac{4C^2D_{total}^2 + 16CT_{total}\left([A]_{total} + [B]_{total}\right)}{64C^2T_{total}^2}}$$

$$= -\frac{D_{total}}{4T_{total}} \pm \sqrt{\frac{D_{total}^2}{16T_{total}^2} + \frac{\left([A]_{total} + [B]_{total}\right)}{4CT_{total}}}$$

$$= -\frac{D_{total}}{4T_{total}} \pm \frac{D_{total}}{4T_{total}}\sqrt{1 + \frac{16T_{total}^2\left([A]_{total} + [B]_{total}\right)}{4CT_{total}D_{total}^2}}$$

$$= \frac{D_{total}}{4T_{total}}\left(\sqrt{1 + \frac{4T_{total}\left([A]_{total} + [B]_{total}\right)}{CD_{total}^2}} - 1\right)$$

$$= \frac{D_{total}}{4T_{total}} \times \frac{\left(\sqrt{1 + \frac{4T_{total}\left([A]_{total} + [B]_{total}\right)}{CD_{total}^2}} - 1\right) \times \left(\sqrt{1 + \frac{4T_{total}\left([A]_{total} + [B]_{total}\right)}{CD_{total}^2}} + 1\right)}{\sqrt{1 + \frac{4T_{total}\left([A]_{total} + [B]_{total}\right)}{CD_{total}^2}} + 1}$$

$$= \frac{\left([A]_{total} + [B]_{total}\right)/C}{D_{total} + \sqrt{D_{total}^2 + 4 \times T_{total}\left([A]_{total} + [B]_{total}\right)/C}}$$

The above equations can be used to describe X_A,

$$\mathrm{X}_A = \frac{[A]_{total}}{[A]_{total} + [B]_{total}}$$

$$= \frac{2C\phi_{2_1}\chi^2\alpha(1-\alpha) + 2C\phi_{2_2}\chi^2\alpha^2 + 4\chi^4C\phi_{4_1}\alpha^1(1-\alpha)^3 + 12\chi^4C\phi_{4_2}\alpha^2(1-\alpha)^2 + 12\chi^4C\phi_{4_3}\alpha^3(1-\alpha)^1 + 4\chi^4C\phi_{4_4}\alpha^4}{4\chi^4CT_{total} + 2\chi^2CD_{total}}$$

$$= \frac{\phi_{2_1}\alpha(1-\alpha) + \phi_{2_2}\alpha^2 + 2\chi^2\phi_{4_1}\alpha^1(1-\alpha)^3 + 6\chi^2\phi_{4_2}\alpha^2(1-\alpha)^2 + 6\chi^2\phi_{4_3}\alpha^3(1-\alpha)^1 + 2\chi^2\phi_{4_4}\alpha^4}{2\chi^2T_{total} + D_{total}}$$

The relative integrations of the aggregated species are defined as follows

$$I_{2_n} = \frac{N\left[A_n B_{N-n}\right]}{\left[A\right]_{total} + \left[B\right]_{total}} = \frac{2M_n C\chi^2 \phi_{2_n} \alpha^n (1-\alpha)^{2-n}}{4\chi^4 CT_{total} + 2\chi^2 CD_{total}} = \frac{M_n \phi_{2_n} \alpha^n (1-\alpha)^{2-n}}{2\chi^2 T_{total} + D_{total}}$$

$$I_{2_2} = \frac{\phi_{2_2} \alpha^2}{2\chi^2 T_{total} + D_{total}} \qquad I_{2_1} = \frac{2\phi_{2_1} \alpha(1-\alpha)}{2\chi^2 T_{total} + D_{total}} \qquad I_{2_0} = \frac{\phi_{2_0} (1-\alpha)^2}{2\chi^2 T_{total} + D_{total}}$$

$$I_{4_n} = \frac{N\left[A_n B_{N-n}\right]}{\left[A\right]_{total} + \left[B\right]_{total}} = \frac{4M_n C\chi^4 \phi_{4_n} \alpha^n (1-\alpha)^{4-n}}{4\chi^4 CT_{total} + 2\chi^2 CD_{total}} = \frac{2M_n \chi^2 \phi_{4_n} \alpha^n (1-\alpha)^{4-n}}{2\chi^2 T_{total} + D_{total}}$$

$$I_{4_4} = \frac{2\chi^2 \phi_{4_4} \alpha^4}{2\chi^2 T_{total} + D_{total}} \qquad I_{4_3} = \frac{8\chi^2 \phi_{4_3} \alpha^3 (1-\alpha)^1}{2\chi^2 T_{total} + D_{total}} \qquad I_{4_2} = \frac{12\chi^2 \phi_{4_2} \alpha^2 (1-\alpha)^2}{2\chi^2 T_{total} + D_{total}}$$

$$I_{4_1} = \frac{8\chi^2 \phi_{4_1} \alpha^1 (1-\alpha)^3}{2\chi^2 T_{total} + D_{total}} \qquad I_{4_0} = \frac{2\chi^2 \phi_{4_0} (1-\alpha)^4}{2\chi^2 T_{total} + D_{total}}$$

VII. Simulated Ensembles: Influence of Aggregate Stability

Introduction.

We carried out detailed simulations of Job plots hoping to understand: (1) how changes in the relative aggregate stabilities deviate from statistical and influence the appearance of the Job plots; (2) how alternative (more complex) aggregate distributions might masquerade as simpler ensembles; (3) how erroneous models would be detected in an experimental setting. The headings in the following sections are based on the model used to simulate the data. Within these sections we will consider the influence of relative aggregate energies (ϕ), changes in absolute concentrations, and consequences of fitting the data to incorrect models.

a. Ensemble: $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$.

Figure 1 presents curves **I-III** which represent simulated $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data at low (**I**), intermediate (**II**), and high (**III**) relative stability of **AB** (ϕ_1). By definition, any combination of ϕ values results in a plot that exhibits symmetry about the x-axis at $X_\mathbf{A} = 0.5$ and the maximum of the **AB** curve at $X_\mathbf{A} = 0.5$. The appearance of the plot will be independent of the absolute concentrations of the subunits.

One might ask how to rule out alternative models in which one of the homoaggregates (**A** for illustration) is a monomer or tetramer (**A** or $\mathbf{A_4}$, respectively.) Can a least-squares fit to models based on **A**-**AB**-$\mathbf{B_2}$ or $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$ ensembles rule out such a possibility? To explore the ability of least-squares fits to distinguish between the models, theoretical data from $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ at low, intermediate and high values of ϕ_1 were fit to alternative models **A**-**AB**-$\mathbf{B_2}$ and $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$. The choice of absolute concentration is arbitrary and, at best, emblematic. In each case, the goodness of fit was evaluated by the sum of the absolute values of the residuals, the absolute difference between the data and the fit summed over all curves. Of course, fitting the $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data to the correct $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ model would give no residuals.

Figure 2 illustrates $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data (symbols) at low (III), intermediate (I) and high (II) ϕ_1 fit to the **A**-**AB**-$\mathbf{B_2}$ (line) model (derived on pp Sxx-Sxx). In each fit, the maximum of the **AB** curve lies toward the **A** side of the plot. Plot IV shows the sums of the residuals as a function of $X_\mathbf{A}$ for plots I-III. The fit is least able to distinguish between the two models when the **AB** aggregate is at an extreme. The fit to the statistical $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ (Plot I) ensemble is the worst and clearly not the correct model. Ensembles of **A**-**AB**-$\mathbf{B_2}$ are most likely to be misinterpreted as $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ when the mixed aggregate is in either high or low integrations relative to the homoaggregates.

Figure 3 demonstrates the analogous experiment when $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data is fit as $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$. The resulting fits are near mirror images of the fits to **A**-**AB**-$\mathbf{B_2}$. The curve for the **AB** aggregate lies toward the $\mathbf{B_2}$ side of the plot. The statistical $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ most obviously displays the mismatch of the models.

b. Ensemble: A, AB, B_2.

The curves in Figure 4 were generated from a model in which a mixture of a monomer (**A**) and dimer (**B_2**) afford a mixed dimer (**AB**). The curves correspond to varying values of ϕ for dimer **AB**. Unlike the ensemble of pure dimers, the curves lack symmetry about the x-axis at X_A=0.5; the maximum of the **AB** aggregate does *not* appear at X_A=0.5. The curves appear most symmetric when the mixed **AB** aggregate is highly favored and most asymmetric when the relative stability of **AB** is low. Consequently, at high populations of **AB**, a **A-AB-B_2** ensemble could easily masquerade a simpler **A_2-AB-B_2** ensemble. Fits of **A-AB- B_2** theoretical data to **A_2-AB-B_2** produce the inverse of the plots in Figure 2; the lines would be the data, the symbols the fit, and the residuals would remain the same. Pairs of ensembles possess inherent differences that will reveal themselves regardless of which ensemble is the data and which is the model.

Theoretical **A-AB-B_2** fit to the **A_2-AB-B_4** model, however, present an important advisory (Figure 5). The subtle differences between the data and the incorrect model at all values of ϕ suggest difficulty distinguishing these two ensembles by Job plot experiments. The residuals' gradual and continuous decrease as the mole fraction of **A** increases offers the most visual clue to the incongruent fit. As in the previous examples, the mismatched model is most evident when the mixed aggregate has a maximum intensity around 0.5.

c. Ensemble: A_4-A_3B_1-A_2B_2-A_1B_3-B_4.

Figure 6 presents curves **I-III** which represent simulated **A_4-A_3B_1-A_2B_2-A_1B_3-B_4** data at low (**I**), intermediate (**II**), and high (**III**) relative stability of **A_4** (ϕ_4). The intermediate case, which is statistically distributed, is the only example which is symmetric about the x-axis at X_A = 0.5. Deviations from statistical distributions result in asymmetric plots; however, the maxima of the curves remain at the stoichiometry of the aggregate.

When characterizing an ensemble of tetrameric aggregates, one might consider whether the ensemble is actually **A_2-A_3B_1-A_2B_2-A_1B_3-B_4**. Application of the **A_2-A_3B_1-A_2B_2-A_1B_3-B_4** model to the **A_4-A_3B_1-A_2B_2-A_1B_3-B_4** data (Figure 7) affords poor fits. A plot (Plot IV) of the residuals reveals that as the dimeric aggregate increases in stability, the overall goodness of fit decreases.

Conclusion. The subtle complexities associated with the myriad of possible enolate ensembles draws attention to the importance of considering multiple models when assigning aggregation numbers to homoaggregated enolates. Fits of ensembles cannot stand alone as unambiguous aggregation assignments although they are essential. Though they may be technically difficult, control experiments such as varying the absolute lithium concentration and solvent swaps play vital roles by providing corroborating evidence for or against a particular model. Unequivocal enolate aggregation assignments require a conglomeration of supporting evidence.

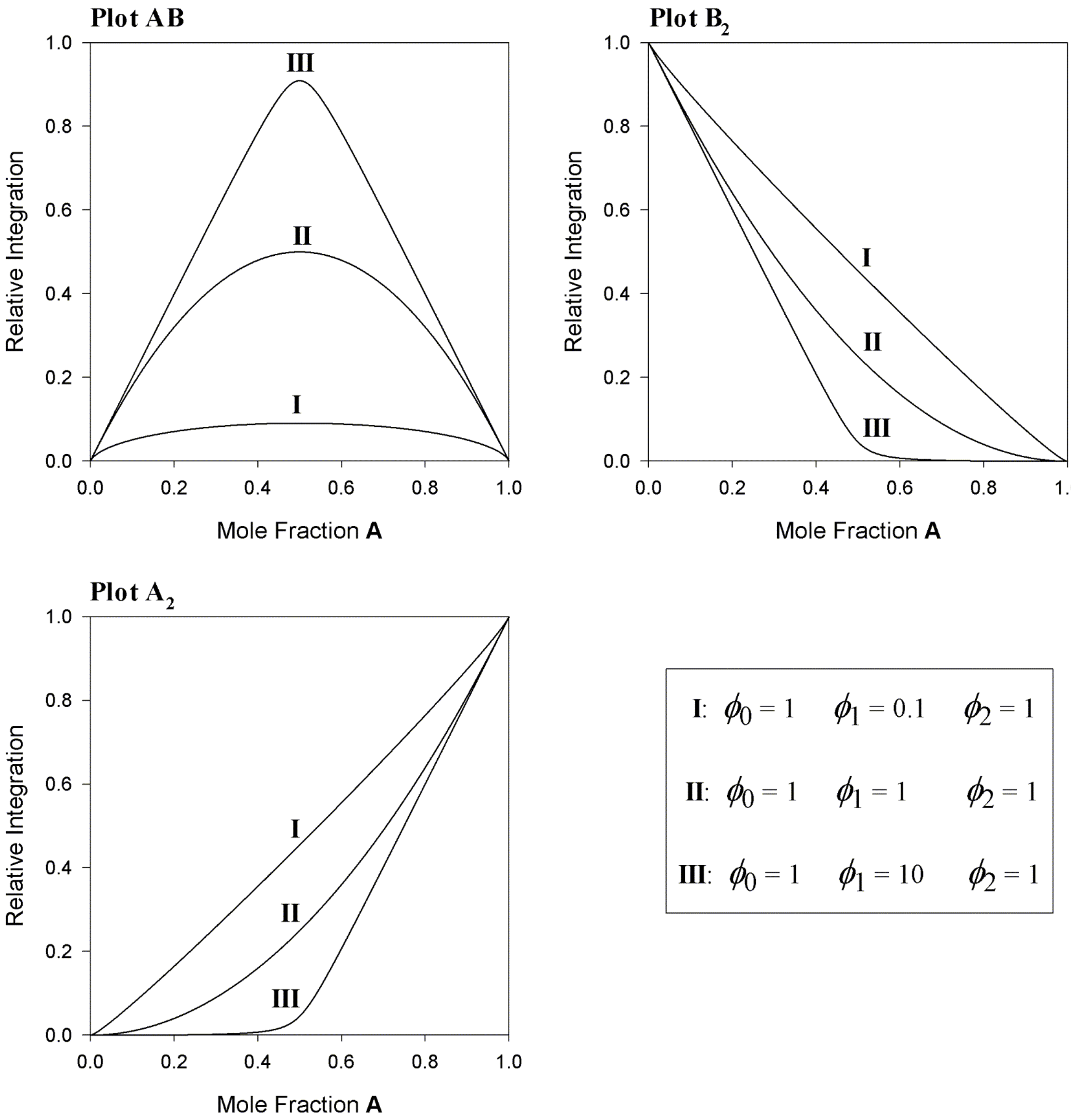


***Figure 1*.** Plots of a dimer ensemble, **A_2-AB-B_2** at low (I), intermediate (II), and high (III) ϕ_1. The curves for each aggregated species are grouped as indicated.

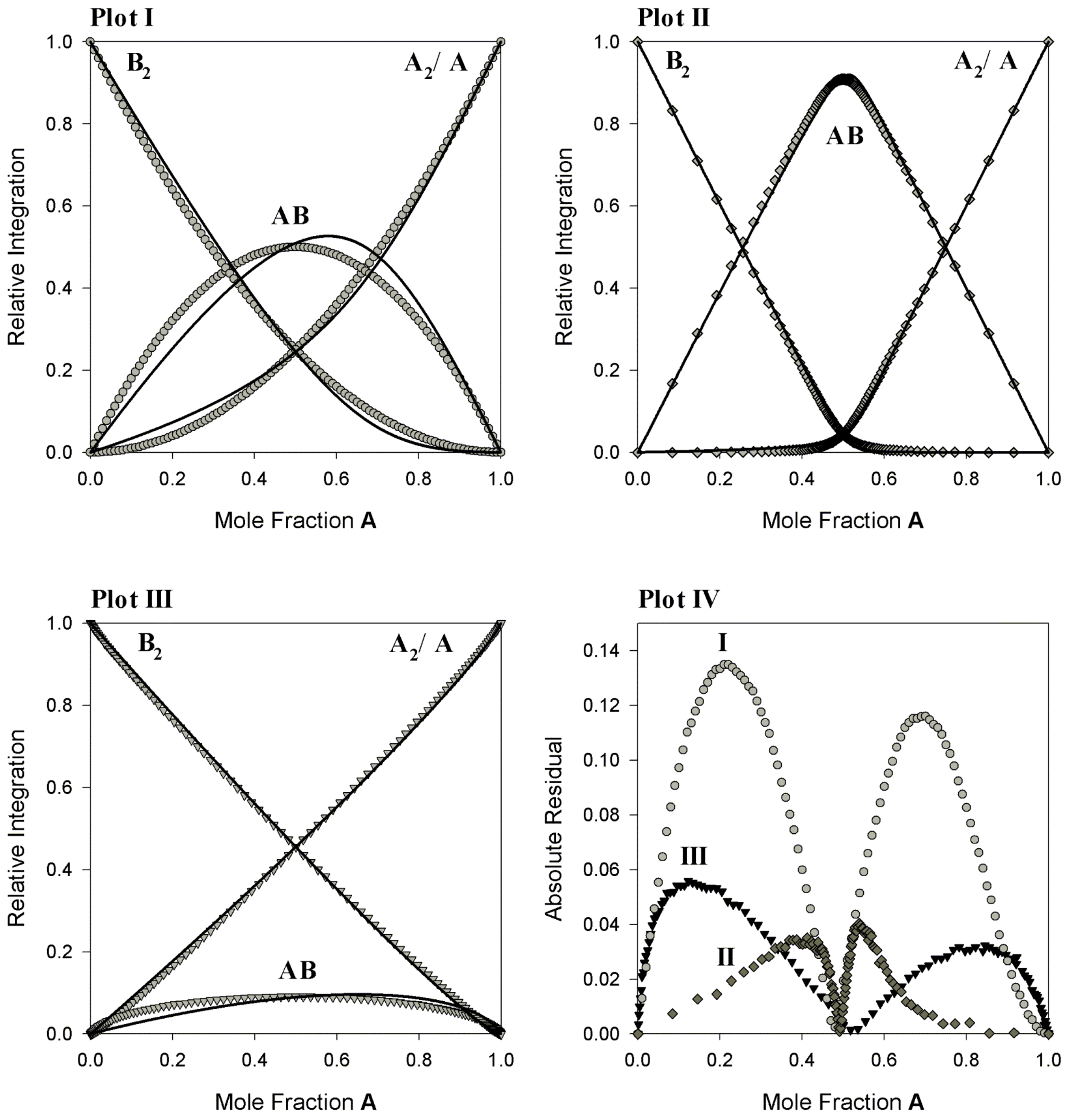


***Figure** 2.* $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data (symbols) at low (III), intermediate (I) and high (II) ϕ_1 fit to the **A**-**AB**-$\mathbf{B_2}$ (line) model. The absolute residual is plotted as a function of mole fraction of **A** in plot IV. Plot I) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_2 = 1$, $\phi_1 = 1$; **A**-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{10} = 0$, $\phi_{11} = 0.542$, $\phi_{20} = 0.549$, $\phi_{21} = 1.886$, $\phi_{22} = 0$, rms = 0.030. Plot II) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_2 = 1$, $\phi_1 = 10$; **A**-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{10} = 0$, $\phi_{11} = 0.167$, $\phi_{20} = 0.177$, $\phi_{21} = 8.088$, $\phi_{22} = 0$, rms = 0.009. Plot III) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_2 = 1$, $\phi_1 = 0.1$; **A**-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{10} = 0$, $\phi_{11} = 1.272$, $\phi_{20} = 1.673$, $\phi_{21} = 0.532$, $\phi_{22} = 0$, rms = 0.011.

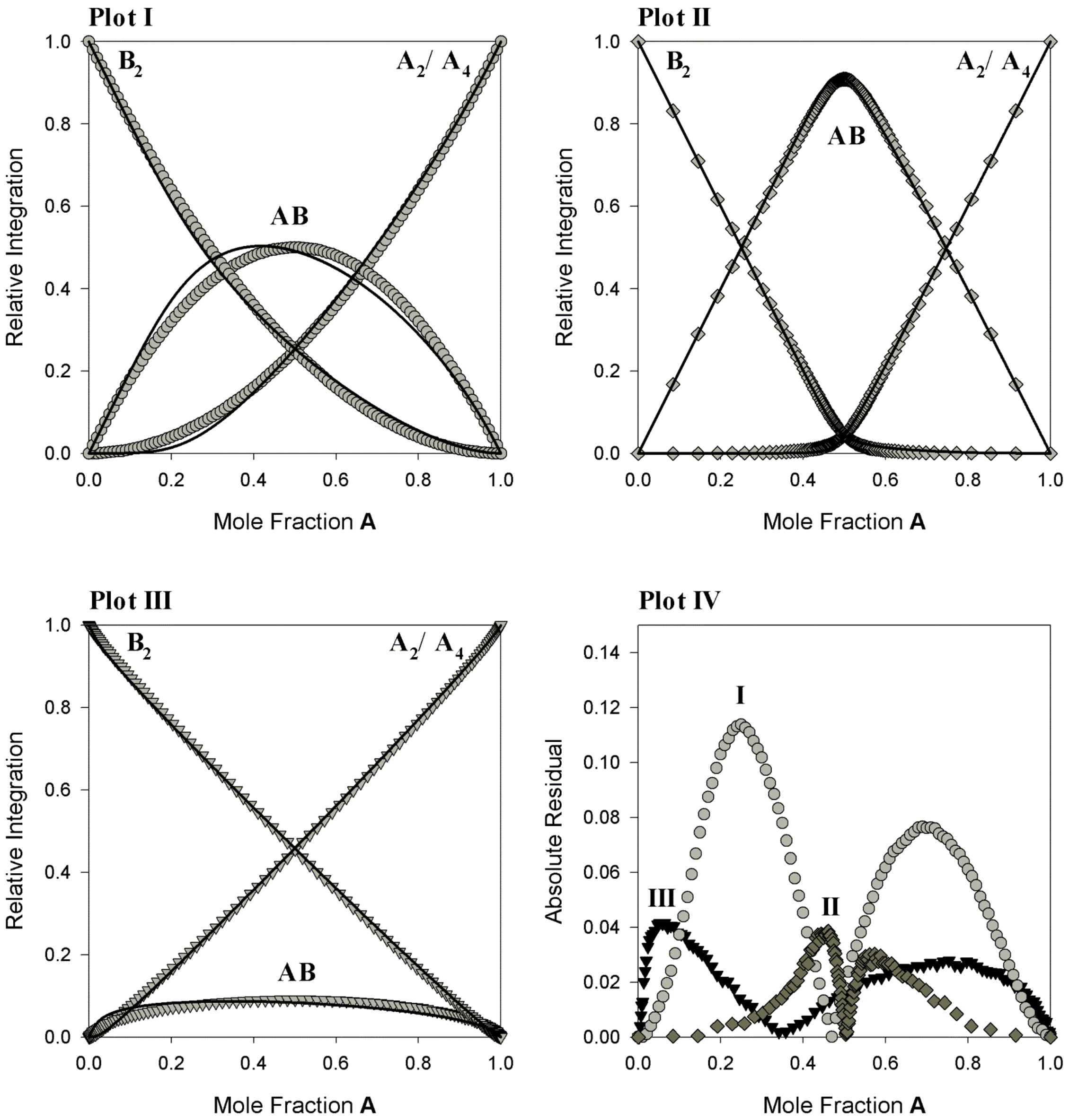


Figure 3. $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$ data (symbols) at low (III), intermediate (I) and high (II) ϕ_1 fit to the $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$ (line) model. The absolute residual is plotted as a function of mole fraction of **A** in plot IV. Plot I) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_1 = \phi_2 = 1$; $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{20} = 1.646$, $\phi_{21} = 0.526$, $\phi_{22} = 0$ $\phi_{40} = \phi_{41} = \phi_{42} = \phi_{43} = 0$, $\phi_{44} = 1.284$, rms = 0.022. Plot II) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_2 = 1$, $\phi_1 = 10$; $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{20} = 0.551$, $\phi_{21} = 1.968$, $\phi_{22} = 0$ $\phi_{40} = \phi_{41} = \phi_{42} = \phi_{43} = 0$, $\phi_{44} = 0.978$, rms = 0.008. Plot III) $\mathbf{A_2}$-**AB**-$\mathbf{B_2}$: $\phi_0 = \phi_2 = 1$, $\phi_1 = 0.1$; $\mathbf{A_4}$-**AB**-$\mathbf{B_2}$ (0.10 M): $\phi_{20} = 7.939$, $\phi_{21} = 0.188$, $\phi_{22} = 0$ $\phi_{40} = \phi_{41} = \phi_{42} = \phi_{43} = 0$, $\phi_{44} = 6.386$, rms = 0.008.

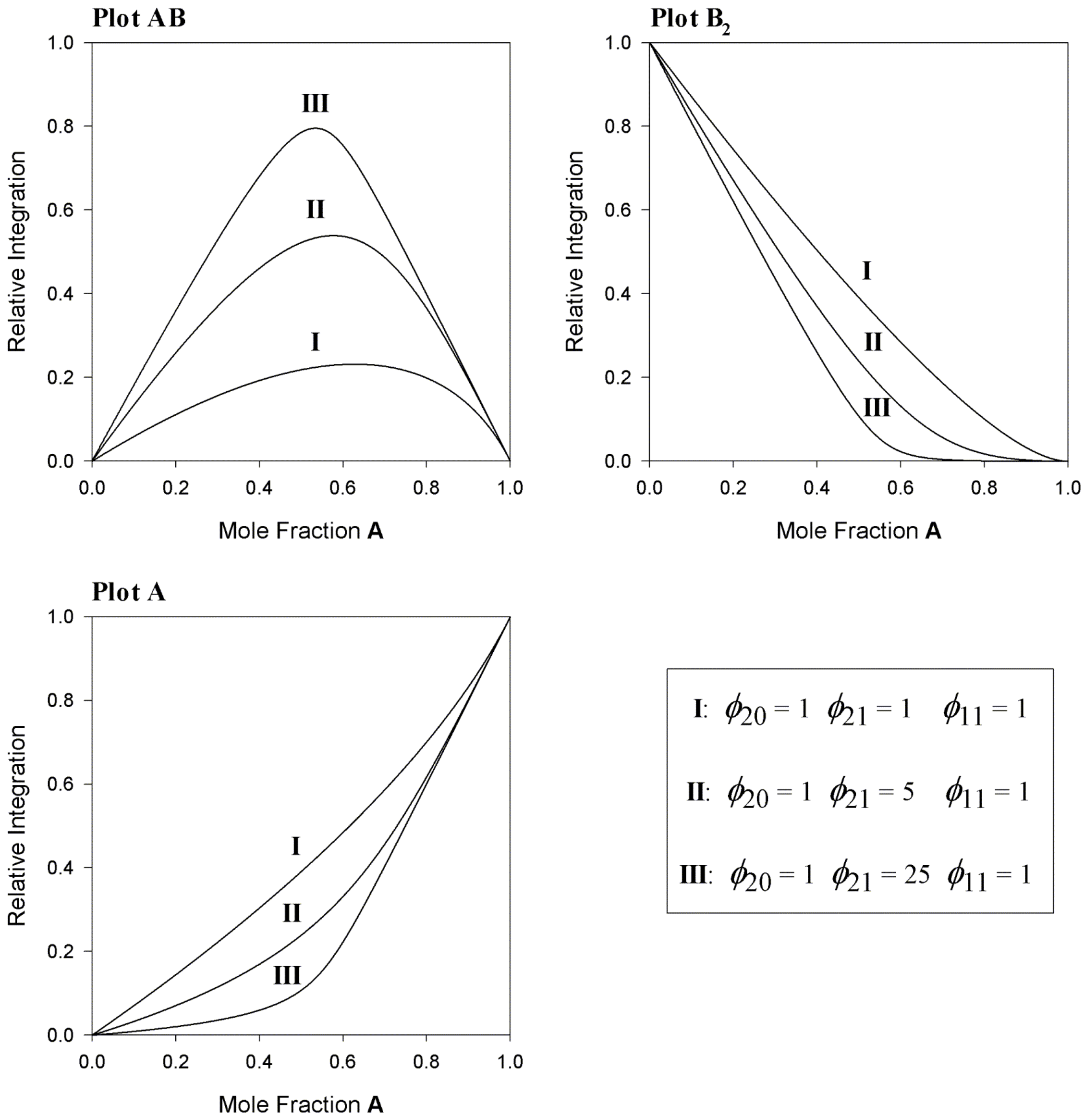


Figure 4. Plots of a monomer-dimer ensemble, **A**-**AB**-**B$_2$** at low (I), intermediate (II), and high (III) ϕ_{21}. The curves for each aggregated species are grouped as indicated.

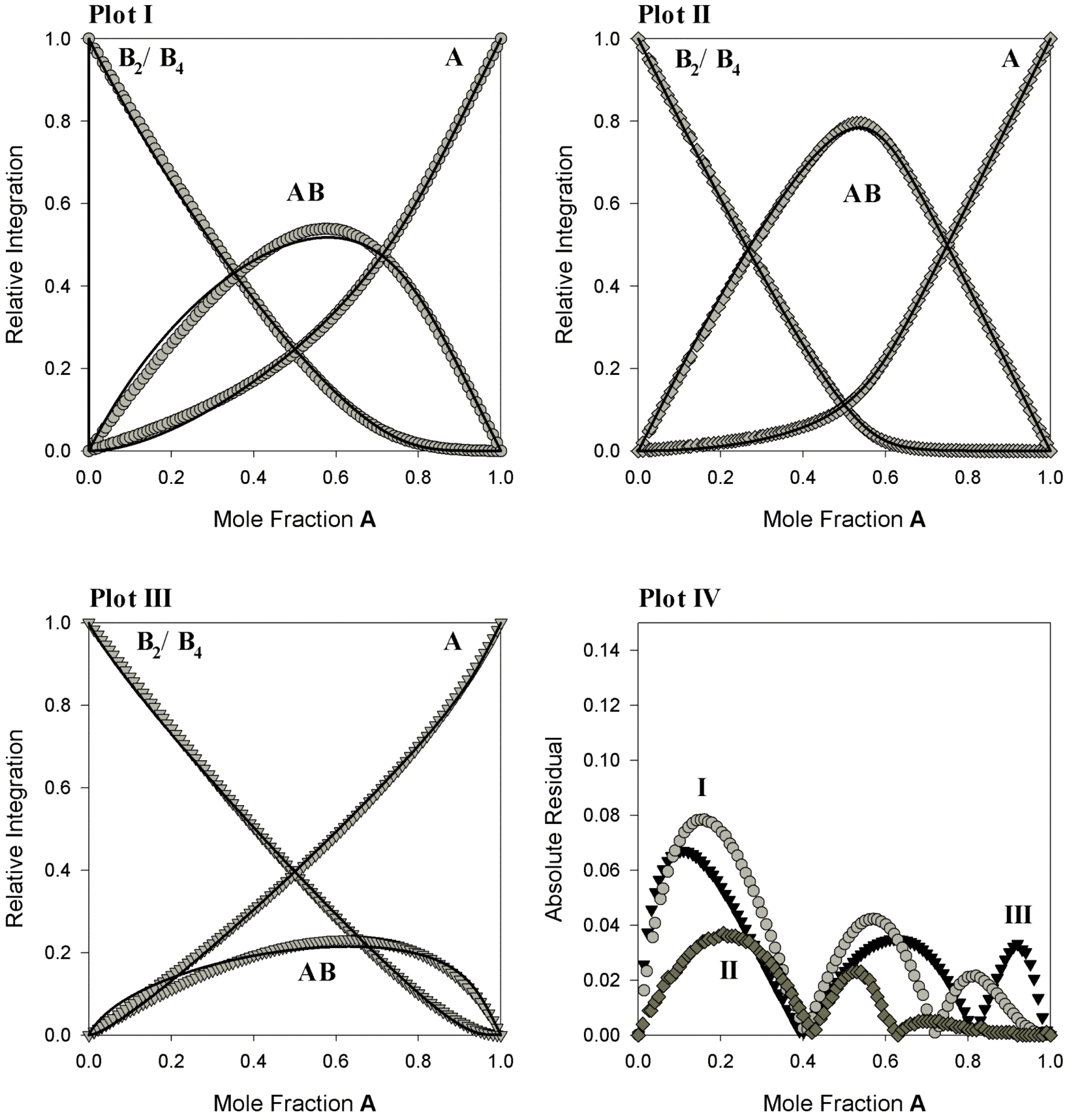


Figure 5. **A-AB-B$_2$** data (symbols) at low (III), intermediate (I) and high (II) ϕ_{21} fit to the **A$_2$-AB-B$_4$** (line) model. The absolute residual is plotted as a function of mole fraction of **A** in plot IV. Plot I) **A$_2$-AB-B$_2$**: $\phi_{20} = \phi_{11} = 1$, $\phi_{21} = 5$; **A$_2$-AB-B$_4$** (0.10 M): $\phi_{20} = 0$, $\phi_{21} = 0.52$, $\phi_{22} = 1.44$ $\phi_{40} = 1.34$; $\phi_{41} = \phi_{42} = \phi_{43} = \phi_{44} = 0$, rms = 0.014. Plot II) **A$_2$-AB-B$_2$**: $\phi_{20} = \phi_{11} = 1$, $\phi_{21} = 25$; **A$_2$-AB-B$_4$** (0.10 M): $\phi_{20} = 0$, $\phi_{21} = 1.11$, $\phi_{22} = 0.97$ $\phi_{40} = 1.01$; $\phi_{41} = \phi_{42} = \phi_{43} = \phi_{44} = 0$, rms = 0.010. Plot III) **A$_2$-AB-B$_2$**: $\phi_{20} = \phi_{11} = 1$, $\phi_{21} = 1$; **A$_2$-AB-B$_4$** (0.10 M): $\phi_{20} = 0$, $\phi_{21} = 0.188$, $\phi_{22} = 1.92$ $\phi_{40} = 1.84$; $\phi_{41} = \phi_{42} = \phi_{43} = \phi_{44} = 0$, rms = 0.012.

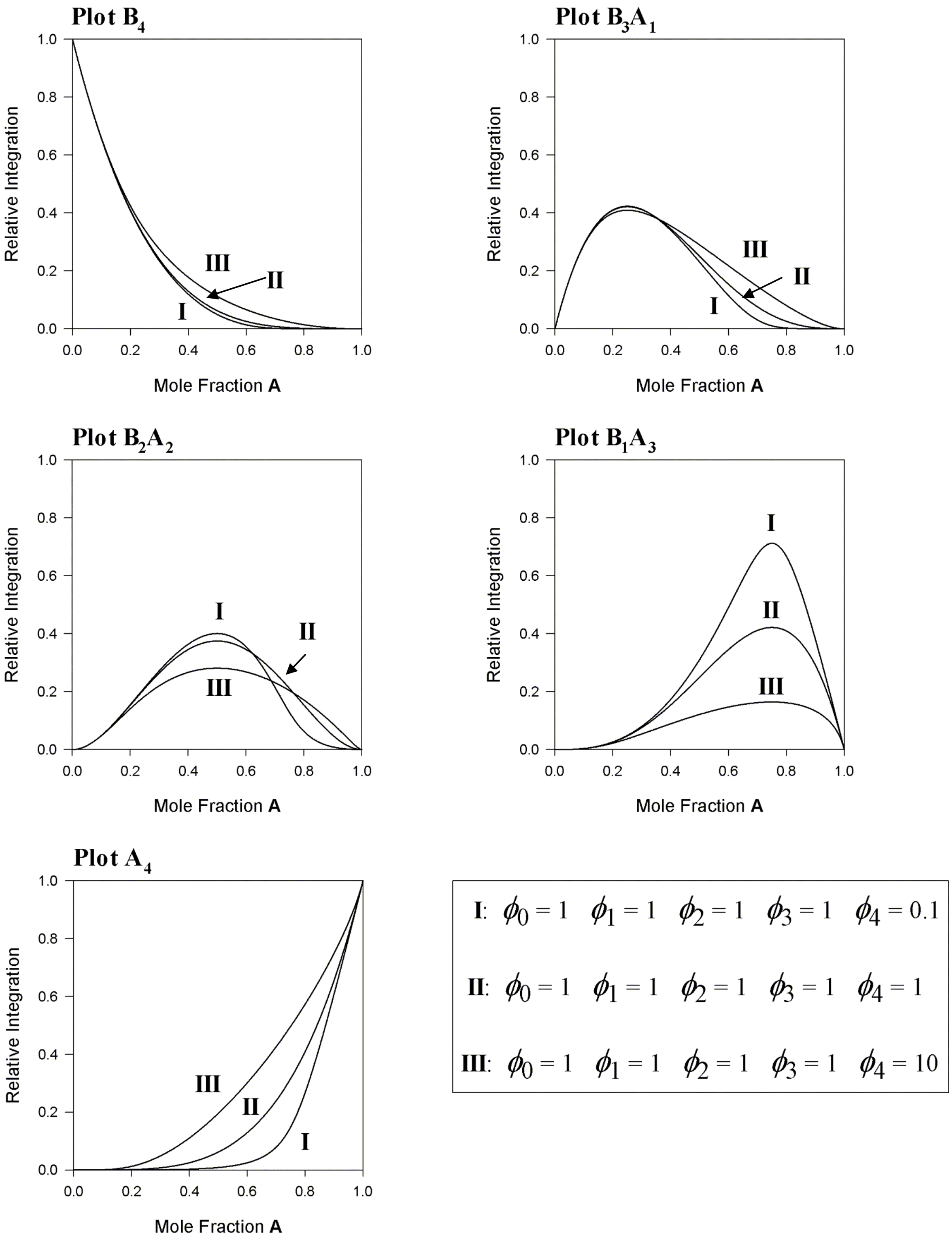


Figure 6. Plots of a tetramer ensemble, $\mathbf{A_4}$-$\mathbf{A_3B_1}$-$\mathbf{A_2B_2}$-$\mathbf{A_1B_3}$-$\mathbf{B_4}$ at low (I), intermediate (II), and high (III) ϕ_4. The curves for each aggregated species are grouped as indicated.

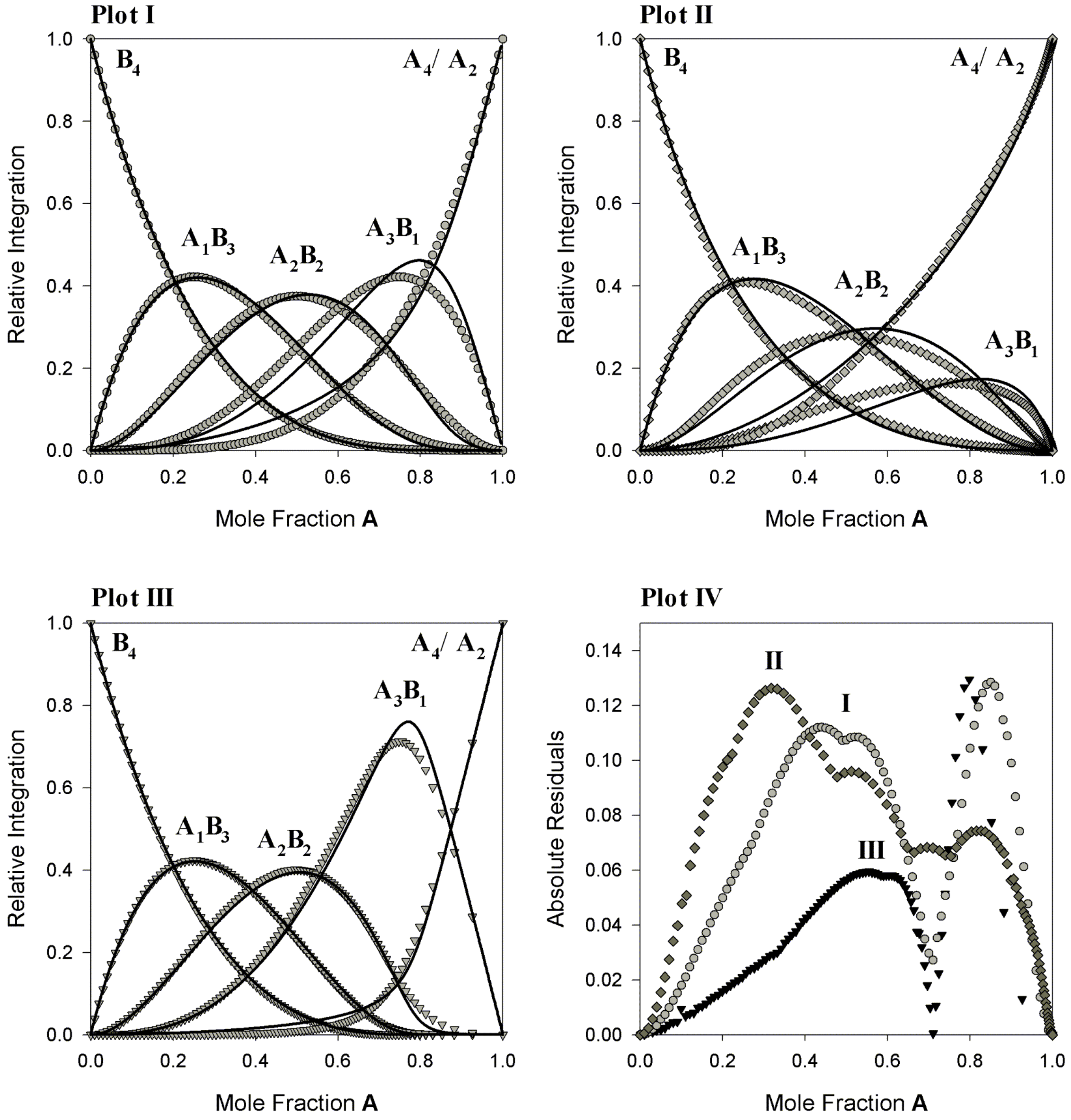


Figure 7. **A_4-A_3B_1-A_2B_2-A_1B_3-B_4** data (symbols) at low (III), intermediate (I) and high (II) ϕ_4 fit to the **A_2-A_3B_1-A_2B_2-A_1B_3-B_4** (line) model. The absolute residual is plotted as a function of mole fraction of **A** in plot IV. Plot I) **A_4-A_3B_1-A_2B_2-A_1B_3-B_4**: $\phi_0 = \phi_1 = \phi_2 = \phi_3 = \phi_4 = 1$; **$A_2$-$A_3B_1$-$A_2B_2$-$A_1B_3$-$B_4$** (0.20 M): $\phi_{20} = \phi_{21} = 0$, $\phi_{22} = 0.207$, $\phi_{40} = 0.932$, $\phi_{41} = 1.026$, $\phi_{42} = 1.098$, $\phi_{43} = 0.959$, $\phi_{44} = 0$, rms = 0.020. Plot II) **A_4-A_3B_1-A_2B_2-A_1B_3-B_4**: $\phi_0 = \phi_1 = \phi_2 = \phi_3 = 1$, $\phi_4 = 10$; **A_2-A_3B_1-A_2B_2-A_1B_3-B_4** (0.20 M): $\phi_{20} = \phi_{21} = 0$, $\phi_{22} = 0.427$, $\phi_{40} = 1.719$, $\phi_{41} = 1.332$, $\phi_{42} = 0.858$, $\phi_{43} = 0.379$, $\phi_{44} = 0$, rms = 0.016. Plot III) **A_4-A_3B_1-A_2B_2-A_1B_3-B_4**: $\phi_0 = \phi_1 = \phi_2 = \phi_3 = 1$, $\phi_4 = 0.1$; **A_2-A_3B_1-A_2B_2-A_1B_3-B_4** (0.20 M): $\phi_{20} = \phi_{21} = 0$, $\phi_{22} = 0.080$, $\phi_{40} = 0.320$, $\phi_{41} = 0.583$, $\phi_{42} = 1.066$, $\phi_{43} = 1.933$, $\phi_{44} = 0$, rms = 0.013.

VIII. Fitting Program Code and Instructions

a. General Description

The data from the Job plot experiments can be fit parametrically to a mathematical model for a specific ensemble. The programs for performing these fits were written for use in MatLab version 7.1. Fitting Job plot data can be achieved without any prior knowledge of programming or use of MatLab by following the directions for the end user (vide infer). Annotated program code is also included. In the program code sections, the primary functions are boxed in by a double line, and the other code is boxed in by a single line so as to be easily distinguished from the annotations. Note that although relative integrations and relative populations are different, here they are used synonymously.

One of three programs fits the experimental data to the model ensemble.

- **Single Aggregate** allows for fits to ensembles composed of a single aggregation state--ensembles of dimers, tetramers, and hexamers. Single aggregate allows constraint of the fit to a symmetric plot for ensembles of dimers or of enantiomers.
- **Monomer_Dimer** allows for fits to ensembles of monomers and dimers.
- **Dimer_Tetramer** allows for fits to ensembles of dimers and tetramers.

The Single_Aggregate functions were extended to allow for fitting data of mixtures of monomers and dimers or mixtures of dimers and tetramers. Note that although the functions share the same or similar names as those used for the Single_Aggregate case, their input and behavior differs. Each program consists of a data file, the experimental result input file, in addition to several other files described below.

- **Try_fit.** The script compares the experimentally measured data against current model parameters by plotting the curves for the model and the experimental data provided in the data file. The script also computes and reports the error between the model and the measurements. The inputs are: 1) XA or Xa 2) phi, phi_monomer, phi_dimer and/or phi_tetramer 3) peak_assignment, peak_assignment_monomer, peak_assignment_dimer, and/or peak_assignment_tetramer 4) Expt_Populations 5) Expt_Errors.

  The outputs are: 1) plot of experimental relative integrations versus XA 2) a plot of the theoretical model according to the phi's provided on the same axis as the experimental data 3) the root mean square difference between theory and experiment. If no errors are given, then all points are weighted equally. If errors are given, then the most precise points are weighted more heavily in the error calculations. For each [A_nB_m], the script computes both the mean error and root mean square error. If the mean error is positive, then the model over-estimates the abundance of [A_nB_m] on average. The root mean square error measures the goodness of the fit.

- **Refine_fit**. The concentration of each species in an ensemble, [A_nB_m], depends on the mole fraction of the subunit **A,** XA(j), and on the relative stability, phi(n+1). This function refines the initial estimate of phi to more closely match the predicted relative integrations to the experimental relative integrations. When the script reaches completion, it reports the new values of phi and the root mean square difference between the predicted and observed populations. The inputs are: 1) XA or Xa 2) phi, phi_monomer, phi_dimer and/or phi_tetramer 3) peak_assignment, peak_assignment_monomer, peak_assignment_dimer, and/or peak_assignment_tetramer 4) Expt_Populations 5) Expt_Errors. The outputs are the refined values of phi, phi_new, phidnew and/or phitnew, and the root mean square error of the new estimate, error. The script Refine_fit_s is used for fitting data from ensembles of a single aggregation state which requires a symmetric plot. Symmetry is required if A and B are enantiomers or if the ensemble is of dimers although the reason is different in each case. The symmetry is achieved in this script by requiring that A_nB_m and A_mB_n have same value of phi. For ensembles which do not have inherent symmetry in the plot, the script refine_fit should be used. The inputs and outputs are the same as in refine_fit.

- **Multimers**. This script computes the concentrations of each species in the ensemble according to the predicted XA(j) and phi's. In this parameterization, the aggregate concentrations are adjusted until the closest XA(j) to the experimental result is obtained. These adjustments in turn determine all the aggregate concentrations. Multimers can be fed multiple values XA(j) and will determine the aggregate concentrations for each value. Parameterizations specific to each fitting program are detailed before the code.

- **Populations**. The concentrations of A_nB_m computed by Multimers are converted by the function in Populations into calculated values for the relative integrations. For each value of XA(j), a set of populations (PP(j,n+1) or Model_populations) is predicted.

- **Error_of_Model**. This script evaluates the fit of the model by comparing each model population to the experimentally measured population, weighted by the accuracy of the measurement.

b. Instructions for the end user

1. Open the program folder and then open the data file.
   Single Aggregate: Data1
   Monomer_Dimer: Data_Monomer_Dimer
   Dimer_Tetramer: Data_Dimer_Tetramer
2. Enter the experimental data as described in the data file. Data may be copied and pasted from Excel or other programs. Save.
3. Open MatLab.
4. Choose the directory where the program is stored from the drop down menu at the top of the workspace.
5. Load the data by entering the name of the data file in the command line.

6. Enter the appropriate Try_fit function for plotting the experimental data and the initial curves removing the Expt_Errors input from the function if no Expt_Errors were entered:
   Single Aggregate: try_fit(XA, phi, peak_assignment, Expt_Populations, Expt_Errors)
   Monomer_Dimer: try_fit(Xa, Ctotal, phi_monomer, peak_assignment_monomer, phi_dimer, peak_assignment_dimer, Expt_Populations, Expt_Errors)
   Dimer_Tetramer: try_fit(Xa, Ctotal, phi_dimer, peak_assignment_dimer, phi_tetramer, peak_assignment_tetramer, Expt_Populations, Expt_Errors)
7. Look at the resulting figure and check that the data points are plotted correctly and that the curves' colors coordinate with the data points' colors. If not, an error in the peak assignment has been made. If a curve is missing, check that the phi's have been input correctly. Entering *whos* in the command line will return information about which parameters the computer has recognized as well as the size of the parameter arrays. If need be, return to the data file and make corrections. Be sure to save, reload the data file, and check the plot again after making the corrections. Enter *clf* in the command line clear the figure.
8. Adjust the initial phi values such that the curves have a reasonable starting point by returning to the data file and entering new values. Be sure to save, reload the data file, and check the plot again. Alternatively, enter *phi = [# # #* etc. *]* in the command line. Use the Try_fit function to check how close the curves are to the data.
9. Enter the function for performing the fit found in the Refine_fit or Refine_fit_s script. If no Expt_Errors were entered, remove the Expt_Errors term from the refine_fit input.
   Single Aggregate: [phi_new, error] = refine_fit(XA, phi, peak_assignment, Expt_Populations, Expt_Errors)
   Single Aggregate symmetric: [phi_new, error] = refine_fit_s(XA, phi, peak_assignment, Expt_Populations, Expt_Errors)
   Monomer_Dimer: try_fit(Xa, Ctotal, phi_monomer, peak_assignment_monomer, phi_dimer, peak_assignment_dimer, Expt_Populations, Expt_Errors)
   Dimer_Tetramer: try_fit(Xa, Ctotal, phi_dimer, peak_assignment_dimer, phi_tetramer, peak_assignment_tetramer, Expt_Populations, Expt_Errors)
10. If the fit stalls, press ctrl+c to abort the fit. A list of where the error occurred will be returned. For fitting ensembles of monomers and dimers or dimers and tetramers, a stalled fit likely indicates the need to set and fix one of the phi's for missing aggregates to 0.00001. The output provides the optimized phi's and the error (root mean square of the weighted sum of squares of the residuals).
11. Replace the initial phi values with the optimized values by entering in the command line: *phi = phi_new* for the single aggregate fit, *phi_monomer = phi_monomer_new* and *phi_dimer = phi_dimer_new* for the monomer_dimer fit, and *phi_dimer = phi_dimer_new* and *phi_tetramer = phi_tetramer_new* for the dimer_tetramer fit.

12. Observe the optimized fit using the try_fit function.
13. Better fits may be obtained using different start values if a local minimum was obtained.

c. Definitions

1. **XA(j)** is the mole fraction of **A** for a set of relative integrations.
2. **Ctotal** is the absolute subunit concentration and is only used in the Monomer_Dimer and Dimer_Tetramer fits.
3. **Expt_Populations** are the relative integrations of the observed aggregates with a range of (j,k) -> k-th NMR peak.
4. **Expt_Errors** is the experimental error in Expt_Populations(j,k) and is an optional input. In the Try_fit script, Expt_Errors are the size of the error bars.
5. **peak_assignment**, **peak_assignment_monomer**, **peak_assignment_dimer**, and **peak_assignment_tetramer** assign each column of Expt_Populations to a specific aggregate. The program expects aggregates to be ordered by increasing number of A subunits.
6. **phi**, **phi_monomer**, **phi_dimer**, and **phi_tetramer** are a measure of the relative stability of the aggregate and is related to the free energy of the species by *kT*ln phi. Phi's must be positive integers and have N+1 values for an ensemble consisting of species with N total subunits. The program expects phi's to be listed in the order of increasing **A** subunit as it is in peak_assignment. Phi_monomer, phi_dimer, and phi_tetramer are used in the monomer_dimer and dimer_tetramer fits.
7. **phi_constant** allows some values of phi to be fixed in the monomer_dimer and dimer_tetramer programs and has the same length as the total number of phi's.
8. **Expt_weights(j,k)** are the amount each experimental data point contributes to the error in the fit. It is calculated by 1. /(Expt_Errors + mean(mean(Expt_Errors))). If no Expt_Errors are entered, all points are weighted equally.
9. **Concentrations**, is the set of concentrations for each aggregate in the ensemble, [A_nB_m]. **Concentration_monomer(j,n+1)**, **Concentration_dimer(j, n+1)**, and **Concentration_tetramer (j, n+1)** are the concentrations of the monomer, dimer and tetramer aggregates in the Monomer_Dimer and Dimer_Tetramer fits.
10. **PP** and **Model_Populations** are the calculated relative populations/integrations for the model of the ensemble.
11. **mean_error** is the root mean square difference in the weighted sum of squares of the residuals over the entire fit.
12. **pop_error(1,j)** is the mean of population j - mean of model value for population j. For example, pop_error(1,1) is the mean amount the prediction of [A_0B_N] misses the measured amount. The value could be negative, zero, or positive.
13. **pop_error(2,j)** is the root mean square error for population j. For example, pop_error(2,1) is the root square amount the prediction of [A_0B_N] missed by. Its value is always positive.
14. **phi_new**, **phidnew**, and **phitnew** are the refined values of phi.

15. **error** is the root mean square error of new estimate.

d. Single Aggregate Fitting Code

d.1. Single Aggregate--Data1

XA(j). The mole fractions are listed in terms of **A** such that the first mole fraction corresponds to the first row of Expt_Populations.

```
XA = [0.000   0.084   0.145   etc.];
```

Expt_Populations are input as a column of data for each aggregate. If an aggregate has two resonances, they should be summed and entered as a single relative integration. Recall that each row must end with a semi-colon.

```
Expt_Populations =[0.000   0.000   1.000   ;
0.000   0.168   0.832   ;
0.000   0.290   0.710   ;
etc.;];
```

Expt_Errors are input as an array the same size as Expt_Populations. Each column and row should correspond to the row and column of Expt_Populations. Expt_Errors is optional and should be left as "Expt_Errors = [;];" if none are provided.

```
Expt_Errors = [ ;];
```

peak_assignment. The program expects the peaks to be listed in the order of increasing **A** subunit as shown below:

Hexamers: peak_assignment = [$[A_0B_6]$ $[A_1B_5]$ $[A_2B_4]$ $[A_3B_3]$ $[A_4B_2]$ $[A_5B_1]$ $[A_6B_0]$]
Tetramers: peak_assignment = [$[A_0B_4]$ $[A_1B_3]$ $[A_2B_2]$ $[A_3B_1]$ $[A_4B_0]$]
Dimers: peak_assignment = [$[A_0B_2]$ $[A_1B_1]$ $[A_2B_0]$]

The column number of the corresponding relative integration is input in the order designated above. If an aggregate was not observed, it should be assigned to column 1. Its absence will be accounted for in phi. For example, if the populations are listed in the order: $[A_2B_2]$ $[A_3B_1]$ $[A_1B_3]$ $[A_0B_4]$ $[A_4B_0]$, then peak_assignment = [4 3 1 2 5]. If a relative integration is a sum of two unresolved resonances, enter the same column for each aggregate contributing to the resonance.

```
peak_assignment = [ 3 2 1 ];
```

phi is listed in the order of increasing **A** subunit as it is in peak_assignment. The phi's provided here will be the start value for the fit. If an aggregate was not observed, it should be assigned a phi value of 0.

```
phi = [ 1  1  1];
```

d.2. Single Aggregate—Try Fit

```
function try_fit(XA, phi, peak_assignment, Expt_Populations, Expt_Errors
```

Code for weighting the Expt_Populations. If no Expt_Errors are entered, all points are weighted equally.

```
   if (nargin<5)
            Expt_weights=ones(size(Expt_Populations));
   else
            Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
   end
```

Code for plotting the experimental data.

```
     hold on ; cscheme='bgrmkcybgrmkcy'; axis([0 1 0 1]); xlabel('X_A');
ylabel('Mole Fractions');
     for j=1:size(Expt_Populations,2)
          if (nargin<5)
             plot(XA, Expt_Populations(:,j),sprintf('%so',cscheme(j)));
          else
             errorbar(XA, Expt_Populations(:,j),
Expt_Errors(:,j),sprintf('%so',cscheme(j)));
          end
     end
```

Code for plotting the model with the provided phi's.

```
     XAc = [0:0.01:1]; TP=Populations(multimers(XAc,phi), peak_assignment);
     for j=1:size(TP,2)
        plot(XAc,TP(:,j),sprintf('%c',cscheme(j)) );
     end
```

Code for computing and reporting the error.

```
   [mean_error, pop_error] = Error_of_Model(XA, phi, peak_assignment,
Expt_Populations, Expt_weights);
   N = length(phi)-1;
          fprintf(1,'\nThe Mean mismatch is %f percent.\n', mean_error*100);
          for j=1:size(pop_error,2)
          fprintf(1,'Predicted value of species A%dB%d +A%dB%d exceeds
measurement by %f percent and mean square error of %f percent.\n ',j-1,N-
j+1,N-j+1,j-1,pop_error(1,j)*100,pop_error(2,j)*100);
          end
```

d.3. Single Aggregate—Refine_fit

```
function [phi_new, error] = refine_fit(XA, phi, peak_assignment,
Expt_Populations, Expt_Errors)
```

If no Expt_Errors are entered, all points are weighted equally.

```
if (nargin<5)
    Expt_weights = ones(size(Expt_Populations));
else
            Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
 end
```

Set-up the parameters.

```
N = length(phi)-1;
param = [ 2:(N+1)];
```

The initial step size for improving the model is 10%.

```
step_size = 0.1*phi(param),
```

Initialize the search.

```
N_no_progress = 0;
N_max_trials = 30;
```

Compute and report the initial quality of the fit.

```
[error_best, temp] = Error_of_Model(XA,phi, peak_assignment,
Expt_Populations) ;
fprintf(1,'\n Initial Error of Fit = %f percent.\n', error_best * 100);
```

Iteratively try to improve fit by changing each parameter in turn.

```
while (N_no_progress < N_max_trials)
    flag = 0;
   for k=1:length(param)
```

Step to the right and to the left.

```
         phi_testr = phi;
         phi_testr(param(k))=abs(phi(param(k)) + step_size(k));
```

```
        [error_testr, temp] = Error_of_Model(XA,phi_testr, peak_assignment,
Expt_Populations, Expt_weights);
        phi_testl = phi;
        phi_testl(param(k))=abs(phi(param(k)) - step_size(k));
        [error_testl, temp] = Error_of_Model(XA,phi_testl,
peak_assignment,Expt_Populations, Expt_weights);
```

Decide if a step should be taken. If the step is positive, continue that direction. If the negative step is better, continue that way. If no improvement occurs, flag that step and begin reducing the step size. N_no_progress is the number of steps since the error last improved. N_max_trials is the number of iterations to perform without the error getting better before ending the script. It is set to 30.

```
      if (error_testr<error_best)
           error_best=error_testr; phi=phi_testr; step_size(k) = step_size(k) * 1.5;
           N_no_progress=0;
      elseif    (error_testl <error_best)
           error_best=error_testl; phi=phi_testl; step_size(k) = step_size(k) * 1.5;
           N_no_progress=0;
      else
         flag = flag + 1;
      end
   end
   if (flag>2)
      step_size = step_size * (0.75 + 0.25*rand);
      N_no_progress=N_no_progress+1;
   end
```

After adjusting each element of rel_weight, report the new fit.

```
   fprintf(1,'\nError - %f , Last Good Step - %d , Mean Step Size - %f \n
',error_best, N_no_progress, 100*mean(step_size./phi(param)));
   fprintf(1,' Phi - %f',phi);
   end
   error=error_best;
   phi_new = phi;
```

d.4. Single Aggregate—Refine_fit_s

```
function [phi_new, error] = refine_fit_s(XA,phi, peak_assignment,
Expt_Populations, Expt_Errors)
```

If no Expt_Errors are entered, all points are weighted equally.

```
if (nargin<5)
    Expt_weights = ones(size(Expt_Populations));
```

```
else
     Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
 end
```

Because some phi's are equivalent in a symmetric plot and the model is unchanged by multiplication, only some of the parameters need to be adjusted. Here the program is told which parameters to adjust.

```
N = length(phi)-1;
param = [ 1:ceil(N/2)];
```

The initial step size for improving the model is 10%.

```
step_size = 0.1*phi(param),
```

Initialize the search.

```
N_no_progress = 0;
N_max_trials = 30;
```

Compute and report the initial quality of the fit.

```
[error_best, temp] = Error_of_Model(XA,phi, peak_assignment,
Expt_Populations, Expt_weights) ;
fprintf(1,'\n Initial Error of Fit = %f percent.\n', error_best * 100);
```

Iteratively try to improve fit by changing each parameter in turn.

```
while (N_no_progress < N_max_trials)
   flag = 0;
   for k=1:length(param) % Try tweaking each parameter in turn.
```

Step to the right and to the left.

```
            phi_testr = phi;
            phi_testr(param(k))=abs(phi(param(k)) + step_size(k));
            phi_testr(N+2-param(k))=phi_testr(param(k));
            [error_testr, temp] = Error_of_Model(XA,phi_testr, peak_assignment,
Expt_Populations, Expt_weights);
            phi_testl = phi;
            phi_testl(param(k))=abs(phi(param(k)) - step_size(k));
            phi_testl(N+2-param(k))=phi_testl(param(k));
            [error_testl, temp] = Error_of_Model(XA,phi_testl,
peak_assignment,Expt_Populations, Expt_weights);
```

Decide if a step should be taken. If the step is positive, continue that direction. If the negative step is better, continue that way. If no improvement occurs, flag that step and begin reducing the step size.

```
    if (error_testr<error_best)
        error_best=error_testr; phi=phi_testr; step_size(k) = step_size(k) * 1.5;
        N_no_progress=0;
   elseif    (error_testl <error_best)
        error_best=error_testl; phi=phi_testl; step_size(k) = step_size(k) * 1.5;
        N_no_progress=0;
   else
     flag = flag + 1; % Failure.  Add it to the list.
    end
end
if (flag>=length(param)) % Failed to improve by stepping in any direction
   step_size = step_size * (0.75 + 0.25*rand);  % Reduce step size
   N_no_progress=N_no_progress+1;
end
```

After adjusting each element of rel_weight, report the new fit.

```
  fprintf(1,'\nError - %f , Last Good Step - %d , Mean Step Size - %f \n
',error_best, N_no_progress, 100*mean(step_size./phi(param)));
  fprintf(1,' Phi - %f',phi);
  end
  error=error_best;
  phi_new = phi;
```

d.5. Multimers

Two subunits A and B are mixed to form an ensemble of N-mers in solution. A given N-mer is described by it's composition, A_nB_m where n+m = N and N = length(phi)-1. Thus, N+1 different species are possible in solution. The concentration of each species is determined by XA(j) and phi. This ensemble is parameterized with the set,

Concentration(j,n+1) = phi(n+1) * Mn(n+1) * C(A_0:B_N)^(1 - n/N) * C(A_N:B_0)^(n/N)

where C(j,n+1) is the concentration of species A_nB_m for mole fraction XA(j) and Mn is the multiplicity of state j (N!/(j!*(N-j)!). The mole fraction is of course,

XA(j) = Sum(n*Concentration(j,n+1)) / Sum(Concentration(j,n+1))

The concentrations are normalized to be mole fractions of aggregates such that

(Sum over n of (Concentration(j,n+1)) = 1

In this parameterization, C(j,1) and C(j,N+1) are adjusted until the closest XA(j) to the experimental result is obtained because XA(j) is the quantity the experimenter adjusts. These adjustments in turn determine all the C(j,n+1)'s. Multimers can be fed multiple values XA(j) and will determine the aggregate concentrations for each value. The returned Concentration(j,n+1) is the concentration of species $[A_nB_m]$ for the j-th value of XA(j).

The returned XA and Concentrations(n+1) are a function of phi and a parameter, A.

C(n+1) = N * Constant * M(n) * phi(n+1) * A^n * (1-A)^(N-n)

where N, Constant, Mn, and A are numbers so that,

sum(C(n+1)) = 1

XA = sum(C(n+1)*n)/N; 0 <= A <= 1.

The bisection method is used to get the value of A for which XA is the one supplied to bisect. The concentration of each species is then returned for that value of a.

```
function Concentration = multimer(XA, phi)
```

For each XA(j), Concentration(j,:) is determined.

```
for j=1:length(XA)
```

Cconc is returned by the function bisect.

```
Concentration(j,:) = bisect(XA(j),phi);
end
function Conc = bisect(XA, phi)
```

Initialize values of A. XA may differ by 1e-6 at the end of bisection and while not close enough, continue to bisect by the difference of Amin and Amax.

```
  tolerance = 1e-6;
  Amax = 1; Amin = 0;
  [Xmin, Conc]=Cparametric(Amin, phi);
  [Xmax, Conc]=Cparametric(Amax, phi);
      while ((Xmax-XA)>tolerance)
      Atest = (Amin+Amax)/2;
    [Xtest, Conc]=Cparametric(Atest,phi);
    if (Xtest>XA)
     Amax = Atest; Xmax=Xtest;
```

```
    else
       Amin = Atest; Xmin=Xtest;
    end
 end
 function [XA, Concs] = Cparametric( A, phi)
```

Parametric form where mole fraction and Concentrations are determined for A, phi and N.

```
N = length(phi)-1;
B = 1-A;
Concs(1)= B^N*phi(1);
Concs(N+1)=A^N*phi(N+1);
Mn=1;
```

Calculate each unscaled concentration.

```
for k=2:N
   idx=k-1;
   Mn = Mn * (N+1-idx)/idx;
   Concs(k) = phi(k)*A^idx*B^(N-idx)*Mn;
end
```

Normalize the concentration and calculate the mole fraction.

```
Concs = Concs / sum(Concs);
XA = sum(Concs.*[0:N]/N);
```

d.6. Single Aggregate—Populations

```
function result = Populations(Concentrations, peak_assignment)
```

For each type of aggregate, add to correct NMR resonance.

```
   result = zeros(size(Concentrations,1),max(peak_assignment));
   N = size(Concentrations,2);
   for j=1:N
      idx = peak_assignment(j);
      result(:,idx) = result(:,idx) + Concentrations(:,j);
   end
```

d.7. Single Aggregate—Error of Model

Function: [mean_error, pop_error] = Error_of_Model(XA, phi, peak_assignment, Expt_Populations, Expt_Errors)

```
function [mean_error, pop_error] = Error_of_Model(XA, phi, peak_assignment,
Expt_Populations, Expt_Errors)
```

If no Expt_weights are given, weight all points equally.

```
   if (nargin<5)
            Expt_weights=ones(size(Expt_Populations));
else
            Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
   end
```

Compute values from the model.

```
   Concentrations = multimers(XA,phi);
   PP = Populations(Concentrations, peak_assignment);
```

Compute the mean error.

```
   diff = PP - Expt_Populations;
   mean_error = sqrt(sum(sum(diff.*diff.*Expt_weights)) /
sum(sum(Expt_weights)));
```

Compute the error for each population independently.

```
   pop_error = sum(diff.*Expt_weights,1) ./ sum(Expt_weights,1);
   pop_error(2,:) = sqrt(sum(diff.*diff.*Expt_weights,1) ./ sum(Expt_weights,1));
```

e. Monomer_Dimer Fitting Code

e.1. Monomer_Dimer -- Data_Monomer_Dimer

XA(j). The mole fractions are listed in terms of **A** such that the first mole fraction corresponds to the first row of Expt_Populations.

```
Xa = [ 0.0000  0.1000  1.0000 etc ];
```

Ctotal must have the same value through out and have the same length as Xa.

```
Ctotal = [ 0.100  0.100  0.100  etc ];
```

Expt_Populations are input as a column of data for each aggregate. If an aggregate has two resonances, they should be summed and entered as a single relative integration. Recall that each row must end with a semi-colon.

```
Expt_Populations = [1.000  0.0000   0.0000;
0.8170 0.1830 0.0000;
0.6274 0.3294 0.0432;
etc; ];
```

Expt_Errors are input as an array the same size as Expt_Populations. Each column and row should correspond to the row and column of Expt_Populations. Expt_Errors is optional and should be left as "Expt_Errors = [;];" if none are provided.

```
Expt_Errors = [ ;];
```

peak_assignment_monomer and **peak_assignment_dimer**. The program expects the peaks to be listed in the order of increasing **A** subunit as shown below:

peak_assignment_monomer = [$[A_0B_1]$ $[A_1B_0]$]
peak_assignment_dimer = [$[A_0B_2]$ $[A_1B_1]$ $[A_2B_0]$]

The column number of the corresponding relative integration is input in the order designated above. If an aggregate was not observed, it should be assigned to column 1. For example, if the populations are listed in the order: $[A_1B_1]$ $[A_0B_1]$ $[A_2B_0]$, then peak_assignment_monomer = [2 1] and peak_assignment_dimer = [1 1 3]. If a relative integration is a sum of two unresolved resonances, enter the same column number for each aggregate contributing to the resonance.

```
peak_assignment_monomer = [ 1 3];
peak_assignment_dimer = [1  2  3];
```

phi_monomer and **phi_dimer** are listed in the order of increasing **A** subunit as it is in peak_assignment. The phi's provided here will be the start value for the fit. If an aggregate was not observed, it should be assigned a phi value of 0. The fit may require that a missing aggregate be assigned a phi of 0.00001 rather than 0 to avoid dividing by zero problem in the fit.

```
phi_monomer = [ 0 1];
phi_dimer = [1 1 0.00001];
```

phi_constant indicates the phi's which should not be changed based on all five phi values in the order $[A_0B_1]$, $[A_1B_0]$, $[A_0B_2]$, $[A_1B_1]$, and $[A_2B_0]$. Values of 0 disallow optimization of the corresponding phi. A value of 1 allows for optimization. For example, to fix the phi for $[A_0B_2]$, phi_constant = [1 1 0 1 1].

```
phi_constant = [1 1 1 1 1];
```

e.2. Monomer_Dimer—Try_fit

```
function try_fit(Xa, Ctotal, phi_monomer, peak_assignment_monomer,
phi_dimer, peak_assignment_dimer, Expt_Populations, Expt_Errors)
```

Code for weighting the Expt_Populations. If no Expt_Errors are entered, all points are weighted equally.

```
  if (nargin<8)
          Expt_weights=ones(size(Expt_Populations));
  else
          Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
  end
```

Code for plotting the experimental data.

```
   hold on ; cscheme='bgrmkcybgrmkcy'; axis([0 1 0 1]); xlabel('X_A');
ylabel('Relative Integration');
   for j=1:size(Expt_Populations,2)
       if (nargin<8)
          plot(Xa, Expt_Populations(:,j),sprintf('%so',cscheme(j)));
       else
          errorbar(Xa, Expt_Populations(:,j),
Expt_Errors(:,j),sprintf('%so',cscheme(j)));
       end
   end
```

Code for plotting the model with the provided phi’s.

```
   Xac = [0:0.01:1];
   Ctotalac = Ctotal(1)*ones(size(Xac));
   [Conc_Monomers, Conc_Dimers] = multimers(Xac, Ctotalac, phi_monomer,
phi_dimer);
   TP=Populations(Conc_Monomers, peak_assignment_monomer,
Conc_Dimers, peak_assignment_dimer);
   for j=1:size(TP,2)
      plot(Xac,TP(:,j),sprintf('%c',cscheme(j)) );
   end
```

Code for computing and reporting the error.

```
  [mean_error, pop_error] = Error_of_Model(Xa, Ctotal, phi_monomer,
peak_assignment_monomer, phi_dimer, peak_assignment_dimer,
Expt_Populations, Expt_weights);
```

```
        fprintf(1,'\nThe Mean mismatch is %f percent.\n', mean_error*100);
        for j=1:size(pop_error,2)
        fprintf(1,'Predicted value of population %d exceeds measurement by %f
percent and mean square error of %f percent.\n
',j,pop_error(1,j)*100,pop_error(2,j)*100);
        end
```

e.3. Monomer_Dimer—Refine_fit

```
function [phi_monomer_new, phi_dimer_new, error] = refine_fit(Xa,
Ctotal,phi_monomer, peak_assignment_monomer, phi_dimer,
peak_assignment_dimer, Expt_Populations, phi_constant, Expt_Errors)
```

If no Expt_Errors are entered, all points are weighted equally.

```
if (nargin<9)
   Expt_weights = ones(size(Expt_Populations));
else
          Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
end
```

Set-up the parameters to merge the monomer and dimer inputs to a single input.

```
phimerge = [phi_monomer, phi_dimer];
idx_monomer = [1 2]; idx_dimer = [ 3 4 5];
param = [1:length(phimerge)];
```

The initial step size for improving the model is 10%.

```
step_size = 0.1*phi_constant.*phimerge(param);
```

Initialize the search. N_no_progress is the number of steps since the error last improved. N_max_trials is the number of iterations to perform without the error getting better before ending the script. It is set to 30.

```
N_no_progress = 0;
N_max_trials = 30;
```

Compute and report the initial quality of the fit.

```
[error_best, temp] = Error_of_Model(Xa,Ctotal,phimerge(idx_monomer),
peak_assignment_monomer, phimerge(idx_dimer), peak_assignment_dimer,
Expt_Populations, Expt_weights);
fprintf(1,'\n Initial Error of Fit = %f percent.\n', error_best * 100);
```

Iteratively try to improve fit by changing each parameter in turn.

```
while (N_no_progress < N_max_trials)
   flag = 0;
   for k=1:length(param)
```

Step to the right and to the left.

```
         phi_testr = phimerge;
         phi_testr(param(k))=abs(phimerge(param(k)) + step_size(k));
         [error_testr, temp] = Error_of_Model(Xa,Ctotal,phi_testr(idx_monomer),
peak_assignment_monomer, phi_testr(idx_dimer), peak_assignment_dimer,
Expt_Populations, Expt_weights);
         phi_testl = phimerge;
         phi_testl(param(k))=abs(phimerge(param(k)) - step_size(k));
         [error_testl, temp] = Error_of_Model(Xa,Ctotal,phi_testl(idx_monomer),
peak_assignment_monomer, phi_testl(idx_dimer), peak_assignment_dimer,
Expt_Populations, Expt_weights);
```

Decide if a step should be taken. If the step is positive, continue that direction. If the negative step is better, continue that way. If no improvement occurs, flag that step and begin reducing the step size.

```
       if (error_testr<error_best)
            error_best=error_testr; phimerge=phi_testr; step_size(k) = step_size(k) *
1.5;
            N_no_progress=0;
      elseif     (error_testl <error_best)
   error_best=error_testl; phimerge=phi_testl; step_size(k) = step_size(k) * 1.5;
            N_no_progress=0;
      else
         flag = flag + 1;
      end
   end
   if (flag>=length(param))
   step_size = step_size * (0.75 + 0.25*rand);
   N_no_progress=N_no_progress+1;
   end
```

After adjusting each element of rel_weight, report the new fit.

```
   fprintf(1,'\nError - %f , Last Good Step - %d , Mean Step Size - %f \n
',error_best, N_no_progress, 100*mean(step_size) );
   fprintf('\n Phi Dimer - ');   fprintf(1,'%f ', phimerge(idx_monomer));
   fprintf(1,'\n Phi Tetramer - '); fprintf(1,'%f ',phimerge(idx_dimer));
   end
   error=error_best;
   phi_monomer_new = phimerge(idx_monomer);
```

```
   phi_dimer_new = phimerge(idx_dimer);
```

e.4. Monomer_Dimer—Mulitmers

Two subunits A and B are mixed to form an ensemble of monomers and dimers in solution. A given N-mer is described by it's composition, A_nB_m where n+m = N and N = 1 and 2. Thus, five different species are possible in solution. The concentration of each species is determined by Xa(j), Chi, and phi_monomer or phi_dimer. The outputs are Concentration_monomer(j,n+1) and Concentration_dimer(j, 1).

In this parameterization, the "relative chemical potential", a, is adjusted until the closest XA(j) to the experimental result is obtained. These adjustments in turn determine Chi, the monomer/dimer scaler, and all the aggregate concentrations. Multimers can be fed multiple values XA(j) and will determine the aggregate concentrations for each value. The returned Concentration(j,n+1) is the concentration of species [A_nB_m] for the j-th value of XA(j).

The returned XA and Concentrations(n+1) are a function of phi and a such that,

[B_1] = Chi/Ctotal * phi_monomer(1) * b
[A_1] = Chi/Ctotal * phi_monomer(2) * a

[B_2] = 2 * Chi^2/Ctotal * phi_dimer(1) * b * b
[AB] = 2 * 2 * Chi^2/Ctotal * phi_dimer(2) * a * b
[A_2] = 2* Chi^2/Ctotal * phi_dimer(3) * a * a

Xa = sum(Conc_monomer.*[0 1]) + sum(Conc_dimer.* [0 0.5 1]);

The bisection method is used to get the value of a for which Xa is the one supplied to bisect. The concentration of each species is then returned for that value of a.

```
function [Concentration_monomer, Concentration_dimer] = multimers(Xa,
Ctotal, phi_monomer, phi_dimer)
```

For each Xa(j), Concentration_monomer(j,:) and Concentration_dimer(j,:) are determined.

```
for j=1:length(Xa)
```

Conc_monomer and Conc_dimer are the total concentrations of monomers and dimers and are returned by the function bisect.

```
  [Concentration_monomer(j,:), Concentration_dimer(j,:)] = bisect(Xa(j),
Ctotal(j),phi_monomer, phi_dimer);
end
```

```
function [Conc_monomer, Conc_dimer ] = bisect(Xa, Ctotal,phi_monomer,
phi_dimer);
```

Initialize values of a. Xa may differ by 1e-6 at the end of bisection and while not close enough, continue to bisect by the difference of amin and amax.

```
   tolerance = 1e-6;
   amax = 1; amin = 0;
   [Xmin, Conc_monomer, Conc_dimer]=Cparametric(amin, phi_monomer,
phi_dimer, Ctotal);
   [Xmax, Conc_monomer, Conc_dimer]=Cparametric(amax, phi_monomer,
phi_dimer, Ctotal);
   while ((Xmax-Xa)>tolerance)
      atest = (amin+amax)/2;
      [Xtest, Conc_monomer, Conc_dimer]=Cparametric(atest, phi_monomer,
phi_dimer, Ctotal);
      if (Xtest>Xa)
        amax = atest; Xmax=Xtest;
     else
        amin = atest; Xmin=Xtest;
     end
  end
function [Xa, Conc_monomer, Conc_dimer]=Cparametric(a, phi_monomer,
phi_dimer, Ctotal)
```

Parametric form where Xa, Mtotal, Dtotal, and Chi are determined for a, phi and N. Note that Chi is actually Chi = Mtotal / (4*Dtotal) * (sqrt(1 + 8 * Dtotal*Ctotal/(Mtotal*Mtotal)) - 1), but the equation has been modified to address of case of Mtotal = 0 or Dtotal = 0. The script will still have trouble if both Mtotal and Dtotal =0 but that indicates a mistake in the choice of phi_monomer and phi_dimer has been made.

```
b=1-a;
Mtotal = phi_monomer(1)*b + phi_monomer(2) * a;
Dtotal = phi_dimer(1)*b*b + 2*phi_dimer(2)*b*a + phi_dimer(3)*a*a;
Chi =( sqrt( Mtotal*Mtotal + 8 * Dtotal*Ctotal ) - Mtotal +
(Dtotal==0)*(2*Mtotal*Ctotal)  ) / (4* Dtotal + (Dtotal==0));
```

Normalize the concentrations of monomers and dimers and calculate the mole fraction.

```
Conc_monomer = Chi/Ctotal *  [ phi_monomer(1)*b, phi_monomer(2) * a] ;
Conc_dimer = 2 * Chi^2/Ctotal * [ phi_dimer(1)*b*b , 2*phi_dimer(2)*b*a ,
phi_dimer(3)*a*a ];
Xa = sum( Conc_monomer.*[0 1]) + sum(Conc_dimer.* [0 0.5 1]);
```

e.5. Monomer_Dimer—Populations

```
function result = Populations(Concentration_monomer,
peak_assignment_monomer, Concentration_dimer, peak_assignment_dimer)
```

For each type of aggregate, add to correct NMR resonance.

```
   result = zeros(size(Concentration_monomer,1), max(
max(peak_assignment_monomer) , max(peak_assignment_dimer) ) );
   N = size(Concentration_monomer,2);
   for j=1:N
      idx = peak_assignment_monomer(j);
      result(:,idx) = result(:,idx) + Concentration_monomer(:,j);
   end
   N = size(Concentration_dimer,2);
   for j=1:N
      idx = peak_assignment_dimer(j);
      result(:,idx) = result(:,idx) + Concentration_dimer(:,j);
   end
```

e.6. Monomer_Dimer—Error of Model

```
function [mean_error, pop_error] = Error_of_Model(Xa, Ctotal, phi_monomer,
peak_assignment_monomer, phi_dimer, peak_assignment_dimer,
Expt_Populations, Expt_Errors)
```

If no Expt_weights are given, weight all points equally.

```
   if (nargin<8)
            Expt_weights=ones(size(Expt_Populations));
   else
            Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
   end
```

Compute values from the model.

```
   [Conc_Monomers, Conc_Dimers] = multimers(Xa, Ctotal, phi_monomer,
phi_dimer);
Model_Populations = Populations(Conc_Monomers,
peak_assignment_monomer, Conc_Dimers, peak_assignment_dimer);
```

Compute the mean error.

```
   diff = Model_Populations - Expt_Populations;
```

```
   mean_error = sqrt(sum(sum(diff.*diff.*Expt_weights)) /
sum(sum(Expt_weights)));
```

Compute the error for each population independently.

```
   pop_error = sum(diff.*Expt_weights,1) ./ sum(Expt_weights,1);
   pop_error(2,:) = sqrt(sum(diff.*diff.*Expt_weights,1) ./ sum(Expt_weights,1));
```

f. Dimer_Tetramer Fitting Code

f.1. Dimer_Tetramer -- Data_Dimer_Tetramer

XA(j). The mole fractions are listed in terms of **A** such that the first mole fraction corresponds to the first row of Expt_Populations.

```
Xa = [ 0.0000  0.1000  1.0000 etc ];
```

Ctotal must have the same value through out and have the same length as Xa.

```
Ctotal = [ 0.100  0.100  0.100  etc ];
```

Expt_Populations are input as a column of data for each aggregate. If an aggregate has two resonances, they should be summed and entered as a single relative integration. Recall that each row must end with a semi-colon.

```
Expt_Populations = [1.000  0.0000   0.0000;
0.8170 0.1830 0.0000;
0.6274 0.3294 0.0432;
etc; ];
```

Expt_Errors are input as an array the same size as Expt_Populations. Each column and row should correspond to the row and column of Expt_Populations. Expt_Errors is optional and should be left as “Expt_Errors = [;];” if none are provided.

```
Expt_Errors = [ ;];
```

peak_assignment_dimer and **peak_assignment_tetramer**. The program expects the peaks to be listed in the order of increasing **A** subunit as shown below:

peak_assignment_dimer = [$[A_0B_2]$ $[A_1B_1]$ $[A_2B_0]$]
peak_assignment_tetramer = [$[A_0B_4]$ $[A_1B_3]$ $[A_2B_2]$ $[A_3B_1]$ $[A_4B_0]$]

The column number of the corresponding relative integration is input in the order designated above. If an aggregate was not observed, it should be assigned to column 1. For example, if the populations are listed in the order: $[A_1B_1]$ $[A_0B_4]$ $[A_2B_0]$, then peak_assignment_dimer = [1 1 3] and peak_assignment_tetramer = [2 1 1 1 1]. If a relative integration is a sum of two unresolved resonances, enter the same column number for each aggregate contributing to the resonance.

```
peak_assignment_dimer = [ 1 2  3 ];
peak_assignment_tetramer = [1  2  3  4  5 ];
```

phi_dimer and **phi_tetramer** are listed in the order of increasing **A** subunit as it is in peak_assignment. The phi's provided here will be the start value for the fit. If an aggregate was not observed, it should be assigned a phi value of 0. The fit may require that a missing aggregate be assigned a phi of 0.00001 rather than 0 to avoid dividing by zero problem in the fit.

```
phi_dimer = [ 0.00001 1  1 ];
phi_tetramer = [1 1 0.00001  1  1  ];
```

phi_constant indicates the phi's which should not be changed based on all five phi values in the order $[A_0B_2]$, $[A_1B_1]$, $[A_2B_0]$, $[A_0B_4]$, $[A_1B_3]$, $[A_2B_2]$, $[A_3B_1]$, $[A_4B_0]$. Values of 0 disallow optimization of the corresponding phi. A value of 1 allows for optimization. For example, to fix the phi for $[A_1B_3]$, phi_constant = [1 1 1 1 0 1 1 1].

```
phi_constant = [1 1 1 1 1 1 1 1];
```

f.2. Dimer_Tetramer—Try_fit

```
function try_fit(Xa, Ctotal, phi_dimer, peak_assignment_dimer, phi_tetramer,
peak_assignment_tetramer, Expt_Populations, Expt_Errors)
```

Code for weighting the Expt_Populations. If no Expt_Errors are entered, all points are weighted equally.

```
   if (nargin<8)
           Expt_weights=ones(size(Expt_Populations));
   else
           Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
   end
```

Code for plotting the experimental data.

```
    hold on ; cscheme='bgrmkcybgrmkcy'; axis([0 1 0 1]); xlabel('X_R');
ylabel('Mole Fractions');
    for j=1:size(Expt_Populations,2)
        if (nargin<8)
          plot(Xa, Expt_Populations(:,j),sprintf('%so',cscheme(j)));
        else
          errorbar(Xa, Expt_Populations(:,j),
Expt_Errors(:,j),sprintf('%so',cscheme(j)));
        end
    end
```

Code for plotting the model with the provided phi's.

```
    Xac = [0:0.01:1];
    Ctotalac = Ctotal(1)*ones(size(Xac));
    [Conc_Dimers, Conc_Tetramers] = multimers(Xac, Ctotalac, phi_dimer,
phi_tetramer);
    TP=Populations(Conc_Dimers, peak_assignment_dimer, Conc_Tetramers,
peak_assignment_tetramer);
    for j=1:size(TP,2)
       plot(Xac,TP(:,j),sprintf('%c',cscheme(j)) );
    end
```

Code for computing and reporting the error.

```
  [mean_error, pop_error] = Error_of_Model(Xa, Ctotal, phi_dimer,
peak_assignment_dimer, phi_tetramer, peak_assignment_tetramer,
Expt_Populations, Expt_weights);
        fprintf(1,'\nThe Mean mismatch is %f percent.\n', mean_error*100);
        for j=1:size(pop_error,2)
        fprintf(1,'Predicted value of population %d exceeds measurement by %f
percent and mean square error of %f percent.\n
',j,pop_error(1,j)*100,pop_error(2,j)*100);
        end
```

f.3. Dimer_Tetramer—Refine_fit

```
function [phi_dimer_new, phi_tetramer_new, error] = refine_fit(Xa,
Ctotal,phi_dimer, peak_assignment_dimer, phi_tetramer,
peak_assignment_tetramer, Expt_Populations, phi_constant, Expt_Errors)
```

If no Expt_Errors are entered, all points are weighted equally.

```
if (nargin<9)
   Expt_weights = ones(size(Expt_Populations));
else
```

```
            Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
end
```

Set-up the parameters to merge the dimer and tetramer inputs to a single input.

```
phimerge = [phi_dimer, phi_tetramer];
idx_dimer = [1 2 3]; idx_tetramer = [ 4 5 6 7 8];
param = [1:length(phimerge)];
```

The initial step size for improving the model is 10%.

```
step_size = 0.1*phi_constant.*phimerge(param);
```

Initialize the search.

```
N_no_progress = 0;
N_max_trials = 30;
```

Compute and report the initial quality of the fit.

```
[error_best, temp] = Error_of_Model(Xa,Ctotal,phimerge(idx_dimer),
peak_assignment_dimer, phimerge(idx_tetramer), peak_assignment_tetramer,
Expt_Populations, Expt_weights);
fprintf(1,'\n Initial Error of Fit = %f percent.\n', error_best * 100);
```

Iteratively try to improve fit by changing each parameter in turn.

```
while (N_no_progress < N_max_trials)
   flag = 0;
   for k=1:length(param)
```

Step to the right and to the left.

```
         phi_testr = phimerge;
         phi_testr(param(k))=abs(phimerge(param(k)) + step_size(k));
         [error_testr, temp] = Error_of_Model(Xa,Ctotal,phi_testr(idx_dimer),
peak_assignment_dimer, phi_testr(idx_tetramer), peak_assignment_tetramer,
Expt_Populations, Expt_weights);
         phi_testl = phimerge;
         phi_testl(param(k))=abs(phimerge(param(k)) - step_size(k));
         [error_testl, temp] = Error_of_Model(Xa,Ctotal,phi_testl(idx_dimer),
peak_assignment_dimer, phi_testl(idx_tetramer), peak_assignment_tetramer,
Expt_Populations, Expt_weights);
```

Decide if a step should be taken. If the step is positive, continue that direction. If the negative step is better, continue that way. If no improvement occurs, flag that step and begin reducing the step size.

```
       if (error_testr<error_best)
             error_best=error_testr; phimerge=phi_testr; step_size(k) = step_size(k) *
1.5;
             N_no_progress=0;
      elseif      (error_testl <error_best)
             error_best=error_testl; phimerge=phi_testl; step_size(k) = step_size(k) *
1.5;
             N_no_progress=0;
      else
         flag = flag + 1;
      end
   end
   if (flag>=length(param))
      step_size = step_size * (0.75 + 0.25*rand);
   N_no_progress=N_no_progress+1;
   end
```

After adjusting each element of rel_weight, report the new fit.

```
   fprintf(1,'\nError - %f , Last Good Step - %d , Mean Step Size - %f \n
',error_best, N_no_progress, 100*mean(step_size) );
   fprintf('\n Phi Dimer - ');   fprintf(1,'%f ', phimerge(idx_dimer));
   fprintf(1,'\n Phi Tetramer - '); fprintf(1,'%f ',phimerge(idx_tetramer));
   end
   error=error_best;
   phi_dimer_new = phimerge(idx_dimer);
   phi_tetramer_new = phimerge(idx_tetramer);
```

f.4. Dimer_Tetramer—Multimers

Two subunits A and B are mixed to form an ensemble of monomers and dimers in solution. A given N-mer is described by it's composition, A_nB_m where n+m = N and N = 1 and 2. Thus, five different species are possible in solution. The concentration of each species is determined by Xa(j), Chi, and phi_dimer or phi_tetramer. The outputs are Concentration_dimer(j,n+1) and Concentration_tetramer(j, 1).

In this parameterization, the “relative chemical potential”, a, is adjusted until the closest XA(j) to the experimental result is obtained. These adjustments in turn determine Chi_squared, the dimer/tetramer scaler, and all the aggregate concentrations. Multimers can be fed multiple values Xa(j) and will determine the aggregate concentrations for each value. The returned Concentration(j,n+1) is the concentration of species $[A_nB_m]$ for the j-th value of Xa(j).

The returned Xa and Concentrations(n+1) are a function of phi and a such that,

$[B_2]$ = 2 * Chi_squared/Ctotal * phi_dimer(1) * b * b
[AB] = 2 * 2 * Chi_squared /Ctotal * phi_dimer(2) * a * b

$[A_2]$ = 2* Chi_squared /Ctotal * phi_dimer(3) * a * a

$[B_4]$ = 4 * Chi_squared^2/Ctotal * phi_tetramer(1) * b^4
$[A_1B_3]$ = 4 * 4 * Chi_squared^2 /Ctotal * phi_tetramer(2) * a * b^3
$[A_2B_2]$ = 4 * 6 * Chi_squared^2 /Ctotal * phi_tetramer(3) * a^2 * b^2
$[A_1B_3]$ = 4 * 4 * Chi_squared^2 /Ctotal * phi_tetramer(4) * a^3 * b
$[A_4]$ = 4* Chi_squared^2 /Ctotal * phi_tetramer(5) * a^4

Xa = sum(Conc_dimer.* [0 0.5 1]) + sum(Conc_tetramer.*[0 0.25 0.5 0.75 1])

The bisection method is used to get the value of a for which Xa is the one supplied to bisect. The concentration of each species is then returned for that value of a.

```
function [Concentration_dimer, Concentration_tetramer] = multimers(Xa, Ctotal,
phi_dimer, phi_tetramer)
```

For each Xa(j), Concentration_dimer(j,:) and Concentration_tetramer(j,:) are determined.

```
for j=1:length(Xa)
```

Conc_dimer and Conc_tetramer are the total concentrations of dimers and tetramers and are returned by the function bisect.

```
  [Concentration_dimer(j,:), Concentration_tetramer(j,:)] = bisect(Xa(j),
Ctotal(j),phi_dimer, phi_tetramer);
end
function [Conc_dimer, Conc_tetramer ] = bisect(Xa, Ctotal,phi_dimer,
phi_tetramer);
```

Initialize values of a. Xa may differ by 1e-6 at the end of bisection and while not close enough, continue to bisect by the difference of amin and amax.

```
   tolerance = 1e-6; % Amount Xr may differ by an end of bisection..
   amax = 1; amin = 0;
   [Xmin, Conc_dimer, Conc_tetramer]=Cparametric(amin, phi_dimer,
phi_tetramer, Ctotal);
   [Xmax, Conc_dimer, Conc_tetramer]=Cparametric(amax, phi_dimer,
phi_tetramer, Ctotal);
   while ((Xmax-Xa)>tolerance) % While not close enough, continue to bisect
difference of rmin and rmax.
      atest = (amin+amax)/2;
      [Xtest, Conc_dimer, Conc_tetramer]=Cparametric(atest, phi_dimer,
phi_tetramer, Ctotal);
      if (Xtest>Xa)
        amax = atest; Xmax=Xtest;
```

```
      else
         amin = atest; Xmin=Xtest;
      end
   end
function [Xa, Conc_dimer, Conc_tetramer]=Cparametric(a, phi_dimer,
phi_tetramer, Ctotal)
```

Parametric form where Xa, Dtotal, Ttotal, and Chi_squared are determined for a, phi and N. Note that Chi is actually Chi_squared = Dtotal / (4*Ttotal) * (sqrt(1 + 4 * Ttotal*Ctotal/(Dtotal*Dtotal)) - 1), but the equation has been modified to address of case of Dtotal = 0 or Ttotal = 0. The script will still have trouble if both Dtotal and Ttotal =0 but that indicates a mistake in the choice of phi_dimer and phi_tetramer has been made.

```
b=1-a;
Dtotal = phi_dimer(1)*b*b + 2 * phi_dimer(2) * a * b + phi_dimer(3) * a*a;
Ttotal = phi_tetramer(1)*b^4 + 4*phi_tetramer(2)*b^3*a +
6*phi_tetramer(3)*b*b*a*a + 4*phi_tetramer(4)*b*a^3 + phi_tetramer(5)*a^4;
Chi_squared =  ( sqrt( Dtotal*Dtotal + 4 * Ttotal*Ctotal ) - Dtotal +
(Ttotal==0)*(2*Dtotal*Ctotal)  ) / (4* Ttotal + (Ttotal==0));
```

Normalize the concentrations of monomers and dimers and calculate the mole fraction.

```
Conc_dimer = 2 * Chi_squared/Ctotal *  [ phi_dimer(1)*b*b , 2*phi_dimer(2)*b*a
, phi_dimer(3)*a*a] ;
Conc_tetramer = 4 * Chi_squared^2/Ctotal * [ phi_tetramer(1)*b*b*b*b,
4*phi_tetramer(2)*b*b*b*a, 6*phi_tetramer(3)*b*b*a*a, 4*phi_tetramer(4)*b*a*a*a ,
phi_tetramer(5)*a*a*a*a ];
Xa = sum( Conc_dimer .*[0 0.5 1]) + sum(Conc_tetramer.* [0 0.25 0.5 0.75 1]);
```

f.5. Dimer_Tetramer—Populations

```
function result = Populations(Concentration_dimer, peak_assignment_dimer,
Concentration_tetramer, peak_assignment_tetramer)
```

For each type of aggregate, add to correct NMR resonance.

```
   result = zeros(size(Concentration_dimer,1), max(
max(peak_assignment_dimer) , max(peak_assignment_tetramer) ) );
   N = size(Concentration_dimer,2);
   for j=1:N % Go through each type of aggregate and add to correct NMR peak.
      idx = peak_assignment_dimer(j);
      result(:,idx) = result(:,idx) + Concentration_dimer(:,j);
   end
   N = size(Concentration_tetramer,2);
   for j=1:N % Go through each type of aggregate and add to correct NMR peak.
```

```
    idx = peak_assignment_tetramer(j);
    result(:,idx) = result(:,idx) + Concentration_tetramer(:,j);
  end
```

f.6. Dimer_Tetramer—Error of Model

```
function [mean_error, pop_error] = Error_of_Model(Xa, Ctotal, phi_dimer,
peak_assignment_dimer, phi_tetramer, peak_assignment_tetramer,
Expt_Populations, Expt_Errors)
```

If no Expt_weights are given, weight all points equally.

```
  if (nargin<8)
        Expt_weights=ones(size(Expt_Populations));
else
        Expt_weights = 1./( Expt_Errors + mean(mean(Expt_Errors)));
  end
```

Compute values from the model.

```
  [Conc_Dimers, Conc_Tetramers] = multimers(Xa, Ctotal, phi_dimer,
phi_tetramer);
  Model_Populations = Populations(Conc_Dimers, peak_assignment_dimer,
Conc_Tetramers, peak_assignment_tetramer);
```

Compute the mean error.

```
  diff = Model_Populations - Expt_Populations;
  mean_error = sqrt(sum(sum(diff.*diff.*Expt_weights)) /
sum(sum(Expt_weights)));
```

Compute the error for each population independently.

```
  pop_error = sum(diff.*Expt_weights,1) ./ sum(Expt_weights,1);
  pop_error(2,:) = sqrt(sum(diff.*diff.*Expt_weights,1) ./ sum(Expt_weights,1));
```