

ADVANCE PUT LECTURE - 02

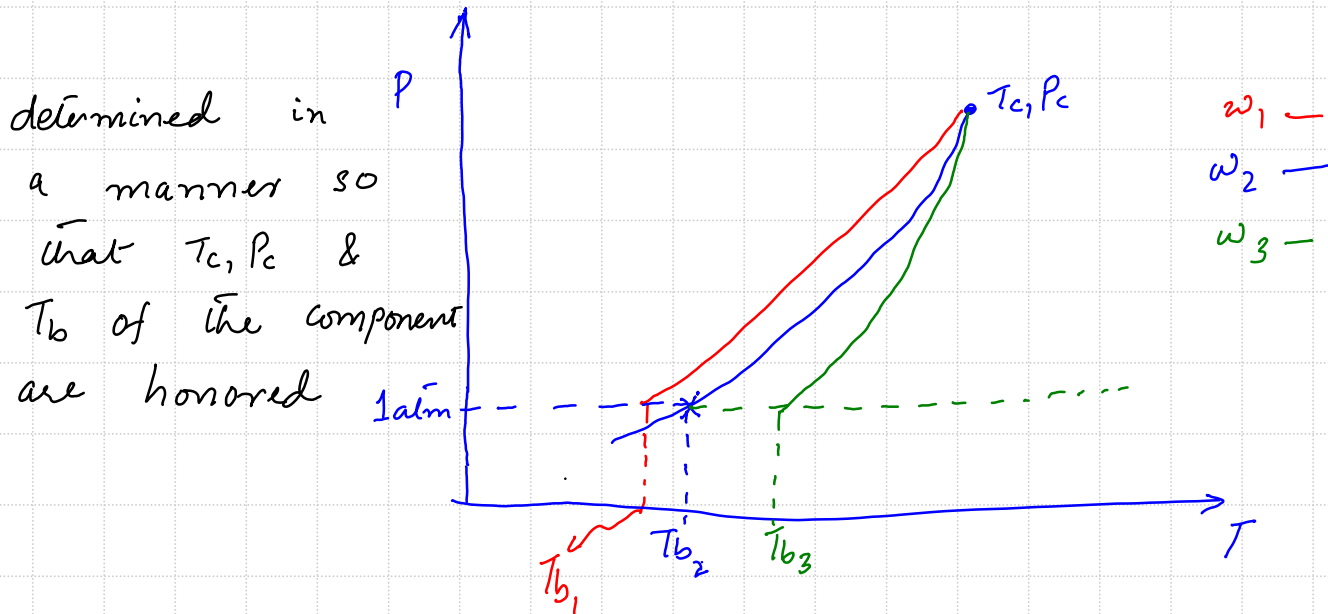
AGENDA:

- ① Recap of Previous lecture
 - Ⓐ Required parameters for EOS calculations
 - Ⓑ How do we get these parameters
 - Ⓒ Recap of Molar distb model
- ② How Twumw & Soreide param gives MW & SG & how does Gamma param affect them?
- ③ Gamma distb model options in Ph2Comp
- ④ Why ω characterisation & Gamma charac are important
- ⑤ using Ph2Comp to do Gamma fitting with different options and see the results

① RECAP OF LECTURE - 01

② EOS Calculations parameters:

- ① MW \rightarrow we have Katz Feroz, Two MW correlation Gamma distb model, Crude Assay data (measured data)
- ② $T_c, P_c \rightarrow$ Two MW, $f(T_b)$; you need T_{bi}
- ③ ω (acentric factor)



④ β (Volume Shift)

Calculated so as to get correct 'SG' of each component: Need SG.

$$(S.G.)_{Eos} \text{ for component } i = (S.G.)_{\text{given}} \text{ for comp } i$$

⑤ molar composition

- ① user input
- ② molar distb models

MOLAR DISTR MODELS

- (a) Exponential discrete
- (b) Gamma continuous

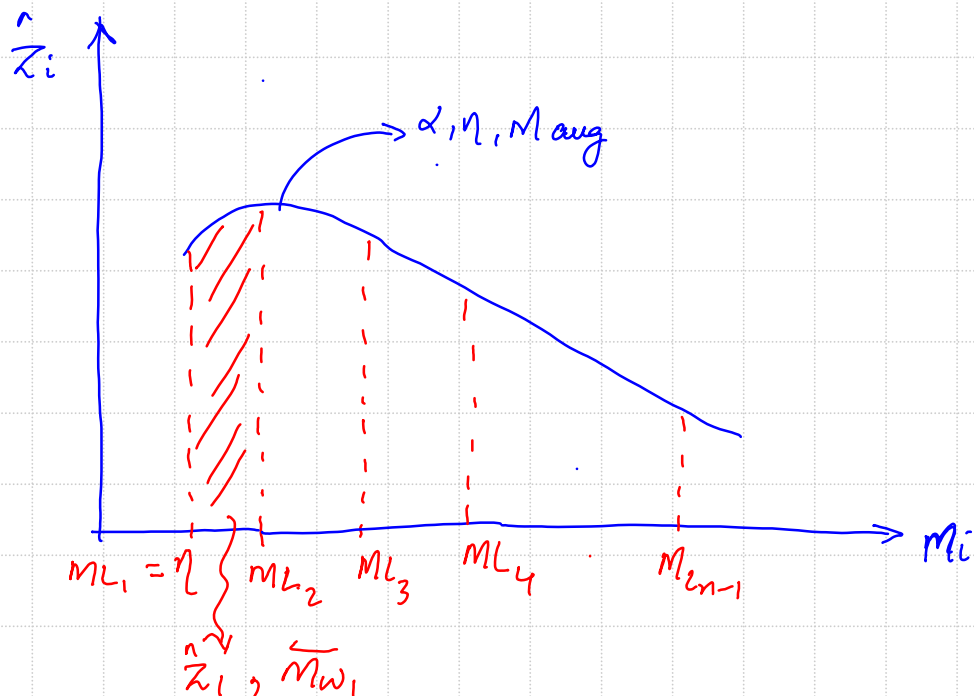
(b) Gamma continuous:

- ① Shape, α
 - ② bound, η
 - ③ Avg, M_{avg}
- } defines the shape of distb model
- ④ LMW's (lower mws) \rightarrow To discretize the Gamma model

Result

\rightarrow molar amounts of each component defined by LMW's

\rightarrow MW of each component



② Twumw & SOREIDE : To get SG & MW

(a) Calculate properties for normal paraffins,
 $M_p, T_{cp}, P_{cp}, \gamma_p$. ($f(T_b)$)
↳ of normal paraffin

(b) $\Delta\gamma = f(\gamma_{given} - \gamma_p)$, $f_T(\Delta\gamma, T_b)$

(c) T_c, P_c, M

In PhzComp

Twumw keyword: value ranges 0-1

• of zero: dependency very small on $\Delta\gamma$

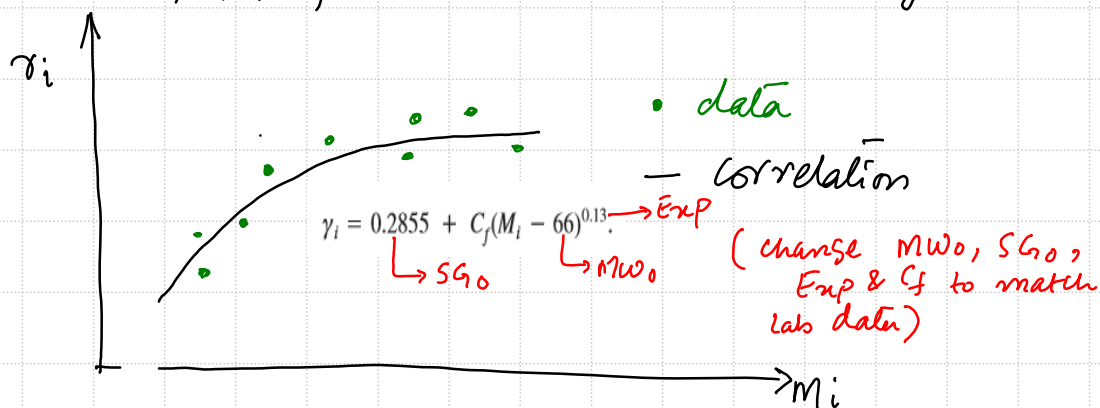
• of one: Full Twumw correlation

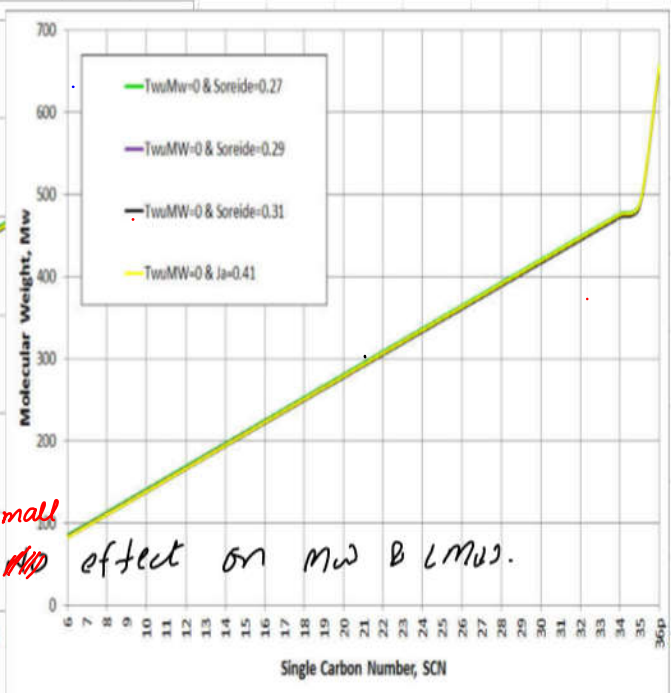
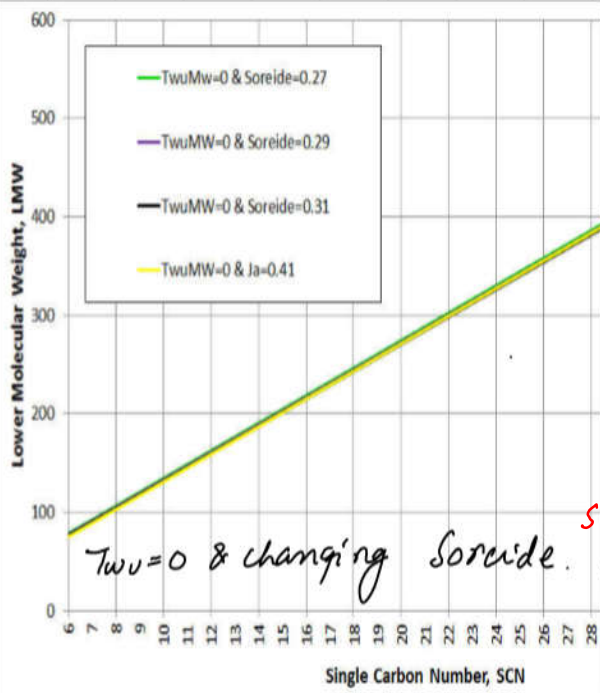
Soreide correlation (MW vs SG relationship)

→ gives SG based MWs

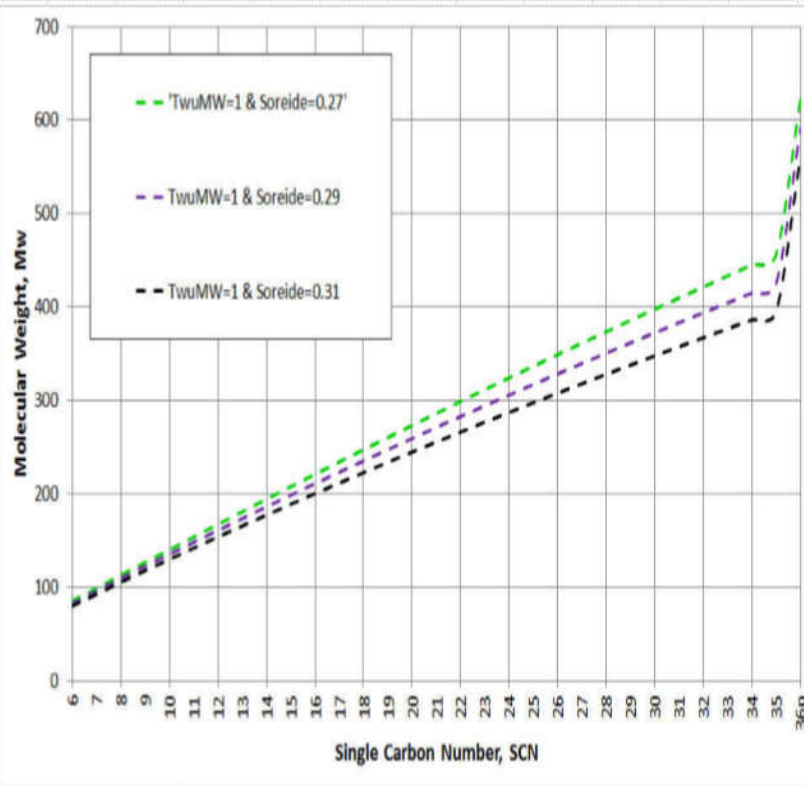
→ Different relationship for different type of fluids (how much aromatic, Paraffinic)

→ normally you have reported $M_{7+}, \gamma_{7+}, M_{n+}, \gamma_{n+}, M \& \gamma$ from Crude Assays





Twu=0 & changing Soreide. Small effect on Mw & LMs.



→ TwuMW=1 & changing Soreide. As $q \uparrow$ Mw \uparrow

Conclusion

- ① we need correct Mw-SG_r relationship & TwuMW to get representative properties for EOS calculation
- ② Correct TwuMW is difficult to find as Mw data is not usually measured on SCN basis. Potential Regression variable in tuning

Gamma modeling in Phz Comp

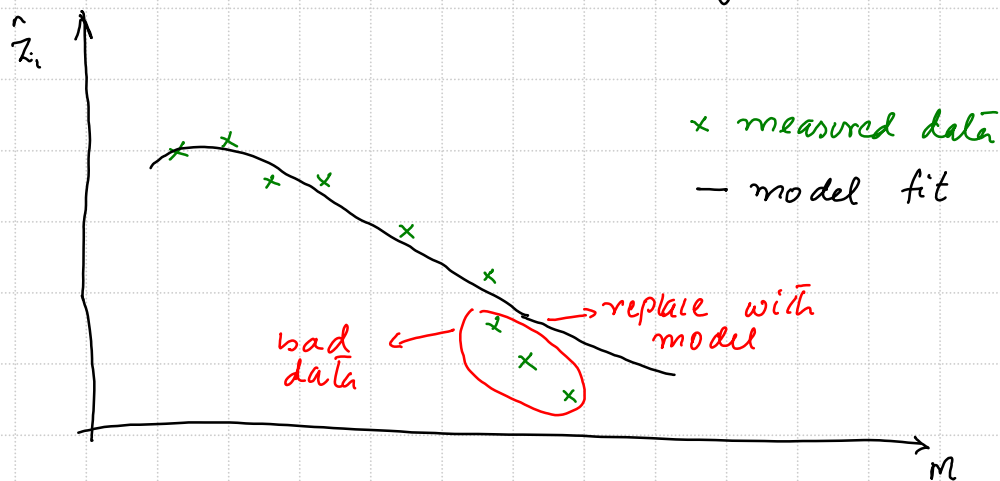
① Fitting Gamma model on reported composition

why do we need model when composition is available?

→ not all labs report the same heaviest fraction and same number of components
→ single EOS has single definition of components

so all streams should be splitted/lumped to EOS defined number of components using the fitted model

→ For BC & replacing bad measured data



② Splitting opto heaviest fraction of EOS charac for all samples.

GAMMA FITTING IN PHZ COMP

① Amount option

② MW option

① Amount Option:-

- ① Min RMS b/w calculated & reported amounts
- ② by changing α, η, M_{avg}
- ③ Need LMW's to be defined & composition to be fitted in

Final Result

- Best fit α, η & M_{avg}
- M_{wi} for each component

② MW Option

- ① Min. RMS b/w calculated & Reported MW's
- ② by changing η, M_{avg}, α
- ③ It calculates LMW's by matching the exact amounts

Result

- Best fit α, η, M_{avg}
- LMW's specific for the sample
- Calculated M_{wi} for each component

Amount option

(+) matching measured data of mass amounts are matched

(+) Fixed LMW's for all samples giving correct amounts. Bcz EOS uses single set of LMW's based on which we will be splitting

(-) LMW need to be defined & should be consistent with MW's

MW option

(-) Matching estimated MW's

(-) Variable LMW's that give correct amounts for each sample

(+) No LMW's need to be defined

Conclusion:

Amount option with max amounts being matched is the best option to use.

Conserve Mass

→ Conserving mass so max amounts measured in lab are honored everywhere
:Step 2: Defining LABSCN for all samples and their respective feeds

```

CHAR      Dynamite-State-3975-16-21-1FH-LABSCN
EOS       PR79
Comp     Mv
H2S      34.080
N2       28.010
CO2      44.010
C1       16.040
C2       30.070
C3       44.100
I-C4     58.120
N-C4     58.120
I-C5     72.150
N-C5     72.150
C6       86.180
C7       92
C8       105
C9       119
C10      134
C11      147
C12      161
C13      175
C14      190
C15      206
C16      222
C17      237
C18      251
C19      263
C20      275
C21      291
C22      305
C23      318
C24      331
C25      345
C26      359
C27      374
C28      388
C29      402
C30p     527
END

```

- ① Lab charac includes component names the lab reports & lab reported MWs.
- ② Input lab feeds in mass if reported otherwise moles
- ③ If moles will be reported then lab MWs will be used to calculate lab measured mass amounts
- ④ If lab does not report MWs explicitly:
 - (a) Lab MWs can be back calculated if wt% & mol% of any stream is given
 - (b) If that is not the case use Katz Feroozabadi MWs

Mix	Dynamite-State-3975-16-21-1FH-WellStream-LABSCN	Moles	0.000	0.369	0.826	67.227	11.570	5.992	0.805	1.932	0.685	0.753	0.887
Mix	Dynamite-State-3975-16-21-1FH-SepOil-LABSCN	Moles	0.000	0.008	0.081	3.099	2.361	3.173	0.857	2.954	2.166	3.220	5.669

```

TWUMW 0
Soreide
: Soreide parameters (best-fit to all data)
SOREIDE
MWO      66
Exponent 0.13
SGO      0.285
Factor   0.29

```

→ Twumw & Soreide will give MW & LMW's for Gamma charac in consistent way

```

:Defining new char for gamma fitting
CHAR      Dynamite-State-3975-16-21-1FH-Gamma-fit
EOS       PR79
Comp     Mv  LMW
H2S
N2
CO2
C1
C2
C3

```

From Twumw & Soreide

```

Mix Dynamite-State-3975-16-21-1FH-WellStream-Gamma Dynamite-State-3975-16-21-1FH-WellStream-LABSCN 1 TANK
Mix Dynamite-State-3975-16-21-1FH-SepOil-Gamma Dynamite-State-3975-16-21-1FH-SepOil-LABSCN 1 TANK

```

→ Importing feeds in new charac with conserved mass so lab

measured mass will be conserved & moles will change based on new MW's

Q Why Gamma charac is needed? why cant we use lab charac for Gamma fitting?

As discussed earlier that for amount option we need LMWS to be defined. In lab charac since MWS are the most important to get the correct masses from modes so if we try to input LMWS by ourselves in lab charac then PhzComp will give error that MW & LMW are not consistent. If we try to estimate LMWS from Two MW correlation against given MWS then we can get consistent LMWS for given MWS but the problem is these LMWS will be different for different samples (lab characterizations).

So during Gamma fitting different set of LMWS will be used for different samples while when we will be splitting them in EOS charac then we will have single set of LMWS. So this does not bring consistency.

So Gamma charac is required:

- (a) to have consistent MWS & LMWS definition for gamma fitting
- (b) to ensure same LMWS used for γ -fitting for all samples and should have same LMWS in EOS charac for splitting.

Notes: Even though Gamma charac will be different for different samples (if samples have different harvest fraction definition) but MWS & LMWS will be same in all including EOS charac bcz we are using same Two MW & sieve for all of them.

Importance of Gamma charac for MW option?

No need of Gamma charac for MW option as we don't need any mws

```
Gamma
split C7 → using  $\gamma$ -model for C7+ fractions
Shape 1 0.5 3
Average 183 170 200 } variables
Bound 90 80 100 }
Fit Dynamite-State-3975-16-21-1FH-SepOil-Gamma C7 amount → Fitting to C7+ fractions
Store Dynamite-State-3975-16-21-1FH-SepOil-Gamma-fit-param → amount option
End → Mass amounts will be fitted
→ storing best fit  $\gamma$ -parameters
```

Instead of amount MW option can also be used. If we want to ignore all components above a certain component like C₂₀ then we write 'Ignore C₂₀' after fit commands. If we want to change weight factor of certain components write "WT component name number" after fit command.

PHAZCOMP CALCULATIONS WITH AMOUNT OPTION:

Component	Mol Wt	
H2S	34.080	34.082
N2	28.010	28.014
CO2	44.010	44.010
C1	16.040	16.043
C2	30.070	30.070
C3	44.100	44.097
I-C4	58.120	58.123
N-C4	58.120	58.123
I-C5	72.150	72.150
N-C5	72.150	72.150
C6	86.180	84.043
C7	92.000	97.812
C8	105.000	111.749
C9	119.000	125.727
C10	134.000	139.716
C11	147.000	153.705
C12	161.000	167.690
C13	175.000	181.672
C14	190.000	195.649
C15	206.000	209.622
C16	222.000	223.591
C17	237.000	237.557
C18	251.000	251.520
C19	263.000	265.481
C20	275.000	279.440
C21	291.000	293.398
C22	305.000	307.354
C23	318.000	321.309
C24	331.000	335.263
C25	345.000	349.217
C26	359.000	363.170
C27	374.000	377.123
C28	388.000	391.077
C29	402.000	405.030
C30p	527.000	418.984

→ Column 1 mws are the ones lab is using

→ Column 2 mws are the ones calculated by two MW used in Gamma charac

values slightly different

→ very large difference. Two MW correlation

does not reorganize C30p. It reorganizes C30 (ignoring 'p') and gives C30 mol. wt which is wrong. So in Gamma charac MW C30p is wrong.

Q Does this wrong MW makes any difference to Gamma fitting?

For the amount option it does not make any difference as we have conserved mass and feed in Gamma charac contains correct masses which we are fitting. The wrong MW will give us wrong moles of C3Op using lab mass but we are fitting mass and not moles.

For MW option, if we are using Gamma charac then we will have to ignore C3Op in fitting as its MW is wrong and we don't want it in regression. If we are using lab charac for fitting with MW option then no need to ignore this component as MW inputted is correct.

Note if we are using multiple samples in lab charac and has defined $MW_{nt} = 1$ and defining Cnt mass by using multiply commands then we also will have to ignore C3Op MW even though we are using lab charac for fitting.

Component	Moles	Mole Fracs	Mass	Mass Fracs	
H2S	0.0000	0.00000	0.000000	0.000	0.000
N2	0.3690	0.36895	0.003690	10.336	10.336
CO2	0.8260	0.82600	0.008260	36.352	36.352
C1	67.2270	67.21443	0.672263	1078.321	1078.321
C2	11.5700	11.57000	0.115699	347.910	347.910
C3	5.9920	5.99241	0.059919	264.247	264.247
I-C4	0.8050	0.80496	0.008050	46.787	46.787
N-C4	1.9320	1.93190	0.019320	112.288	112.288
I-C5	0.6850	0.68500	0.006850	49.423	49.423
N-C5	0.7530	0.75300	0.007530	54.329	54.329
C6	0.8870	0.90956	0.008870	76.442	76.442
C7	1.3120	1.23403	0.013120	120.704	120.704
C8	1.5440	1.45075	0.015440	162.120	162.120
C9	0.9850	0.93230	0.009850	117.215	117.215
C10	0.7450	0.71452	0.007450	99.830	99.830
C11	0.5360	0.51262	0.005360	78.792	78.792
C12	0.4350	0.41765	0.004350	70.035	70.035
C13	0.4270	0.41132	0.004270	74.725	74.725
C14	0.3590	0.34864	0.003590	68.210	68.210
C15	0.3300	0.32430	0.003300	67.980	67.980
C16	0.2610	0.25914	0.002610	57.942	57.942
C17	0.2360	0.23545	0.002360	55.932	55.932
C18	0.2280	0.22753	0.002280	57.228	57.228
C19	0.1840	0.18228	0.001840	48.392	48.392
C20	0.1430	0.14073	0.001430	39.325	39.325
C21	0.1330	0.13191	0.001330	38.703	38.703
C22	0.1130	0.11213	0.001130	34.465	34.465
C23	0.0990	0.09798	0.000990	31.482	31.482
C24	0.0970	0.09577	0.000970	32.107	32.107
C25	0.0870	0.08595	0.000870	30.015	30.015
C26	0.0770	0.07612	0.000770	27.643	27.643
C27	0.0690	0.06843	0.000690	25.806	25.806
C28	0.0620	0.06151	0.000620	24.056	24.056
C29	0.0550	0.05459	0.000550	22.110	22.110
C30p	0.4380	0.55092	0.004380	230.826	230.826
Totals:	100.0010	1.000000	3692.077	1.000000	

moles in lab charac } \neq { moles in Gamma charac
 mass amounts in tank defined in lab charac } = { mass amounts in tank defined in Gamma charac.

Always compare mass and moles and not the fraction amounts.

Component	Mol Wt	LMW
H2S	34.082	
N2	28.014	
CO2	44.010	
C1	16.043	
C2	30.070	
C3	44.097	
I-C4	58.123	
N-C4	58.123	
I-C5	72.150	
N-C5	72.150	
C6	84.043	77.029
C7	97.812	90.799 97.81
C8	111.749	104.735 104.74
C9	125.727	118.714 118.71
C10	139.716	132.702 132.70
C11	153.705	146.691 146.69
C12	167.690	160.677 160.68
C13	181.672	174.658 174.66
C14	195.649	188.635 188.64
C15	209.622	202.608 202.61
C16	223.591	216.578 216.58
C17	237.557	230.544 230.54
C18	251.520	244.507 244.51
C19	265.481	258.468 258.47
C20	279.440	272.427 272.43
C21	293.398	286.384 286.38
C22	307.354	300.340 300.34
C23	321.309	314.295 314.30
C24	335.263	328.249 328.25
C25	349.217	342.203 342.20
C26	363.170	356.157 356.16
C27	377.123	370.110 370.11
C28	391.077	384.063 384.06
C29	405.030	398.017 398.02
C30p	418.984	411.971 411.97

LMW calc in Gamma charac by TwoMw & Sorcede
 MWs taken from Gamma fit Results table both exactly same (second ones are round off to two decimal places) except C7 LMW. Because C7 LMW has to be equal to calculated 'n' during fitting

Shape Parameter (Alpha) : 0.69580
 Average MW Multiplier : 1.01815
 Bounding MW Multiplier : 1.00000
 Origin MW Multiplier : 1.00000
 Number of Iterations : 4
 Beta Parameter : 133.534
 Average Plus MW : 190.726
 Bounding MW : 97.812
 Origin MW : 97.812
 RMS % Error : 0.364

variables
RMS reduced b/w these two

Component	Lower MW	Reported MW	Calculated MW	Reported Moles	Calculated Moles	Reported Mass	Calculated Mass	Percent Deviation	Relative Weight
C7	97.81	97.81	100.62	0.127900	0.135105	0.066783	0.072570	0.58	1.00
C8	104.74	111.75	111.22	0.163798	0.144373	0.097713	0.085719	-1.20	1.00
C9	118.71	125.73	125.41	0.107599	0.103662	0.072217	0.069397	-0.28	1.00
C10	132.70	139.72	139.46	0.083527	0.082262	0.062297	0.061240	-0.11	1.00
C11	146.69	153.70	153.47	0.060309	0.067778	0.049485	0.055529	0.60	1.00
C12	160.68	167.69	167.47	0.049156	0.056983	0.044004	0.050944	0.69	1.00
C13	174.66	181.67	181.47	0.048350	0.048520	0.046890	0.047002	0.01	1.00
C14	188.64	195.65	195.45	0.040991	0.041677	0.042812	0.043484	0.07	1.00
C15	202.61	209.62	209.43	0.038105	0.036029	0.042640	0.040279	-0.24	1.00
C16	216.58	223.59	223.40	0.030506	0.031299	0.036412	0.037326	0.09	1.00
C17	230.54	237.56	237.37	0.027748	0.027295	0.035189	0.034586	-0.06	1.00
C18	244.51	251.52	251.33	0.026792	0.023877	0.035973	0.032036	-0.39	1.00
C19	258.47	265.48	265.30	0.021413	0.020942	0.030346	0.029659	-0.07	1.00
C20	272.43	279.44	279.26	0.016558	0.018407	0.024699	0.027441	0.27	1.00
C21	286.38	293.40	293.22	0.015543	0.016209	0.024344	0.025372	0.10	1.00
C22	300.34	307.35	307.17	0.013248	0.014296	0.021736	0.023443	0.17	1.00
C23	314.30	321.31	321.13	0.011499	0.012627	0.019724	0.021646	0.19	1.00
C24	328.25	335.26	335.08	0.011326	0.011166	0.020270	0.019973	-0.03	1.00
C25	342.20	349.22	349.04	0.010074	0.009884	0.018780	0.018417	-0.04	1.00
C26	356.16	363.17	362.99	0.008979	0.008758	0.017408	0.016971	-0.04	1.00
C27	370.11	377.12	376.95	0.008103	0.007767	0.016313	0.015629	-0.07	1.00
C28	384.06	391.08	390.90	0.007255	0.006893	0.015145	0.014385	-0.08	1.00
C29	398.02	405.03	404.86	0.006419	0.006122	0.013878	0.013232	-0.06	1.00
C30p	411.97	418.98	535.83	0.064803	0.050245	0.144943	0.143721	-0.12	1.00
Totals	97.81	187.33	190.73	1.000000	0.982178	1.000000	1.000000	1.81*	0.00*

Same from Gamma Charac

From Gamma charac

From r-charac

From Calc mass & Calc. Mws

Weight factors for each component

Mws from best fit Gamma model & LMws provided

418 is MW C30p calculated by Twomw. Considering it C30 however
 535 is MW calculated by Gamma model by integrating from LMW of C30p to infinity. so 535 is correct/representative MW of C30p rather than 418.

So Gamma model is needed to get the correct MW of Cn+ which cannot be obtained from Twomw alone

BC of Gamma fitting can be done:

- by visualizing the fitting results in a plot
- looking at overall RMS
- calculated mass plus $\pm 10\%$ of lab value
- calculated MW of Cn+ $\pm 10\%$ of lab value

PHAZCOMP CALCULATIONS WITH MW OPTION:

Everything is same until Gamma fit results which are shown below:

Shape Parameter (Alpha) ... : 0.69554
 Average MW Multiplier ... : 1.01574
 Bounding MW Multiplier ... : 0.98104
 Origin MW Multiplier ... : 1.00000
 Number of Iterations ... : 4

Beta Parameter ... : 135.350
 Average Plus MW ... : 190.441
 Bounding MW ... : 96.300
 Origin MW ... : 96.300
 RMS % Error ... : 0.578

variables
min RMS b/w two

Component	Reported Mass	Calculated Mass	Reported Moles	Calculated Moles	Lower MW	Reported MW	Calculated MW	Percent Deviation	Relative Weight
C7	0.066783	0.066783	0.127557	0.126650	96.30	91.148	98.16	98.86	0.72
C8	0.097713	0.097713	0.163666	0.166408	102.61	104.923	111.94	110.09	-1.65
C9	0.072217	0.072217	0.107581	0.107353	118.91	118.844	125.86	126.12	0.21
C10	0.062297	0.062297	0.083539	0.082770	134.01	132.804	139.82	141.12	0.93
C11	0.049485	0.049485	0.060330	0.059869	148.74	146.772	153.79	154.97	0.77
C12	0.044004	0.044004	0.049180	0.049245	161.55	160.741	167.75	167.53	-0.13
C13	0.046890	0.046890	0.048379	0.048662	173.81	174.707	181.72	180.66	-0.58
C14	0.042812	0.042812	0.041020	0.041241	187.88	188.668	195.68	194.63	-0.54
C15	0.042640	0.042640	0.038135	0.038255	201.72	202.624	209.64	208.98	-0.31
C16	0.036412	0.036412	0.030533	0.030571	216.61	216.576	223.59	223.31	-0.12
C17	0.035189	0.035189	0.027775	0.027802	230.32	230.525	237.54	237.30	-0.10
C18	0.035973	0.035973	0.026819	0.026731	244.60	244.470	251.48	252.32	0.33
C19	0.030346	0.030346	0.021436	0.021270	260.42	258.412	265.43	267.50	0.78
C20	0.024699	0.024699	0.016576	0.016472	274.90	272.351	279.36	281.13	0.63
C21	0.024344	0.024344	0.015562	0.015515	287.60	286.289	293.30	294.19	0.30
C22	0.021736	0.021736	0.013264	0.013258	301.05	300.225	307.24	307.38	0.05
C23	0.019724	0.019724	0.011514	0.011551	313.96	314.160	321.17	320.14	-0.32
C24	0.020270	0.020270	0.011341	0.011399	326.56	328.094	335.11	333.39	-0.51
C25	0.018780	0.018780	0.010088	0.010137	340.50	342.027	349.04	347.36	-0.48
C26	0.017408	0.017408	0.008992	0.009031	354.49	355.959	362.97	361.38	-0.44
C27	0.016313	0.016313	0.008115	0.008144	368.55	369.892	376.91	375.55	-0.36
C28	0.015145	0.015145	0.007265	0.007283	382.85	383.824	390.84	389.92	-0.23
C29	0.013878	0.013878	0.006428	0.006435	397.29	397.756	404.77	404.34	-0.11
C30p	0.144943	0.148308	0.064904	0.051765	411.69	411.689	418.70	537.16	28.29
Totals	1.000000	1.003365	1.000000	0.987818	96.30	187.49	190.44	1.57	0.00

mass amounts are exactly matched except for C30p by changing Lmws mass amounts are matched b/c mass is conserved

Lmws calculated so to match mass amounts } ≠ { Lmws from r-charac
 will vary from sample to sample therefore mw option does not ensure fitting based on common Lmws

Representative mw of C30p from Gamma mode
 mw C30p from Gamma charac was wrong so C30p was to be ignored
 no need to ignore if mw of C30p would be correct (if lab charac was used for fitting)

wt=0 ignore