

# *Computerized Design of Robust Separations in HPLC*

Applica, Olten  
08.11.2006

Imre Molnár  
Institut für angewandte Chromatographie  
Berlin, Germany

# *Introduction*

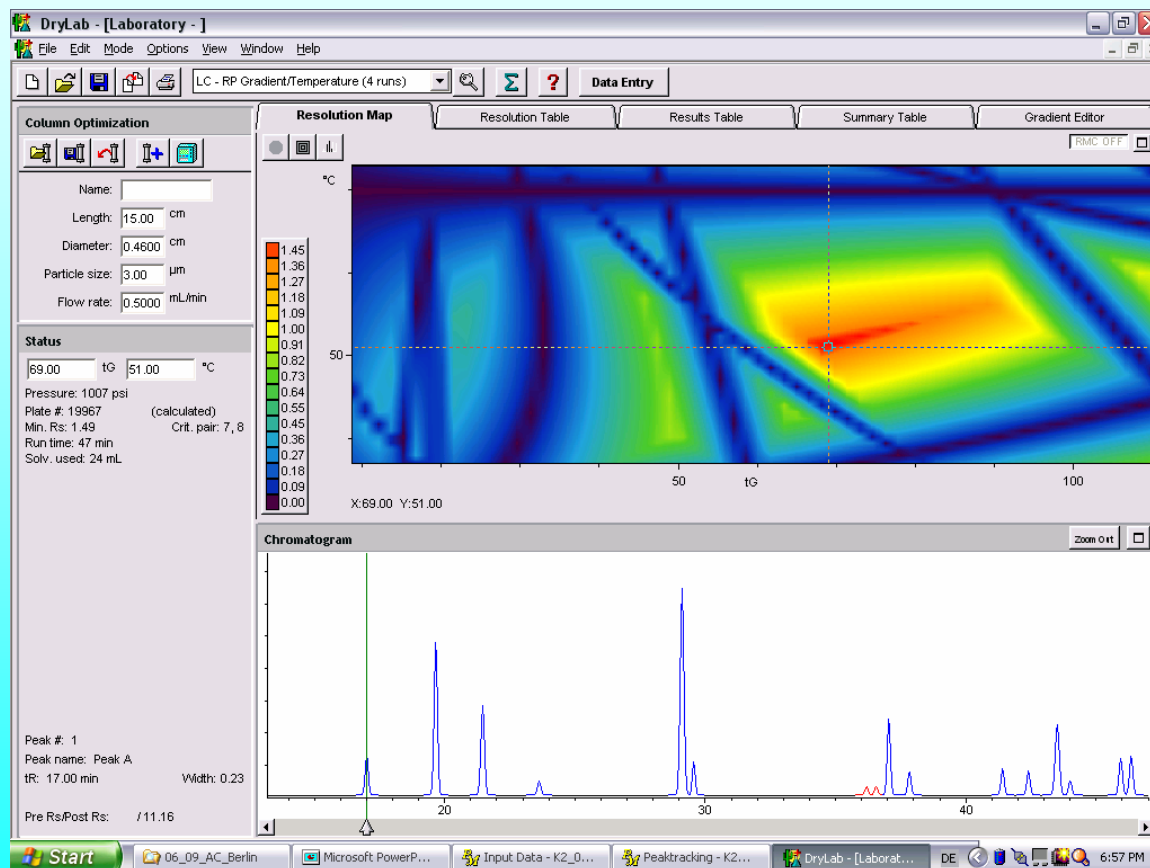
- Csaba Horváth, Yale, RP-HPLC, 1976 -> pH-retention-calculations - *moving bands*
- Lloyd Snyder, John Dolan, 1986 - present -> Development of DryLab -> platform of communication about HPLC-methods
- Resolution Maps = Method quality
- Method quality -> Product quality

# *Themes*

- A. Success in HPLC
- B. Systematic RPC
- C. Moving Peaks
- D. Peak Match
- E. Precision
- F. Robustness
- G. Exploiting Column Selectivities

# A. Success in HPLC

- Don't make lots of experiments *slow* but
- reduce the no.of bad experiments *fast*



30x100 = 3000  
bad experiments  
can be substituted

better

by  
5-10 promising  
experiments

## *B. Systematic RPC*

$$\begin{aligned} \ln k = & A + B\mathcal{D} + C\Delta A + \\ & + D(K^e - 1) V^{2/3} \gamma + E + \\ & + \ln (RT/P_0 V) \end{aligned}$$

$$C = N \gamma / RT \quad (\gamma \sim \%A = \%H_2O)$$

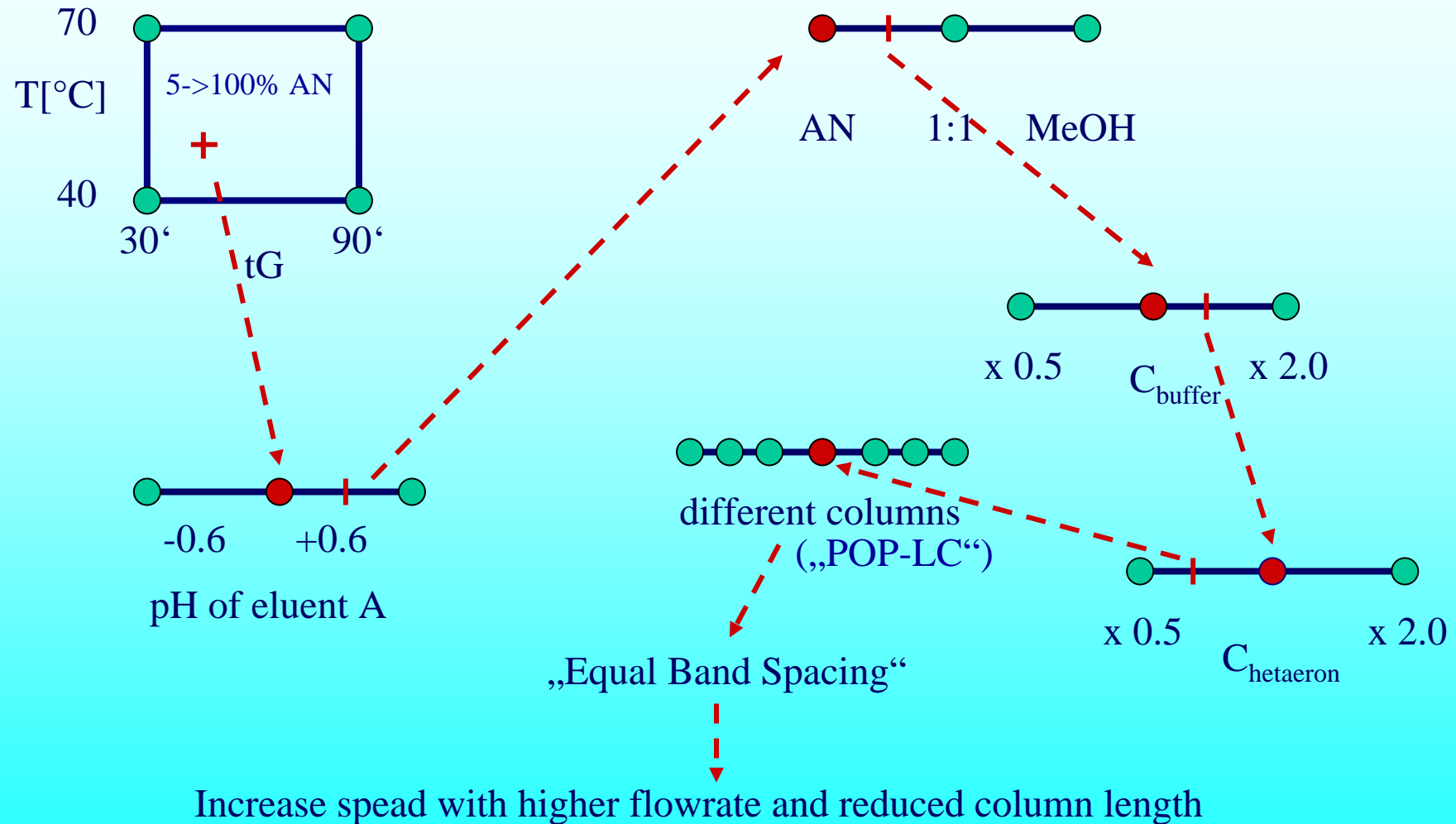
### "Solvophobic Theory"

Cs.Horváth, W.Melander, I.Molnar,  
J.Chromatogr., **125** (1976) 129.

# *Systematic RPC*

- Learn more with less experiments
- 4x (tG vs T) + 2x pH + 2x ternary composition + 6x diff.columns
- Automated generation of experiments
- Coordinate data in PeakMatch
- Transfer data to DryLab
- Evaluate DryLab-model

# Systematic MD-Strategies require for reduced analysis time maximized critical resolution



## *C. Moving peaks: Examples*

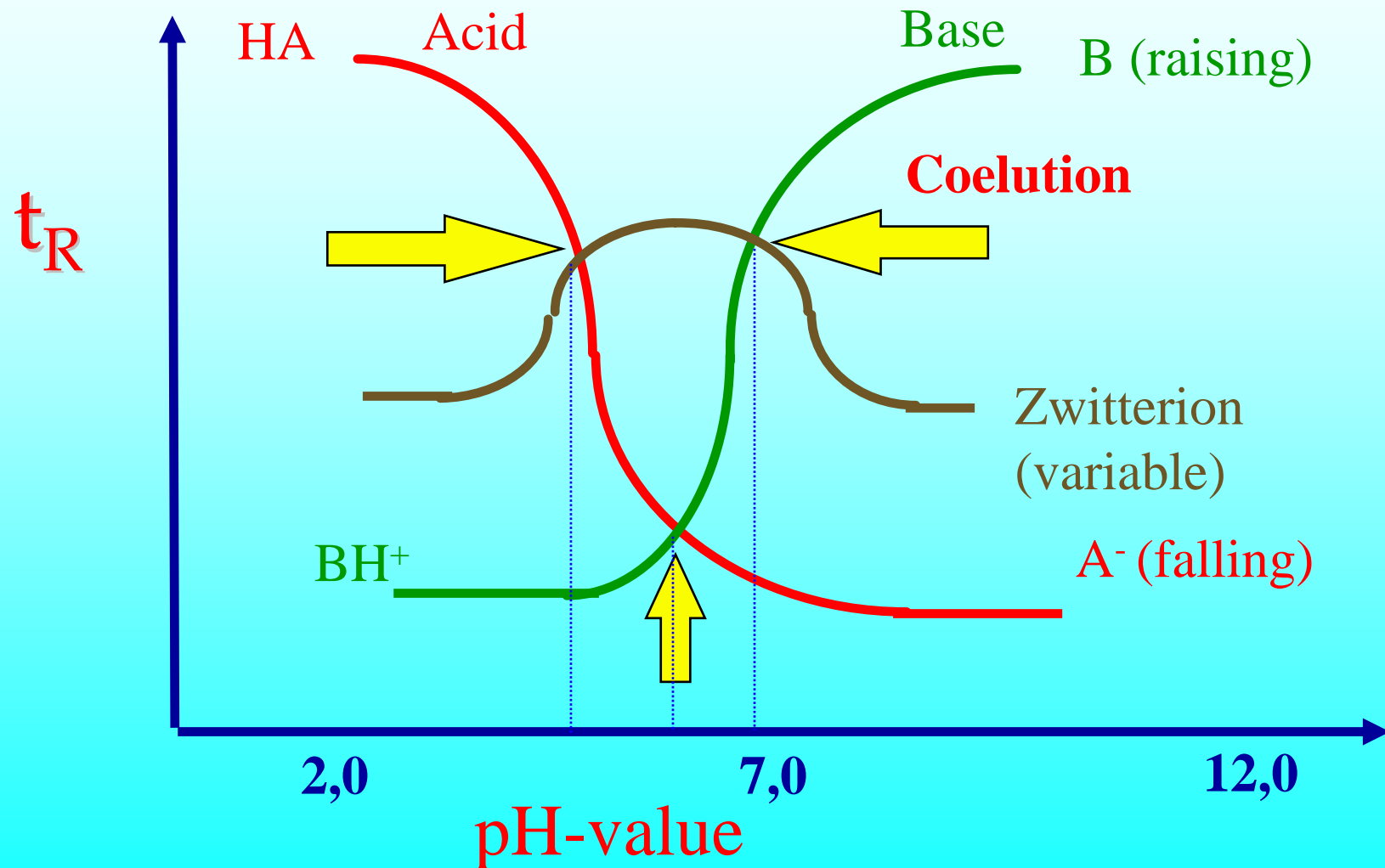
- Moving peaks with pH - isocratic model
- Moving peaks with pH - gradient model

Controlling a method means to control  
peak movements

Download examples from homepage: [www.molnar-institut.com](http://www.molnar-institut.com)



# Parameter-changes cause *continuous* selectivity changes in RPC

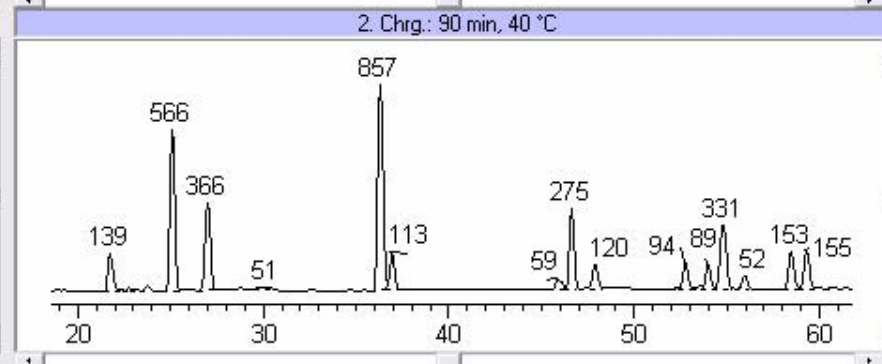
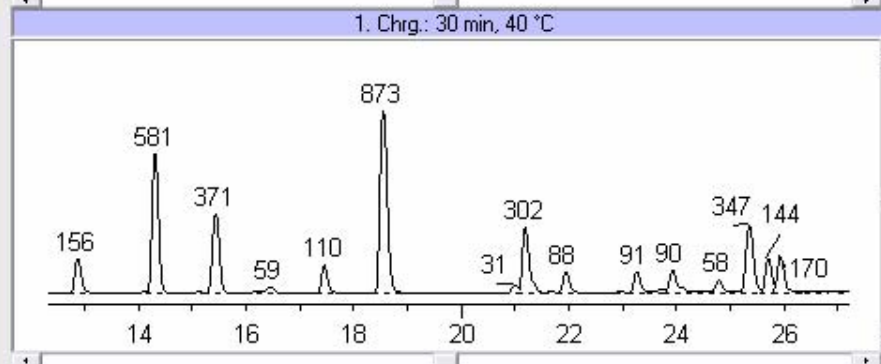
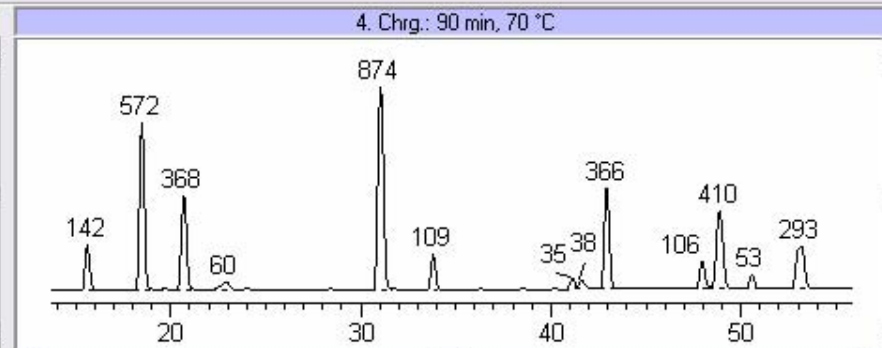
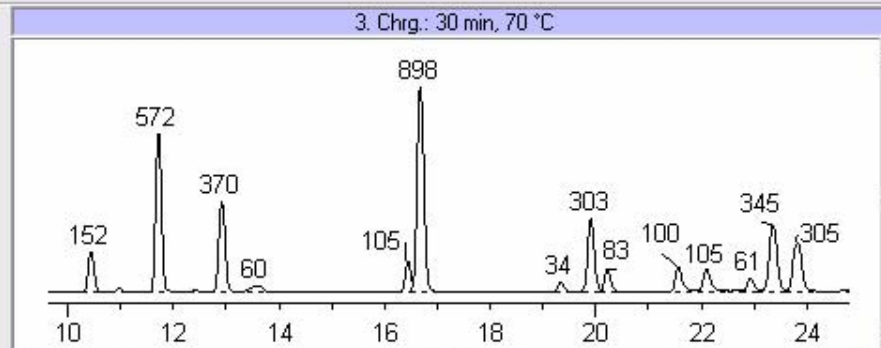


# Advantages of computerized models of separations

- Transparency of good and bad choices
- Saving the time for unnecessary runs
- Maximized resolution of separations
- Improved communication about working conditions and better development reports
- Method transfer greatly enhanced

## *D. Peak Match*

- Different runs give often confusing results - challenge to go after
- Comparisons are complicated, if trial and error experiments were carried out - systematic work is more economic
- Semi- or full automation is needed to get the data organized and to simplify the process



Vertical toolbar with icons for zooming, panning, and other plot controls.

**View Options**

Activate Chromatogram Toolbar

**Divide Peak Areas by Factor**

100000  in Chromatogram

100000  in Peak Table

**Remove small peaks**

30  smaller than

Run

	1. Chrg.: 30 min, 40 °C		2. Chrg.: 90 min, 40 °C		3. Chrg.: 30 min, 70 °C		4. Chrg.: 90 min, 70 °C			
	tR	Area	tR	Area	tR	Area	tR	Area	StdDev(%)	
1	UNKNOWN2	12.83	156	21.63	139	10.40	152	15.50	142	4.7
2	Cpnd 1	14.27	581	24.99	566	11.68	572	18.38	572	0.9
3	Cpnd 2	15.40	371	26.90	366	12.88	370	20.59	368	0.5
4	Cpnd 3	16.43	59	30.14	51	13.57	60	22.81	60	6.6
5	Cpnd 4	17.41	110	36.84	113	16.40	105	33.71	109	2.6
6	Cpnd 5	18.51	873	36.20	857	16.64	898	30.94	874	1.7
7	Cpnd 6	20.96	31	45.80	28	19.30	34	41.04	35	8.6
8	Cpnd 6 Splitted	21.15	31	45.80	31	19.87	31	41.53	38	9.3
9	Cpnd 7	21.15	271	46.52	275	19.87	272	42.83	276	0.8
10	Cpnd 8	21.91	88	47.79	90	20.18	83	42.83	90	3.3
11	Cpnd 9	23.22	91	52.66	94	21.52	100	47.84	106	5.9
12	Cpnd 10	23.89	90	53.88	89	22.06	105	48.76	87	7.7
<b>Sum of peak areas</b>			<b>3471</b>		<b>3390</b>		<b>3493</b>		<b>3426</b>	<b>1.2</b>

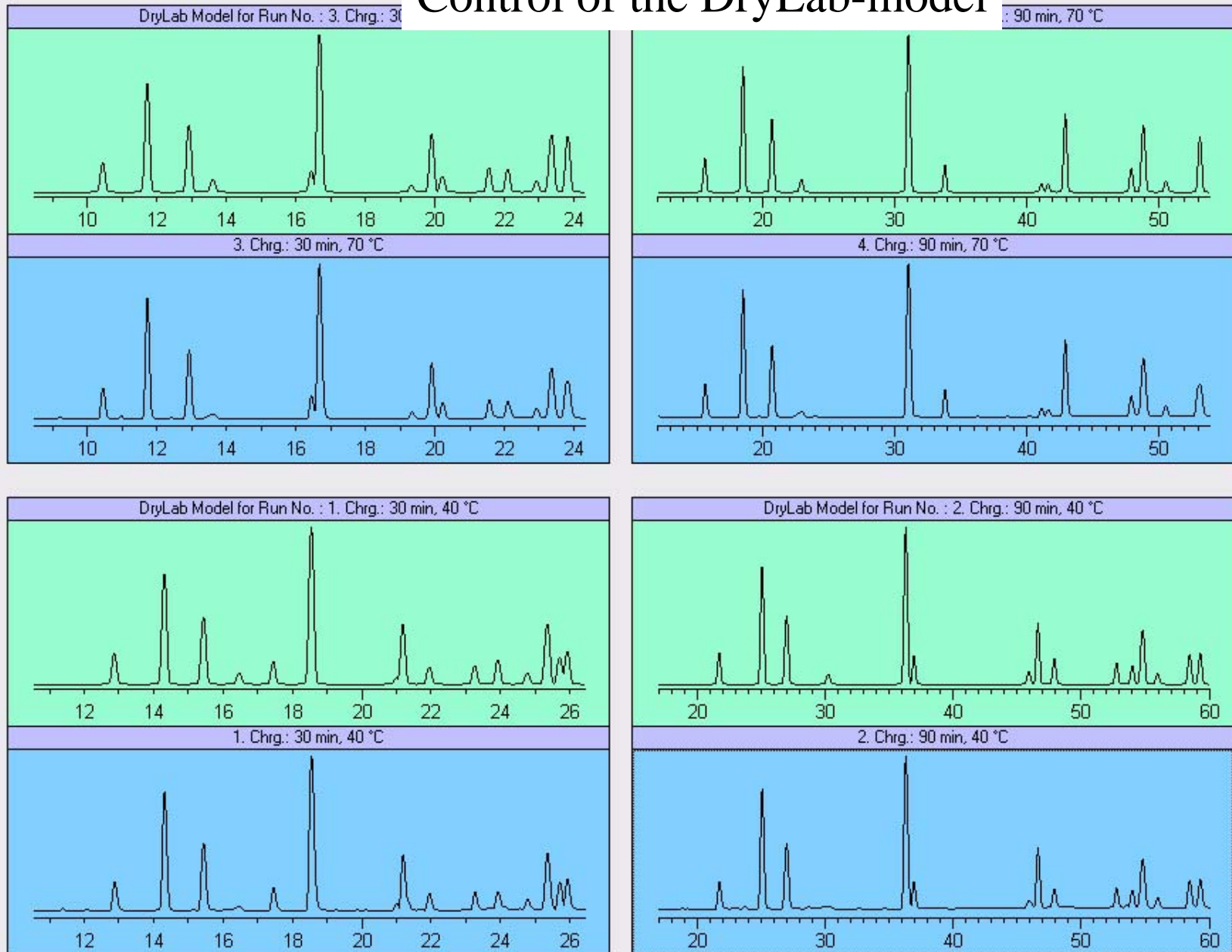
Sum of Selected Peakareas =

NUM

## *Peak Match (cont.)*

- Chromatograms + Tables on the same page
- Tools and colours to reduce errors
- Automated data transfer to DryLab
- Comparison of original- w. model-chromatograms
- Automated location of optimum conditions
- Robustness calculations

# Control of the DryLab-model



**Options**

Load Exper.

Load Sim.

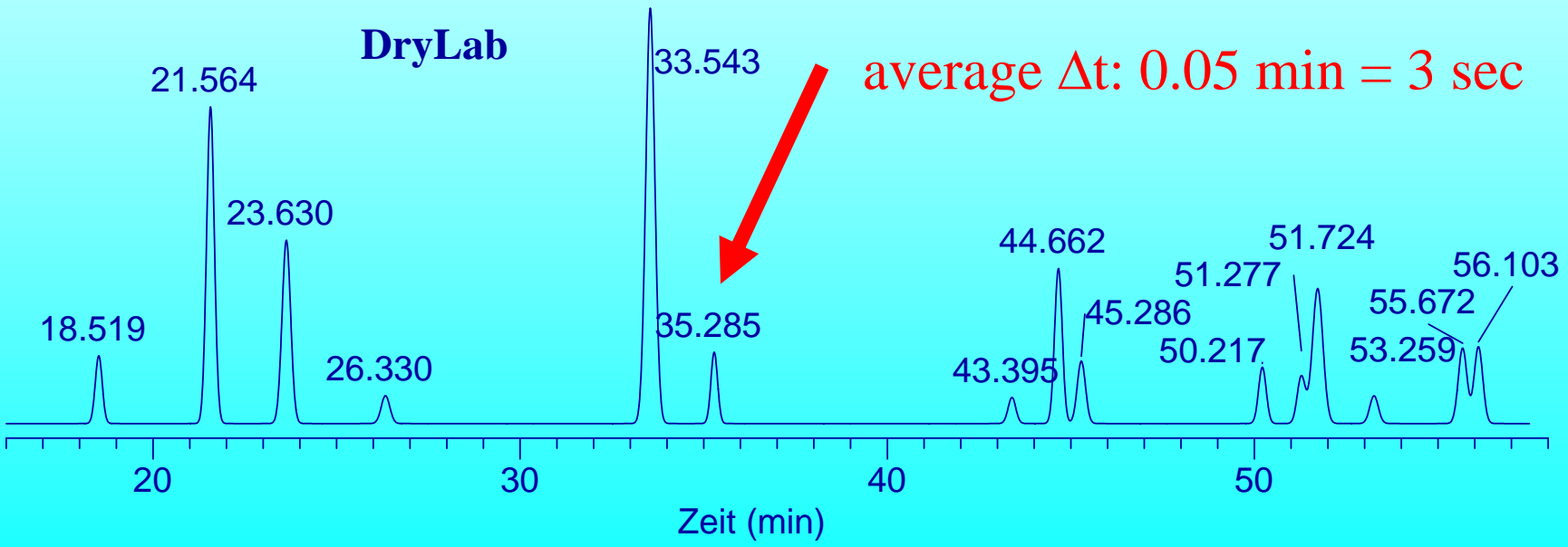
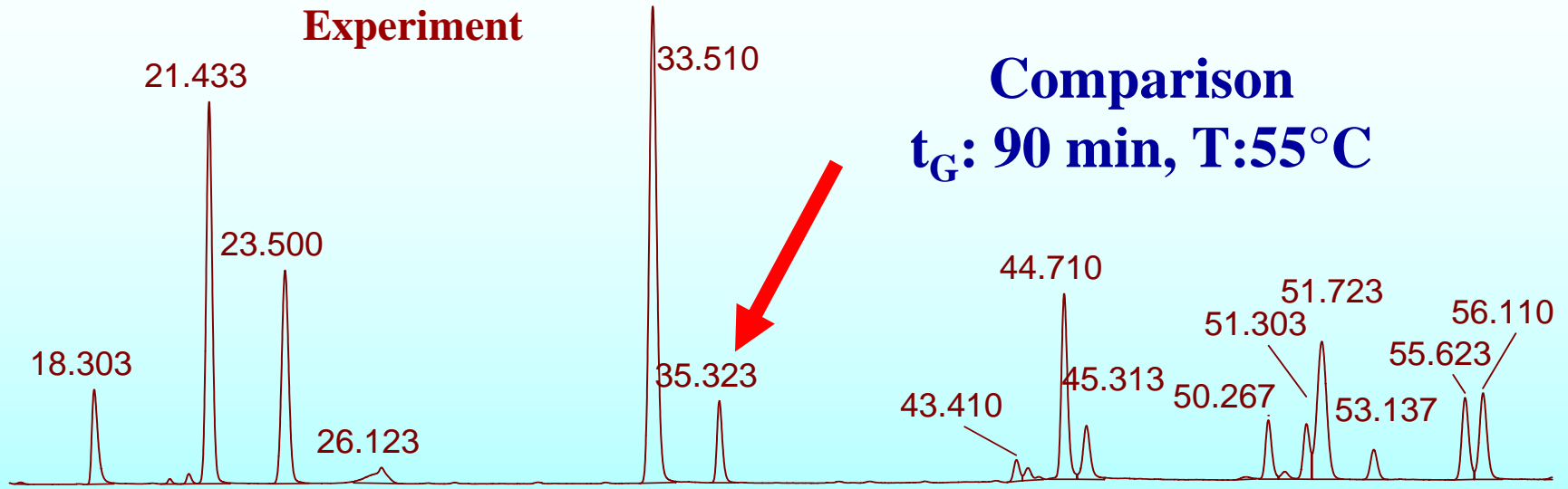
Toolbar

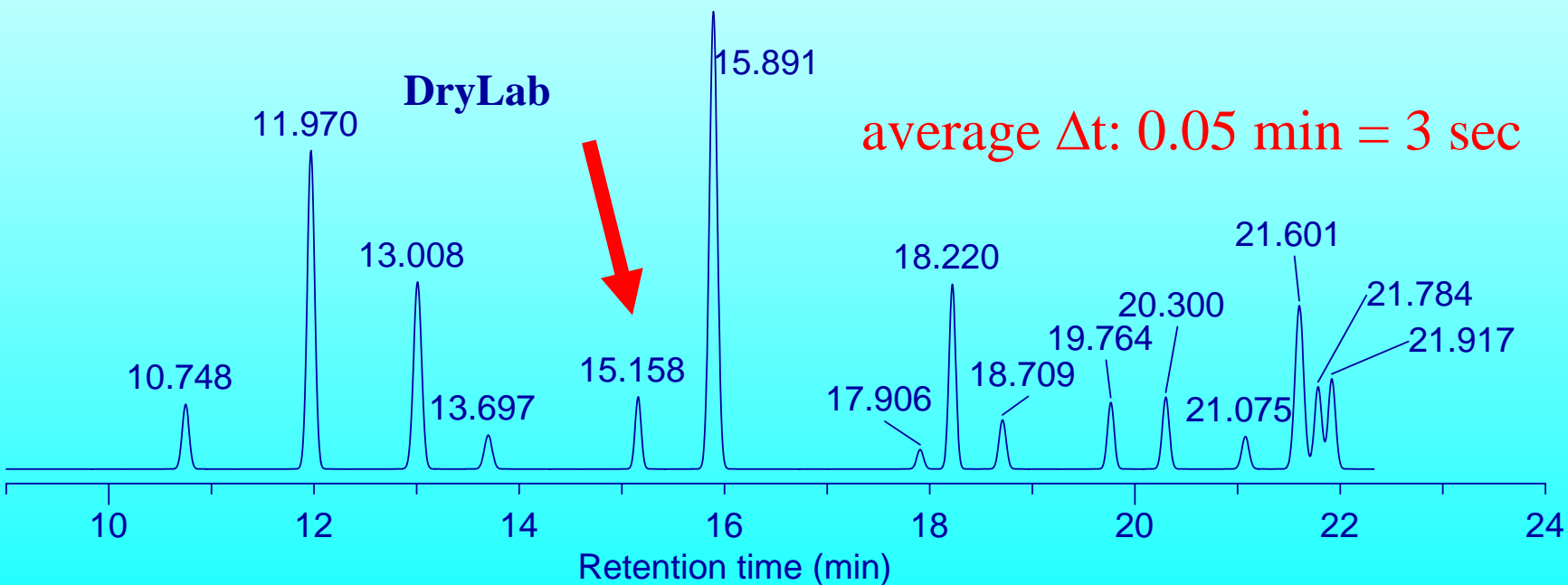
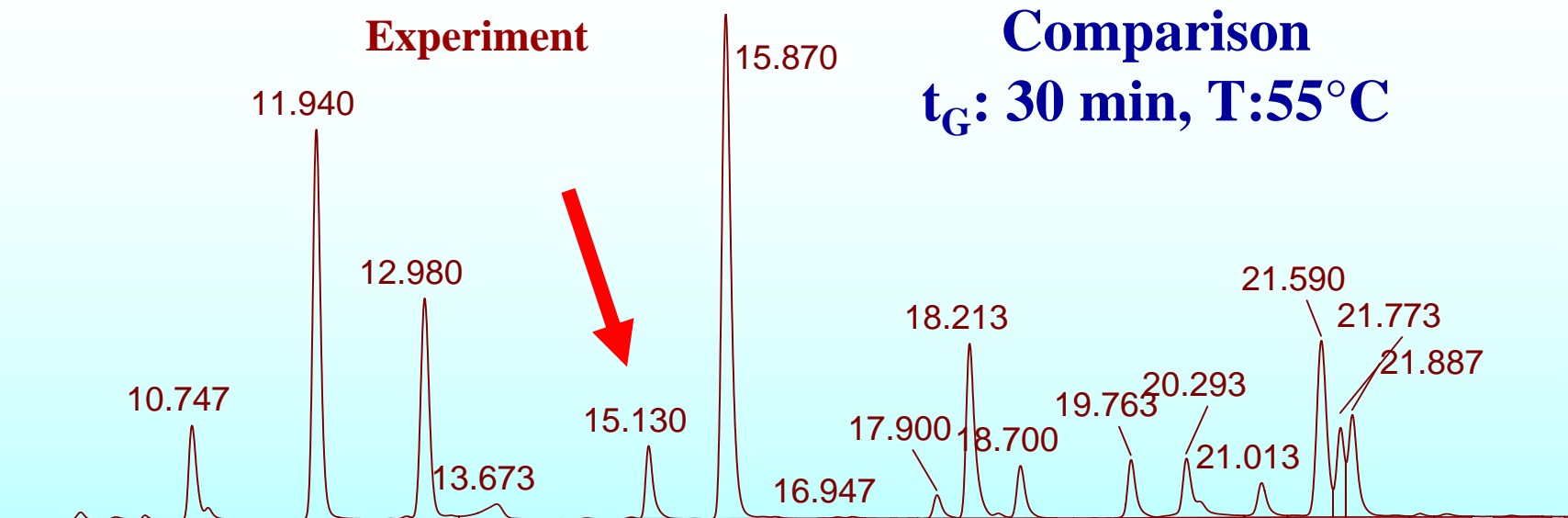
**Legend**

Sim.

Exper.

# *E. Precision of predicted data*



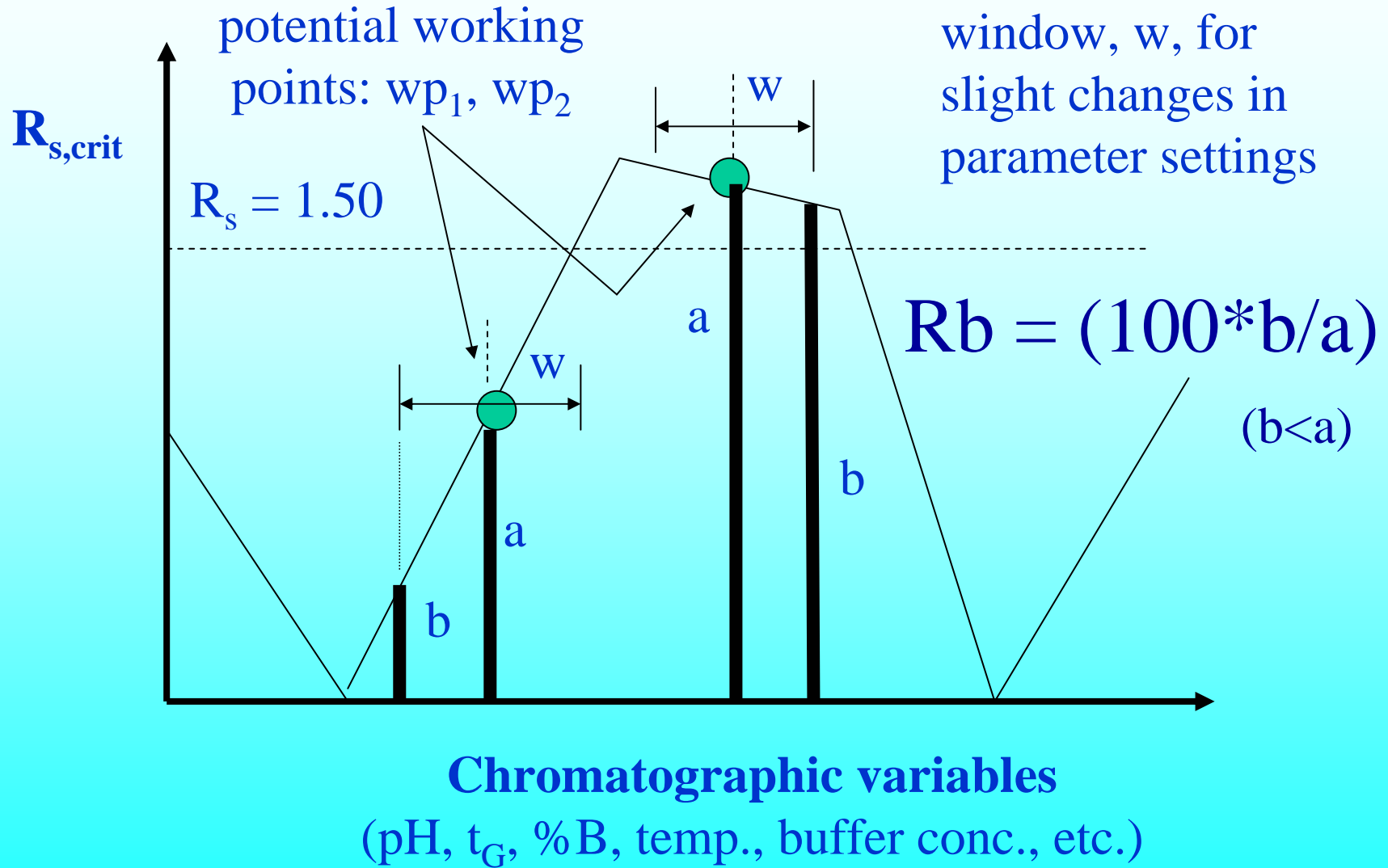




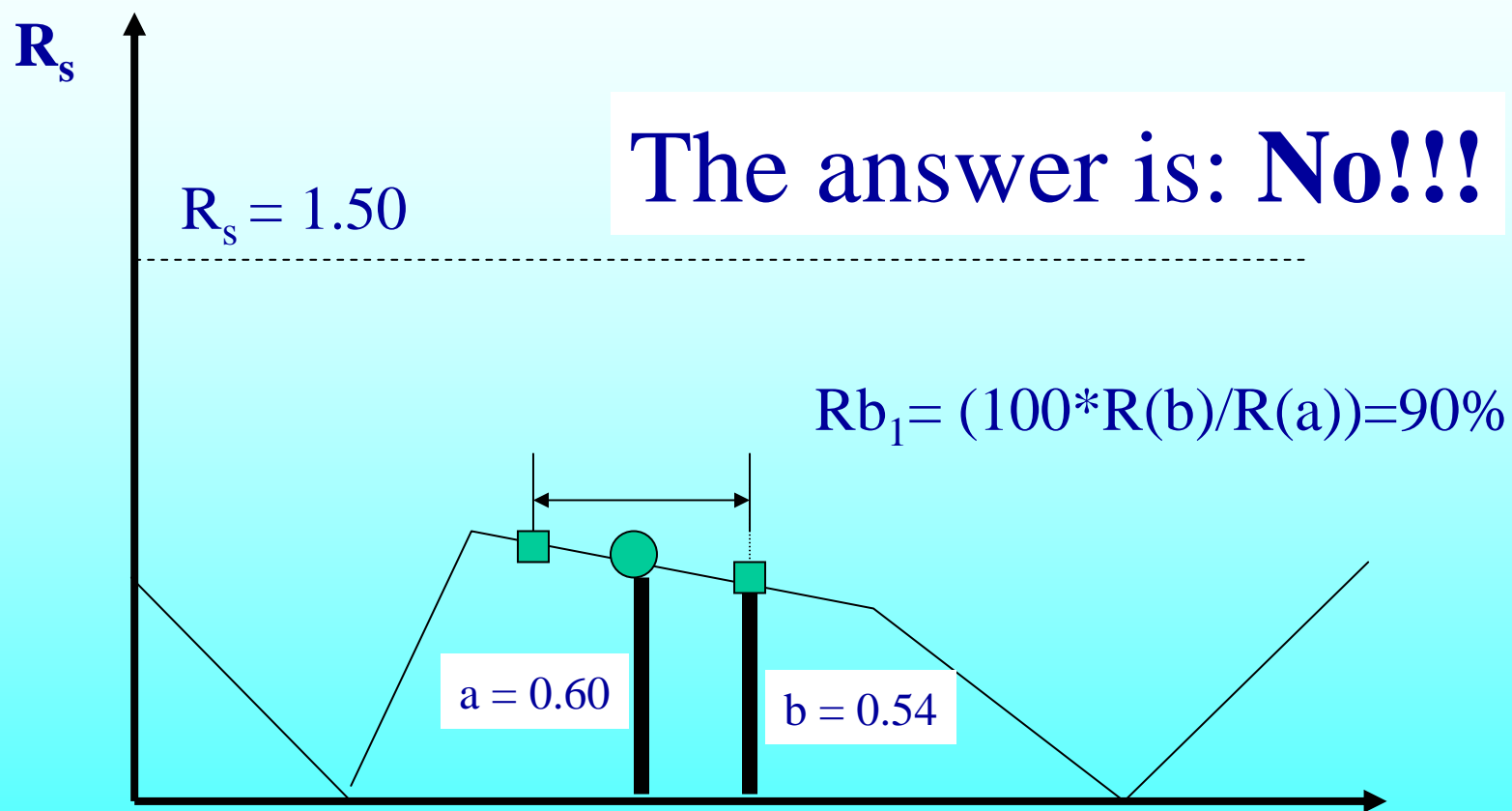
## *F. Robustness*

- Capability of the method to remain stable at small variations of the experimental parameters
- A method is robust, if it is chromatographically safe, and gives us reliable results.  
*Incorrect methods can not be robust*
- Robustness can be visualized by maps of the critical resolution in the vicinity of the working point

# Estimation of Robustness

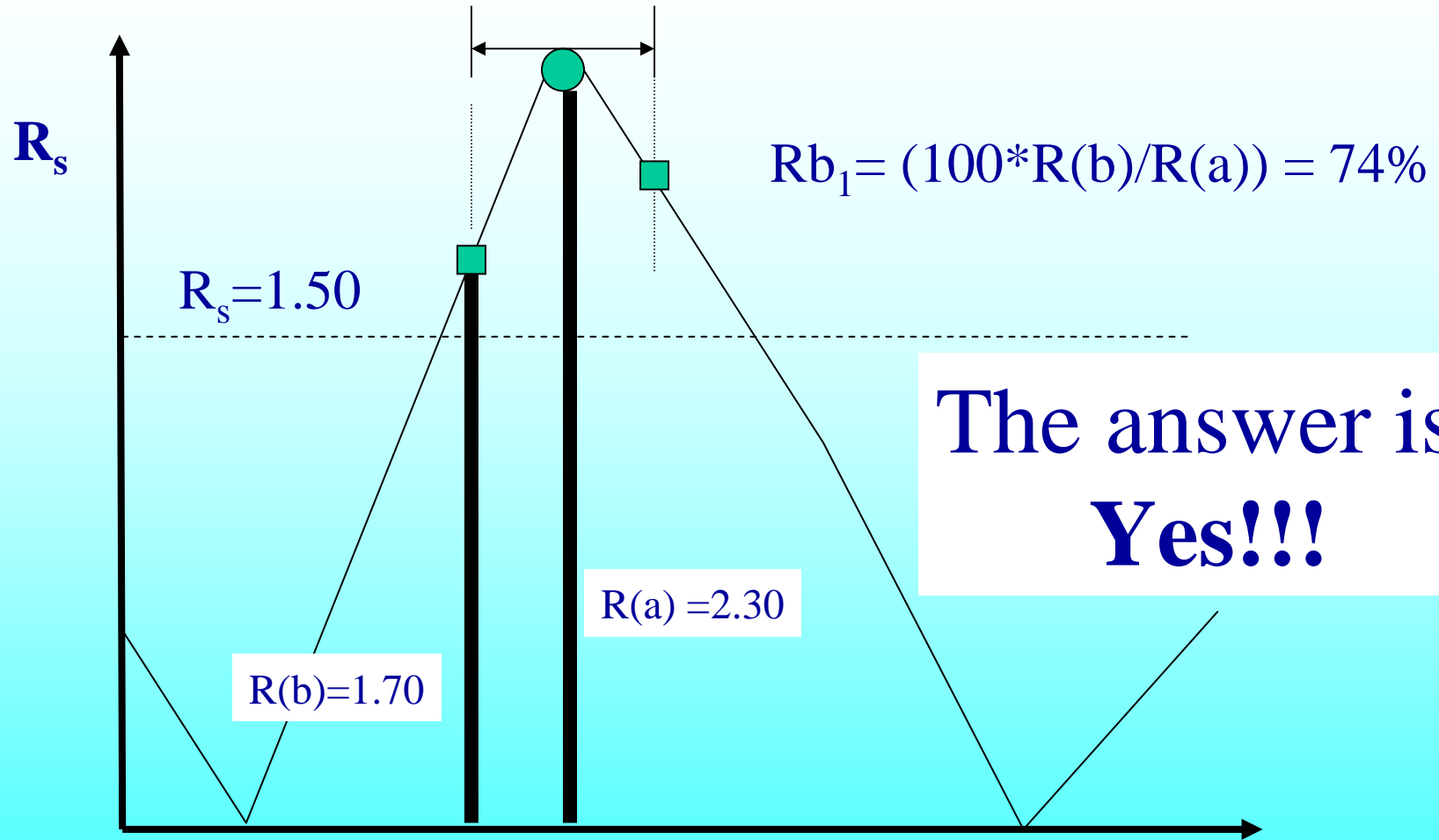


# Is this method robust?



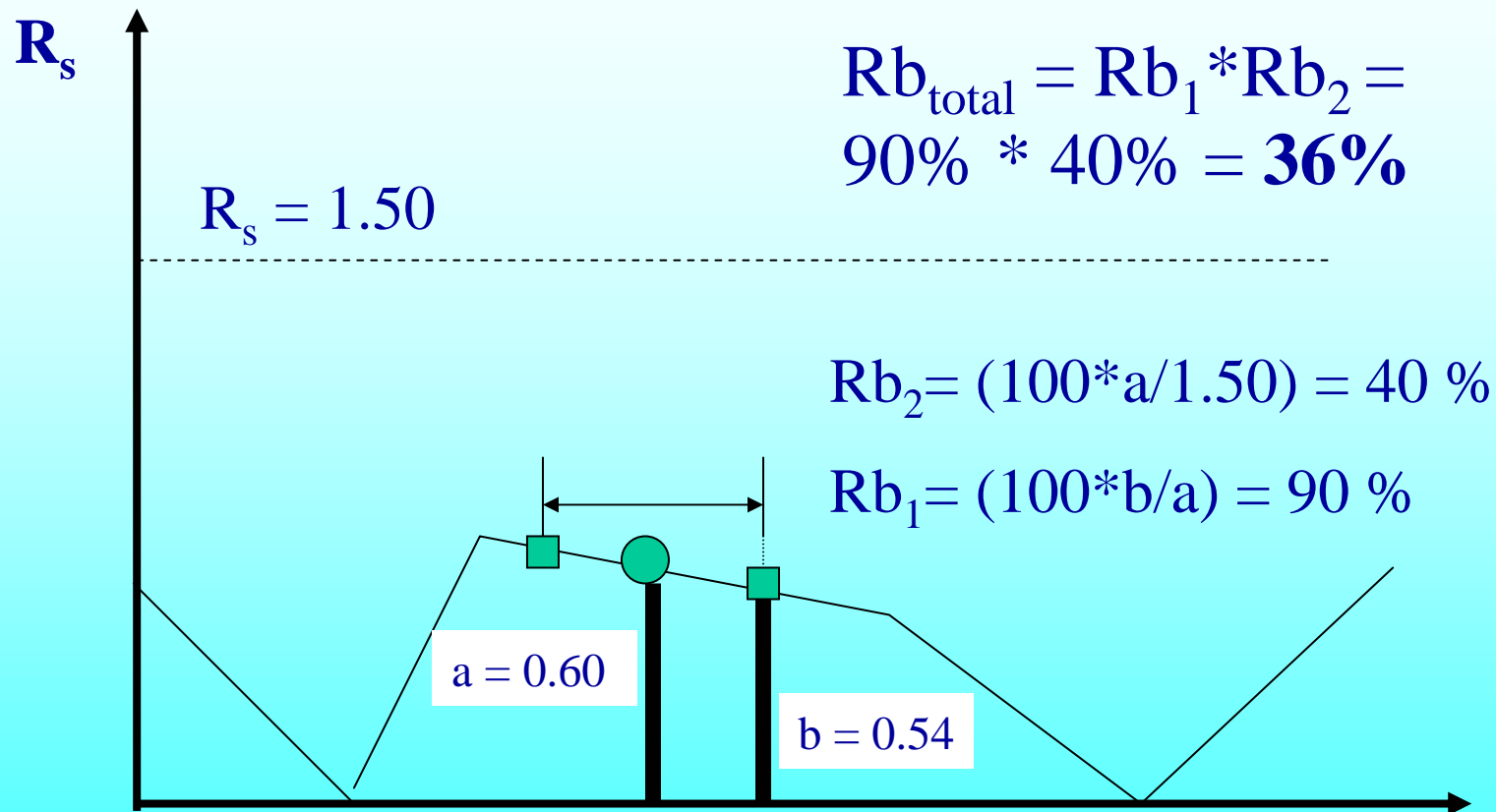
**Chromatographic variables**  
(pH, tG, %B, temp., buffer conc., etc)

# Is this method robust?



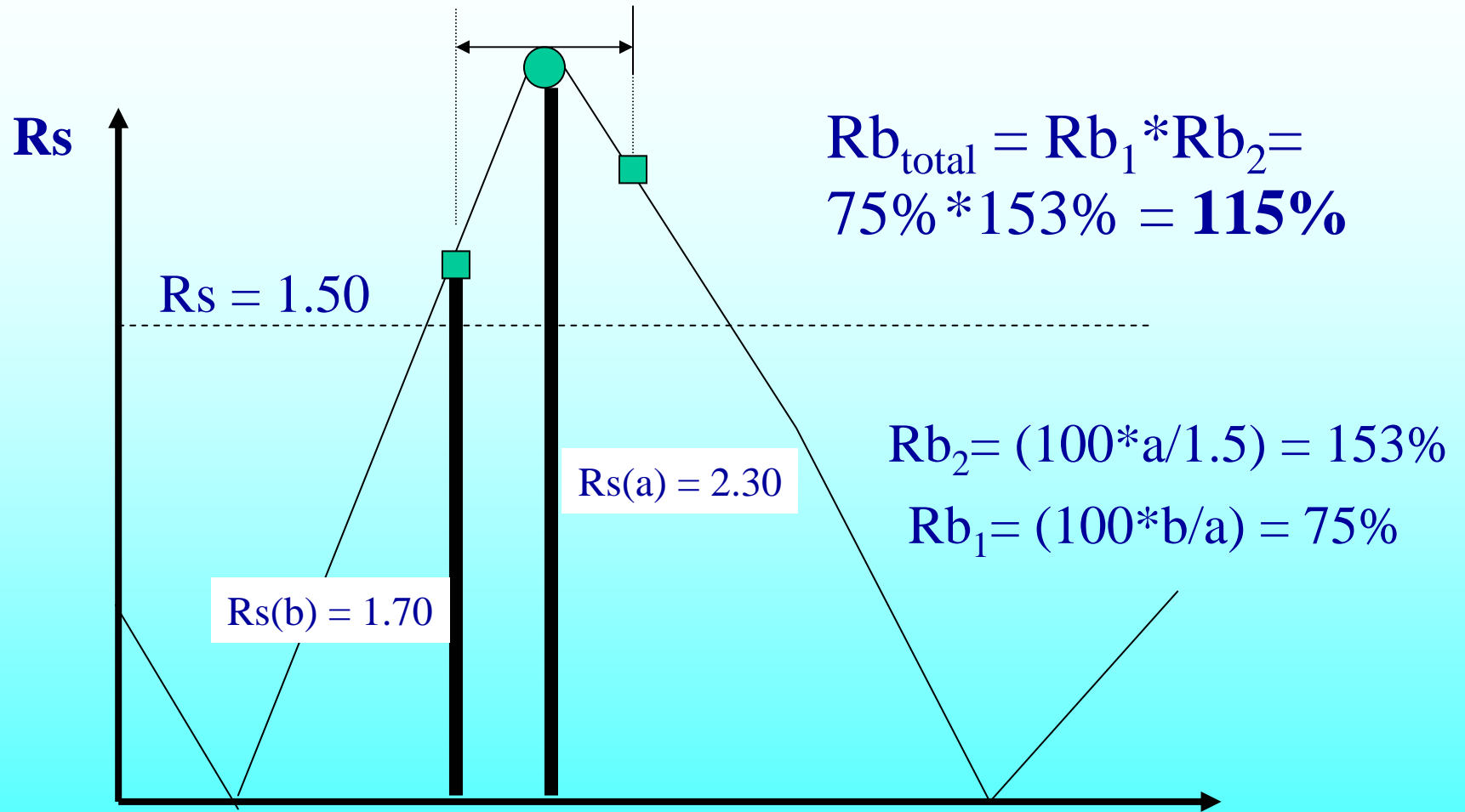
**Chromatographic variables**  
(pH, tG, %B, temp., buffer conc., etc)

# How robust is this method?



**Chromatographic variables**  
(pH, tG, %B, temp., buffer conc., etc)

# How robust is this method?



**Chromatographic variables**  
(pH, tG, %B, temp., buffer conc., etc)

# Contributions to robustness

- Contribution  $Rb_1$  from the slope of  $R_{s,crit}$  in the vicinity of the working point vs. the lower  $R_s$ -value in the working window
- Contribution  $Rb_2$  from the absolute value of  $R_{s,crit}$  at the working point.  $R_{s,crit} = 1.50$  is equal to  $Rb_2 = 100\%$

$$Rb_{total} = Rb_1 * Rb_2$$

## *G. Exploiting Column Selectivities*

### *Column Match<sup>®</sup> Database*

- Database with 300 columns using 6 Parameter
- Compares the 10 most similar and the 10 most different columns
- Selection of sample classes (acids, bases)



## Column Match: Select a Column

Back to Main Menu

"Auto-tune" Parameters

Select Sources &

Match: Close Reasonable Questionable

Column: Alltech Alltima C18

Relative Importance:

Show Columns of Type

All

Same Only

Different Only

Level of Detail

More Detail

Less Detail

Parameter							Ret'n	Type	Source
H	S	A	B	C (2.8)	C (7.0)				
0.993	-0.014	0.037	-0.013	0.093	0.391	11.5	B	Alltech	
100%	100%	100%	0%	0%	0%				

**Most Similar**

Rank	Fs	Column
1	0.0	Alltima C18
2	0.5	CAPCELL C18 M G
3	0.5	Capcell Pak C18 MGII
4	1.3	Supelcosil LC-18-DB
5	1.4	Alltima HP C18
6	1.5	ACE 5 C18-300
7	1.6	Luna C18
8	1.6	Hichrom 300 5 RPB
9	1.6	Ultrasphere Octyl
10	1.8	GROM-SIL 120 ODS-3 CP

Parameter							Relative Retention	Type	Source
H	S	A	B	C (2.8)	C (7.0)				
0.993	-0.014	0.037	-0.013	0.093	0.391	1.0	B	Alltech	
1.005	-0.010	0.042	-0.007	0.079	0.007	0.9	B	Shiseido	
1.011	-0.011	0.047	-0.006	0.007	-0.009	0.9	B	Shiseido	
0.981	-0.026	0.054	0.116	0.484	0.534	0.5	A	Supelco	
0.987	-0.026	0.059	0.011	0.190	0.193	0.4	B	Alltech	
0.968	-0.024	0.003	0.006	0.232	0.208	0.3	B	MacMod/ACT	
1.018	-0.025	0.072	0.008	-0.361	-0.036	0.9	B	Phenomenex	
0.944	-0.028	0.044	0.015	0.226	0.216	0.2	B	HiChrom	
0.896	-0.016	0.004	0.086	0.157	0.546	0.5	B	Beckman	
1.029	-0.019	0.093	-0.005	0.099	0.123	0.9	B	GROM Analytik	

**Most Different**

Rank	Fs	Column
1	54.7	Alltima HP C18 Amide
2	49.4	Inertsil ODS-EP
3	33.2	Purospher RP-18
4	29.8	ZirChrom-PS
5	27.7	Bonus RP
6	27.3	Inertsil CN-3
7	26.9	ZirChrom-EZ
8	26.0	Prontosil 120-5-C8 ace-EPS
9	25.9	ACE 5CN
10	25.6	Discovery CN

Parameter							Relative Retention	Type	Source
H	S	A	B	C (2.8)	C (7.0)				
0.466	-0.072	-1.763	-0.259	-0.978	-0.033	0.3	EP	Alltech	
0.825	0.056	-1.590	0.054	-0.600	-0.049	0.6	B	GL Science	
0.585	0.254	-0.560	-1.309	-1.934	1.109	0.5	B	Merck	
0.644	-0.284	-0.303	0.089	1.823	1.820	0.0	Other	ZirChrom	
0.737	0.074	-0.831	0.379	-2.800	-0.836	0.4	EP	Agilent	
0.369	0.049	-0.808	0.083	-2.607	-1.297	0.1	CN	GL Science	
1.110	0.100	-0.770	-0.070	2.170	2.170	0.1	Other	ZirChrom	
0.554	-0.028	-0.808	0.226	-0.255	0.121	0.3	EP	Bischoff	
0.409	-0.107	-0.729	-0.008	-0.086	0.441	0.1	CN	MacMod/ACT	
0.404	-0.111	-0.709	-0.009	-0.029	0.491	0.1	CN	Supelco	

# *Summary*

- Systematic experiments are more economic than trial and error
- Semi-automation makes model setup easy
- Visible method quality in resolution maps
- Smooth method transfer
- Method robustness quantified
- Shorter analysis time
- More reliable product quality

Thanks to

Lloyd Snyder

John Dolan

Tom Jupille

Hans-Jürgen Rieger

More information:

[www.molnar-institut.com](http://www.molnar-institut.com)