

## **Main guidelines to successfully apply the R based algorithm for pattern reconstruction procedure of chlorinated paraffins.**

**Background:** In majority of cases there are 2 types of reference standards available for quantification of chlorinated paraffins. Namely, single-chain standards (e.g. Chloroparaffin C11 65.25% Cl) or standards which contain either C10-C13 (SCCPs), C14-C17 (MCCPs) or C18-C21 (LCCPs) altogether in one mix (e.g. Chloroparaffin C10-C13 55,5% Cl). This algorithm can be used for both types. However, different calibration sheets must be used. In case of single-chain standards please use sheets, which end with "Single chain". In case of group standards, please use sheets, which end with "All chains".

This quantification approach can be applied for both – GC-MS and LC-MS analysis to process results for SCCPs, MCCPs or LCCPs. It is also possible to substitute all area values with ratios (Target/ISTD) in case internal standard approach has been used. General workflow for pattern reconstruction and quantification of CPs is as follows:

- 1.) Measurement of calibration solutions.
- 2.) Fill acquired calibration data in corresponding Excel sheets.
- 3.) Sample measurement.
- 4.) Fill acquired sample data in corresponding Excel sheet.
- 5.) Pattern reconstruction and quantification in R.

*Contact [ingus.perkons\[at\]bior.lv](mailto:ingus.perkons[at]bior.lv) if you experience any serious problems with the R. code or provided .xlsx documents. This is a part of supplementary material for article ([link](#)). Please refer to the article for further information.*

**Note: Authors do not take any responsibility for the accuracy of the quantification/pattern reconstruction data obtained with this approach. Additionally, this algorithm should be used for research/educational purposes only.**

**If using multiple chain standards** – measure a calibration curve for each standard mixture. In order to accurately enter calibration results – please use Excel document - "[CP calibration - multiple chains.xlsx](#)".

**If using single chain standards** – I suggest to create several specific mixtures of standard solutions, where one measurement covers four different  $C_{n-n+3}$  standards. Although, single-chain CP standards can be measured separately, there is no need to analyze them one by one, as standards with different carbon chain lengths do not overlap, thus 4 different single-chain standards can be measured in one single run. Nevertheless, it is possible to measure mixtures which contain e.g. only two chain length standards. In such case – leave the unnecessary homologue rows blank. In order to accurately enter calibration results – please use Excel document - "[CP calibration - single chains.xlsx](#)".

Each Excel document which is used to store calibration data, contains 3 sheets - "SCCPs", "MCCPs", and "LCCPs". Unfortunately, this R algorithm can only simultaneously process data for either SCCPs, MCCPs or LCCPs, but not all three (or two) groups together.

#### **Each sheet contains several important columns:**

**Column A - "Standard mixture"** – Contains arbitrary name for each calibration mixture. Must be different for each  $C_{n-n+3}$  CP group. I personally prefer to name them "Type-A/B/C/D/E" (e.g. SCCP-A, MCCP-C, etc.).

**Column B - "Standard used"** – Contains name of reference standard used for the particular standard mixture in calibration curve.

**Column C - "Chain length"** – Chain length of each CP homologue

**Column D - "Type"** – Chlorinated paraffin type: SCCP, MCCP or LCCP

**Column E - "Homologue"** – Molecular formula of CP homologues.

**Columns F,G,H,I,J,K,L,M - "Calibration levels"** – Calibration levels used to construct calibration curve. By default, there are a maximum of 8 calibration levels, however, you don't need to fill all of them. Concentration levels (conc. values) can be changed as you want and number of levels is up to you. However, it's important that the last calibration level is in column "M". You can delete unnecessary/unused calibration levels starting from column "F".

**Columns N,O,P,Q,R,S,T,U - "Areas"** – From column "N" to "U" you can store acquired peak areas (or ratios in case of internal standard applications) for each homologue. If no homologue is detected, just leave those cells blank (it will be greyed out).

**Columns V and W** - contains  $R^2$  (square of the Pearson product moment correlation coefficient) and response factor (RF) for each homologue (slope of the linear regression line through data points,  $b = 0$ ). Both columns are calculated automatically from the given calibration data.

**Columns Z,AA,AB,AC,AD,AE** - contain all the necessary data, which must be copied (using Paste->Values) to "input\_ref.xls" document, which will be later used for pattern reconstruction procedure in R.

## Running ".R" scripts

To run the code you'll need to install R-Stats from one of the CRAN mirrors (<https://cran.r-project.org/mirrors.html>) and, preferably, RStudio - an integrated development environment (IDE), which can be downloaded from <https://www.rstudio.com/products/rstudio/#Desktop>. For this code three R packages are necessary ("readxl", "ggplot2", and "dplyr"). When running the code for the first time they will be installed automatically. An in-depth guide for running the algorithm is provided below. Additional information regarding R and RStudio can be found online in developer homepages - <https://cran.r-project.org> and <https://www.rstudio.com>, respectively.

**Note:** There are two ".R" files uploaded in repository. In case of single chain CP standards use **"ParaffinCrawler-Chain.R"**, while for multiple chain standards use **"ParaffinCrawler-Group.R"**

## A guide on how to perform the procedure is illustrated below (example of single chain SCCP standards)

### 1.) Measure reference mixtures at different calibration levels

An example composition

Standard	SCCP-A	SCCP-B	SCCP-C	SCCP-D	SCCP-E
C10 50%	x				
C11 45%	x				
C12 52%	x				
C13 59%	x				
C10 55%		x			
C11 50%		x			
C12 55%		x			
C13 65%		x			
C10 60%			x		
C11 55%			x		
C12 60%			x		
C13 69%			x		
C10 65%				x	
C11 60%				x	
C12 65%				x	
C13 75%				x	
C11 69%					x
C12 69%					x

2.) Fill standard mixture "SCCP-A" information data in "CP calibration - single chains.xlsx" document columns A-B.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y				
1						Calibration LEVELS								Calibration LEVELS									Response factor of each homologue per 1 ng/μL		Data which must be cop				
2	Standard mixture	Standard used	Chain length	Type	Homologue	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8	R <sup>2</sup>							
3						C, ng/μL								Area								Area							
4	A-SCCP	C10 50%	C10	SCCP	C10H17CI5																	#N/A	#N/A		A				
5	A-SCCP	C10 50%	C10	SCCP	C10H16CI6																	#N/A	#N/A		A				
6	A-SCCP	C10 50%	C10	SCCP	C10H15CI7																	#N/A	#N/A		A				
7	A-SCCP	C10 50%	C10	SCCP	C10H14CI8																	#N/A	#N/A		A				
8	A-SCCP	C10 50%	C10	SCCP	C10H13CI9																	#N/A	#N/A		A				
9	A-SCCP	C10 50%	C10	SCCP	C10H12CI10																	#N/A	#N/A		A				
10	A-SCCP	C10 50%	C10	SCCP	C10H11CI11																	#N/A	#N/A		A				
11	A-SCCP	C11 45%	C11	SCCP	C11H19CI5																	#N/A	#N/A		A				
12	A-SCCP	C11 45%	C11	SCCP	C11H18CI6																	#N/A	#N/A		A				
13	A-SCCP	C11 45%	C11	SCCP	C11H17CI7																	#N/A	#N/A		A				
14	A-SCCP	C11 45%	C11	SCCP	C11H16CI8																	#N/A	#N/A		A				
15	A-SCCP	C11 45%	C11	SCCP	C11H15CI9																	#N/A	#N/A		A				
16	A-SCCP	C11 45%	C11	SCCP	C11H14CI10																	#N/A	#N/A		A				
17	A-SCCP	C11 45%	C11	SCCP	C11H13CI11																	#N/A	#N/A		A				
18	A-SCCP	C12 52%	C12	SCCP	C12H21CI5																	#N/A	#N/A		A				
19	A-SCCP	C12 52%	C12	SCCP	C12H20CI6																	#N/A	#N/A		A				
20	A-SCCP	C12 52%	C12	SCCP	C12H19CI7																	#N/A	#N/A		A				
21	A-SCCP	C12 52%	C12	SCCP	C12H18CI8																	#N/A	#N/A		A				
22	A-SCCP	C12 52%	C12	SCCP	C12H17CI9																	#N/A	#N/A		A				
23	A-SCCP	C12 52%	C12	SCCP	C12H16CI10																	#N/A	#N/A		A				
24	A-SCCP	C12 52%	C12	SCCP	C12H15CI11																	#N/A	#N/A		A				
25	A-SCCP	C13 59%	C13	SCCP	C13H23CI5																	#N/A	#N/A		A				
26	A-SCCP	C13 59%	C13	SCCP	C13H22CI6																	#N/A	#N/A		A				
27	A-SCCP	C13 59%	C13	SCCP	C13H21CI7																	#N/A	#N/A		A				
28	A-SCCP	C13 59%	C13	SCCP	C13H20CI8																	#N/A	#N/A		A				
29	A-SCCP	C13 59%	C13	SCCP	C13H19CI9																	#N/A	#N/A		A				
30	A-SCCP	C13 59%	C13	SCCP	C13H18CI10																	#N/A	#N/A		A				
31	A-SCCP	C13 59%	C13	SCCP	C13H17CI11																	#N/A	#N/A		A				
32																						#N/A	#N/A						
33																						#N/A	#N/A						
34																						#N/A	#N/A						
35																						#N/A	#N/A						
36																						#N/A	#N/A						

3.) Fill standard mixture "SCCP-A" calibration levels in "CP calibration - single chains.xlsx" document columns F-M.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1						Calibration LEVELS								Calibration LEVELS								R <sup>2</sup>	Response factor of each homologue per 1 ng/μL	Data which must be co		
2	Standard mixture	Standard used	Chain length	Type	Homologue	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8					
3						C, ng/μL								Area												
4	A-SCCP	C10 50%	C10	SCCP	C10H17CI5			0.5	1	2	4	8	16										#N/A	#N/A		
5	A-SCCP	C10 50%	C10	SCCP	C10H16CI6			0.5	1	2	4	8	16										#N/A	#N/A		
6	A-SCCP	C10 50%	C10	SCCP	C10H15CI7			0.5	1	2	4	8	16										#N/A	#N/A		
7	A-SCCP	C10 50%	C10	SCCP	C10H14CI8			0.5	1	2	4	8	16										#N/A	#N/A		
8	A-SCCP	C10 50%	C10	SCCP	C10H13CI9			0.5	1	2	4	8	16										#N/A	#N/A		
9	A-SCCP	C10 50%	C10	SCCP	C10H12CI10			0.5	1	2	4	8	16										#N/A	#N/A		
10	A-SCCP	C10 50%	C10	SCCP	C10H11CI11			0.5	1	2	4	8	16										#N/A	#N/A		
11	A-SCCP	C11 45%	C11	SCCP	C11H19CI5	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
12	A-SCCP	C11 45%	C11	SCCP	C11H18CI6	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
13	A-SCCP	C11 45%	C11	SCCP	C11H17CI7	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
14	A-SCCP	C11 45%	C11	SCCP	C11H16CI8	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
15	A-SCCP	C11 45%	C11	SCCP	C11H15CI9	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
16	A-SCCP	C11 45%	C11	SCCP	C11H14CI10	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
17	A-SCCP	C11 45%	C11	SCCP	C11H13CI11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
18	A-SCCP	C12 52%	C12	SCCP	C12H21CI5	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
19	A-SCCP	C12 52%	C12	SCCP	C12H20CI6	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
20	A-SCCP	C12 52%	C12	SCCP	C12H19CI7	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
21	A-SCCP	C12 52%	C12	SCCP	C12H18CI8	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
22	A-SCCP	C12 52%	C12	SCCP	C12H17CI9	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
23	A-SCCP	C12 52%	C12	SCCP	C12H16CI10	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
24	A-SCCP	C12 52%	C12	SCCP	C12H15CI11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		
25	A-SCCP	C13 59%	C13	SCCP	C13H23CI5			0.5	1	2	4	8	16										#N/A	#N/A		
26	A-SCCP	C13 59%	C13	SCCP	C13H22CI6			0.5	1	2	4	8	16										#N/A	#N/A		
27	A-SCCP	C13 59%	C13	SCCP	C13H21CI7			0.5	1	2	4	8	16										#N/A	#N/A		
28	A-SCCP	C13 59%	C13	SCCP	C13H20CI8			0.5	1	2	4	8	16										#N/A	#N/A		
29	A-SCCP	C13 59%	C13	SCCP	C13H19CI9			0.5	1	2	4	8	16										#N/A	#N/A		
30	A-SCCP	C13 59%	C13	SCCP	C13H18CI10			0.5	1	2	4	8	16										#N/A	#N/A		
31	A-SCCP	C13 59%	C13	SCCP	C13H17CI11			0.5	1	2	4	8	16										#N/A	#N/A		
32																										

4.) Fill acquired areas for standard mixture "SCCP-A" calibration levels in "CP calibration - single chains.xlsx" document columns N-U.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Standard mixture	Standard used	Chain length	Type	Homologue	Calibration LEVELS								Calibration LEVELS								R <sup>2</sup>	Response factor of each homologue per 1 ng/μL	Data which must be c		
2						1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8					
3						C, ng/μL								Area	Area	Area	Area	Area	Area	Area	Area					
4	A-SCCP	C10 50%	C10	SCCP	C10H17CI5	0.13	0.25	0.5	1	2	4	8	16					25000	49000	94000	201000	#N/A	#N/A			
5	A-SCCP	C10 50%	C10	SCCP	C10H16CI6	0.1	0.25	0.5	1	2	4	8	16									0.998447235	25157			
6	A-SCCP	C10 50%	C10	SCCP	C10H15CI7	0.1	0.25	0.5	1	2	4	8	16					12500	24000	50000	110000	200000	400000	0.999205151	24953	
7	A-SCCP	C10 50%	C10	SCCP	C10H14CI8	0.1	0.25	0.5	1	2	4	8	16	1000	2500	5000	10000	20000	40000	80000	160000	0.999997653	10005			
8	A-SCCP	C10 50%	C10	SCCP	C10H13CI9	0.1	0.25	0.5	1	2	4	8	16	500	1250	2500	5000	10000	20000	40000	80000	0.999997653	5002			
9	A-SCCP	C10 50%	C10	SCCP	C10H12CI10	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
10	A-SCCP	C10 50%	C10	SCCP	C10H11CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
11	A-SCCP	C11 45%	C11	SCCP	C11H19CI5	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
12	A-SCCP	C11 45%	C11	SCCP	C11H18CI6	0.1	0.25	0.5	1	2	4	8	16	3000	7500	15000	30000	60000	120000	240000	480000	0.999997653	30014			
13	A-SCCP	C11 45%	C11	SCCP	C11H17CI7	0.1	0.25	0.5	1	2	4	8	16	4000	10000	20000	40000	80000	160000	320000	640000	0.999997653	40018			
14	A-SCCP	C11 45%	C11	SCCP	C11H16CI8	0.1	0.25	0.5	1	2	4	8	16	2100	5250	10500	21000	42000	84000	168000	336000	0.996516383	20635			
15	A-SCCP	C11 45%	C11	SCCP	C11H15CI9	0.1	0.25	0.5	1	2	4	8	16	700	1750	3500	7000	14000	28000	56000	112000	0.999997653	7003			
16	A-SCCP	C11 45%	C11	SCCP	C11H14CI10	0.1	0.25	0.5	1	2	4	8	16	300	750	1500	3000	6000	12000	24000	48000	0.999997653	3001			
17	A-SCCP	C11 45%	C11	SCCP	C11H13CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
18	A-SCCP	C12 52%	C12	SCCP	C12H21CI5	0.1	0.25	0.5	1	2	4	8	16	500	1250	2500	5000	10000	20000	40000	80000	0.999997653	5002			
19	A-SCCP	C12 52%	C12	SCCP	C12H20CI6	0.1	0.25	0.5	1	2	4	8	16	4500	11250	22500	45000	90000	180000	360000	720000	0.999997653	45020			
20	A-SCCP	C12 52%	C12	SCCP	C12H19CI7	0.1	0.25	0.5	1	2	4	8	16	3700	9250	18500	37000	74000	148000	296000	592000	0.999997653	37017			
21	A-SCCP	C12 52%	C12	SCCP	C12H18CI8	0.1	0.25	0.5	1	2	4	8	16	2000	5000	10000	20000	40000	80000	160000	320000	0.999997653	20009			
22	A-SCCP	C12 52%	C12	SCCP	C12H17CI9	0.1	0.25	0.5	1	2	4	8	16			2500	5000	10000	20000	40000	80000	1	5000			
23	A-SCCP	C12 52%	C12	SCCP	C12H16CI10	0.1	0.25	0.5	1	2	4	8	16				5000	10000	20000	40000	80000	1	5000			
24	A-SCCP	C12 52%	C12	SCCP	C12H15CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
25	A-SCCP	C13 59%	C13	SCCP	C13H23CI5			0.5	1	2	4	8	16				7000	14000	28000	56000	112000	1	7000			
26	A-SCCP	C13 59%	C13	SCCP	C13H22CI6			0.5	1	2	4	8	16			15000	30000	60000	120000	240000	480000	1	30000			
27	A-SCCP	C13 59%	C13	SCCP	C13H21CI7			0.5	1	2	4	8	16	4500	11250	22500	45000	90000	180000	360000	720000	1	45000			
28	A-SCCP	C13 59%	C13	SCCP	C13H20CI8			0.5	1	2	4	8	16	2700	6750	13500	27000	54000	108000	216000	432000	1	27000			
29	A-SCCP	C13 59%	C13	SCCP	C13H19CI9			0.5	1	2	4	8	16	1200	3000	6000	12000	24000	48000	96000	192000	1	12000			
30	A-SCCP	C13 59%	C13	SCCP	C13H18CI10			0.5	1	2	4	8	16	200	500	1000	2000	4000	8000	16000	32000	1	2000			
31	A-SCCP	C13 59%	C13	SCCP	C13H17CI11			0.5	1	2	4	8	16									#N/A	#N/A			
32																					#N/A	#N/A				
33																					#N/A	#N/A				

5.) Repeat steps 2.-4. for all remaining standard mixtures.

#	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
22	A-SCCP	C12 52%	C12	SCCP	C12H17C9	0.1	0.25	0.5	1	2	4	8	16			2500	5000	10000	20000	40000	80000		1	5000		A-SCCP	C12 52%	C12	SCCP	
23	A-SCCP	C12 52%	C12	SCCP	C12H16C10	0.1	0.25	0.5	1	2	4	8	16				5000	10000	20000	40000	80000		1	5000		A-SCCP	C12 52%	C12	SCCP	
24	A-SCCP	C12 52%	C12	SCCP	C12H15C11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		A-SCCP	C12 52%	C12	SCCP	
25	A-SCCP	C13 59%	C13	SCCP	C13H23C5			0.5	1	2	4	8	16				7000	14000	28000	56000	112000		1	7000		A-SCCP	C13 59%	C13	SCCP	
26	A-SCCP	C13 59%	C13	SCCP	C13H22C6			0.5	1	2	4	8	16			15000	30000	60000	120000	240000	480000		1	30000		A-SCCP	C13 59%	C13	SCCP	
27	A-SCCP	C13 59%	C13	SCCP	C13H21C7			0.5	1	2	4	8	16			4500	11250	22500	45000	90000	180000		1	45000		A-SCCP	C13 59%	C13	SCCP	
28	A-SCCP	C13 59%	C13	SCCP	C13H20C8			0.5	1	2	4	8	16			2700	6750	13500	27000	54000	108000		1	27000		A-SCCP	C13 59%	C13	SCCP	
29	A-SCCP	C13 59%	C13	SCCP	C13H19C9			0.5	1	2	4	8	16			1200	3000	6000	12000	24000	48000		1	12000		A-SCCP	C13 59%	C13	SCCP	
30	A-SCCP	C13 59%	C13	SCCP	C13H18C10			0.5	1	2	4	8	16			200	500	1000	2000	4000	8000		1	2000		A-SCCP	C13 59%	C13	SCCP	
31	A-SCCP	C13 59%	C13	SCCP	C13H17C11			0.5	1	2	4	8	16										#N/A	#N/A		A-SCCP	C13 59%	C13	SCCP	
32	B-SCCP	C10 55%	C10	SCCP	C10H17C5		0.25	0.5	1	2	4	8	16										#N/A	#N/A		B-SCCP	C10 55%	C10	SCCP	
33	B-SCCP	C10 55%	C10	SCCP	C10H16C6		0.25	0.5	1	2	4	8	16				4000	8000	16000	32000			1	4000		B-SCCP	C10 55%	C10	SCCP	
34	B-SCCP	C10 55%	C10	SCCP	C10H15C7	0.1	0.25	0.5	1	2	4	8	16			2000	4000	8000	16000	32000	64000	128000		1	16000		B-SCCP	C10 55%	C10	SCCP
35	B-SCCP	C10 55%	C10	SCCP	C10H14C8	0.1	0.25	0.5	1	2	4	8	16			4000	8000	16000	32000	64000	128000	256000		1	32000		B-SCCP	C10 55%	C10	SCCP
36	B-SCCP	C10 55%	C10	SCCP	C10H13C9	0.1	0.25	0.5	1	2	4	8	16				1000	2000	4000	8000	16000	32000		1	4000		B-SCCP	C10 55%	C10	SCCP
37	B-SCCP	C10 55%	C10	SCCP	C10H12C10	0.1	0.25	0.5	1	2	4	8	16										1	1600		B-SCCP	C10 55%	C10	SCCP	
38	B-SCCP	C10 55%	C10	SCCP	C10H11C11		0.25	0.5	1	2	4	8	16					1600	3200	6400	12800	25600		#N/A	#N/A		B-SCCP	C10 55%	C10	SCCP
39	B-SCCP	C11 50%	C11	SCCP	C11H19C5	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		B-SCCP	C11 50%	C11	SCCP	
40	B-SCCP	C11 50%	C11	SCCP	C11H18C6	0.1	0.25	0.5	1	2	4	8	16					8000	16000	32000	64000	128000		1	8000		B-SCCP	C11 50%	C11	SCCP
41	B-SCCP	C11 50%	C11	SCCP	C11H17C7	0.1	0.25	0.5	1	2	4	8	16					18000	36000	72000	144000	288000		1	36000		B-SCCP	C11 50%	C11	SCCP
42	B-SCCP	C11 50%	C11	SCCP	C11H16C8	0.1	0.25	0.5	1	2	4	8	16					7000	14000	28000	56000	112000		1	28000		B-SCCP	C11 50%	C11	SCCP
43	B-SCCP	C11 50%	C11	SCCP	C11H15C9	0.1	0.25	0.5	1	2	4	8	16			2100	4200	8400	16800	33600	67200	134400		1	16800		B-SCCP	C11 50%	C11	SCCP
44	B-SCCP	C11 50%	C11	SCCP	C11H14C10	0.1	0.25	0.5	1	2	4	8	16				960	1920	3840	7680	15360	30720		1	3840		B-SCCP	C11 50%	C11	SCCP
45	B-SCCP	C11 50%	C11	SCCP	C11H13C11				1	2	4	8	16										#N/A	#N/A		B-SCCP	C11 50%	C11	SCCP	
46	B-SCCP	C12 55%	C12	SCCP	C12H21C5	0.1	0.25	0.5	1	2	4	8	16					4000	8000	16000	32000	64000		1	4000		B-SCCP	C12 55%	C12	SCCP
47	B-SCCP	C12 55%	C12	SCCP	C12H20C6	0.1	0.25	0.5	1	2	4	8	16				9000	18000	36000	72000	144000	288000		1	36000		B-SCCP	C12 55%	C12	SCCP
48	B-SCCP	C12 55%	C12	SCCP	C12H19C7	0.1	0.25	0.5	1	2	4	8	16				3700	7400	14800	29600	59200	118400		1	29600		B-SCCP	C12 55%	C12	SCCP
49	B-SCCP	C12 55%	C12	SCCP	C12H18C8	0.1	0.25	0.5	1	2	4	8	16				2000	4000	8000	16000	32000	64000		1	16000		B-SCCP	C12 55%	C12	SCCP
50	B-SCCP	C12 55%	C12	SCCP	C12H17C9	0.1	0.25	0.5	1	2	4	8	16				1500	3000	6000	12000	24000	48000		1	12000		B-SCCP	C12 55%	C12	SCCP
51	B-SCCP	C12 55%	C12	SCCP	C12H16C10	0.1	0.25	0.5	1	2	4	8	16										1	4000		B-SCCP	C12 55%	C12	SCCP	
52	B-SCCP	C12 55%	C12	SCCP	C12H15C11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		B-SCCP	C12 55%	C12	SCCP	
53	B-SCCP	C13 65%	C13	SCCP	C13H23C5		0.25	0.5	1	2	4	8	16					4800	9600	19200	38400	76800		1	9600		B-SCCP	C13 65%	C13	SCCP
54	B-SCCP	C13 65%	C13	SCCP	C13H22C6	0.1	0.25	0.5	1	2	4	8	16										1	48000		B-SCCP	C13 65%	C13	SCCP	
55	B-SCCP	C13 65%	C13	SCCP	C13H21C7	0.1	0.25	0.5	1	2	4	8	16				6000	12000	24000	48000	96000	192000		1	28000		B-SCCP	C13 65%	C13	SCCP
56	B-SCCP	C13 65%	C13	SCCP	C13H20C8	0.1	0.25	0.5	1	2	4	8	16				3500	7000	14000	28000	56000	112000		1	28000		B-SCCP	C13 65%	C13	SCCP
57	B-SCCP	C13 65%	C13	SCCP	C13H19C9	0.1	0.25	0.5	1	2	4	8	16				2000	4000	8000	16000	32000	64000		1	16000		B-SCCP	C13 65%	C13	SCCP
58	B-SCCP	C13 65%	C13	SCCP	C13H18C10	0.1	0.25	0.5	1	2	4	8	16					2800	5600	11200	22400	44800		1	5600		B-SCCP	C13 65%	C13	SCCP
59	B-SCCP	C13 65%	C13	SCCP	C13H17C11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		B-SCCP	C13 65%	C13	SCCP	
60	C-SCCP	C10 60%	C10	SCCP	C10H17C5	0.13	0.25	0.5	1	2	4	8	16										#N/A	#N/A		C-SCCP	C10 60%	C10	SCCP	
61	C-SCCP	C10 60%	C10	SCCP	C10H16C6	0.1	0.25	0.5	1	2	4	8	16					1600	3200	6400	12800	25600		1	1600		C-SCCP	C10 60%	C10	SCCP
62	C-SCCP	C10 60%	C10	SCCP	C10H15C7	0.1	0.25	0.5	1	2	4	8	16				4000	8000	16000	32000	64000	128000		1	32000		C-SCCP	C10 60%	C10	SCCP
63	C-SCCP	C10 60%	C10	SCCP	C10H14C8	0.1	0.25	0.5	1	2	4	8	16				7000	14000	28000	56000	112000	224000		1	56000		C-SCCP	C10 60%	C10	SCCP
64	C-SCCP	C10 60%	C10	SCCP	C10H13C9	0.1	0.25	0.5	1	2	4	8	16				3500	7000	14000	28000	56000	112000		1	28000		C-SCCP	C10 60%	C10	SCCP
65	C-SCCP	C10 60%	C10	SCCP	C10H12C10	0.1	0.25	0.5	1	2	4	8	16				2000	4000	8000	16000	32000	64000		1	8000		C-SCCP	C10 60%	C10	SCCP
66	C-SCCP	C10 60%	C10	SCCP	C10H11C11	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		C-SCCP	C10 60%	C10	SCCP	
67	C-SCCP	C11 55%	C11	SCCP	C11H19C5	0.1	0.25	0.5	1	2	4	8	16										#N/A	#N/A		C-SCCP	C11 55%	C11	SCCP	
68	C-SCCP	C11 55%	C11	SCCP	C11H18C6	0.1	0.25	0.5	1	2	4	8	16					1600	3200	6400	12800	25600		1	1600		C-SCCP	C11 55%	C11	SCCP



6.) Check if there are no unexpected errors in your sheet and copy the calculated information from column Z-AE to an Excel document "input\_ref.xlsx" starting from 2nd row (use Paste->Paste special->Values). Do not clear the first row of "input\_ref.xlsx" sheet!

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Standard mixture	Standard used	Chain length	Type	Homologue	Calibration LEVELS								Calibration LEVELS								R <sup>2</sup>	Response factor of each homologue per 1 ng/μL	Data which must be		
2						1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8					
3						C, ng/μL								Area	Area	Area	Area	Area	Area	Area	Area				Area	
4	A-SCCP	C10 50%	C10	SCCP	C10H17CI5	0.13	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
5	A-SCCP	C10 50%	C10	SCCP	C10H16CI6	0.1	0.25	0.5	1	2	4	8	16				25000	49000	94000	201000		0.998447235		25157		
6	A-SCCP	C10 50%	C10	SCCP	C10H15CI7	0.1	0.25	0.5	1	2	4	8	16				12500	24000	50000	110000	200000	400000	0.999205151		24953	
7	A-SCCP	C10 50%	C10	SCCP	C10H14CI8	0.1	0.25	0.5	1	2	4	8	16	1000	2500	5000	10000	20000	40000	80000	160000	0.999997653		10005		
8	A-SCCP	C10 50%	C10	SCCP	C10H13CI9	0.1	0.25	0.5	1	2	4	8	16	500	1250	2500	5000	10000	20000	40000	80000	0.999997653		5002		
9	A-SCCP	C10 50%	C10	SCCP	C10H12CI10	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
10	A-SCCP	C10 50%	C10	SCCP	C10H11CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
11	A-SCCP	C11 45%	C11	SCCP	C11H19CI5	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
12	A-SCCP	C11 45%	C11	SCCP	C11H18CI6	0.1	0.25	0.5	1	2	4	8	16	3000	7500	15000	30000	60000	120000	240000	480000	0.999997653		30014		
13	A-SCCP	C11 45%	C11	SCCP	C11H17CI7	0.1	0.25	0.5	1	2	4	8	16	4000	10000	20000	40000	80000	160000	320000	640000	0.999997653		40018		
14	A-SCCP	C11 45%	C11	SCCP	C11H16CI8	0.1	0.25	0.5	1	2	4	8	16	2100	5250	10500	21000	42000	84000	168000	336000	0.996516383		20635		
15	A-SCCP	C11 45%	C11	SCCP	C11H15CI9	0.1	0.25	0.5	1	2	4	8	16	700	1750	3500	7000	14000	28000	56000	112000	0.999997653		7003		
16	A-SCCP	C11 45%	C11	SCCP	C11H14CI10	0.1	0.25	0.5	1	2	4	8	16	300	750	1500	3000	6000	12000	24000	48000	0.999997653		3001		
17	A-SCCP	C11 45%	C11	SCCP	C11H13CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
18	A-SCCP	C12 52%	C12	SCCP	C12H21CI5	0.1	0.25	0.5	1	2	4	8	16	500	1250	2500	5000	10000	20000	40000	80000	0.999997653		5002		
19	A-SCCP	C12 52%	C12	SCCP	C12H20CI6	0.1	0.25	0.5	1	2	4	8	16	4500	11250	22500	45000	90000	180000	360000	720000	0.999997653		45020		
20	A-SCCP	C12 52%	C12	SCCP	C12H19CI7	0.1	0.25	0.5	1	2	4	8	16	3700	9250	18500	37000	74000	148000	296000	592000	0.999997653		37017		
21	A-SCCP	C12 52%	C12	SCCP	C12H18CI8	0.1	0.25	0.5	1	2	4	8	16	2000	5000	10000	20000	40000	80000	160000	320000	0.999997653		20009		
22	A-SCCP	C12 52%	C12	SCCP	C12H17CI9	0.1	0.25	0.5	1	2	4	8	16			2500	5000	10000	20000	40000	80000	1		5000		
23	A-SCCP	C12 52%	C12	SCCP	C12H16CI10	0.1	0.25	0.5	1	2	4	8	16				5000	10000	20000	40000	80000	1		5000		
24	A-SCCP	C12 52%	C12	SCCP	C12H15CI11	0.1	0.25	0.5	1	2	4	8	16									#N/A	#N/A			
25	A-SCCP	C13 59%	C13	SCCP	C13H23CI5			0.5	1	2	4	8	16				7000	14000	28000	56000	112000	1		7000		
26	A-SCCP	C13 59%	C13	SCCP	C13H22CI6			0.5	1	2	4	8	16			15000	30000	60000	120000	240000	480000	1		30000		
27	A-SCCP	C13 59%	C13	SCCP	C13H21CI7			0.5	1	2	4	8	16	4500	11250	22500	45000	90000	180000	360000	720000	1		45000		
28	A-SCCP	C13 59%	C13	SCCP	C13H20CI8			0.5	1	2	4	8	16	2700	6750	13500	27000	54000	108000	216000	432000	1		27000		
29	A-SCCP	C13 59%	C13	SCCP	C13H19CI9			0.5	1	2	4	8	16	1200	3000	6000	12000	24000	48000	96000	192000	1		12000		
30	A-SCCP	C13 59%	C13	SCCP	C13H18CI10			0.5	1	2	4	8	16	200	500	1000	2000	4000	8000	16000	32000	1		2000		
31	A-SCCP	C13 59%	C13	SCCP	C13H17CI11			0.5	1	2	4	8	16									#N/A	#N/A			

[illegible]



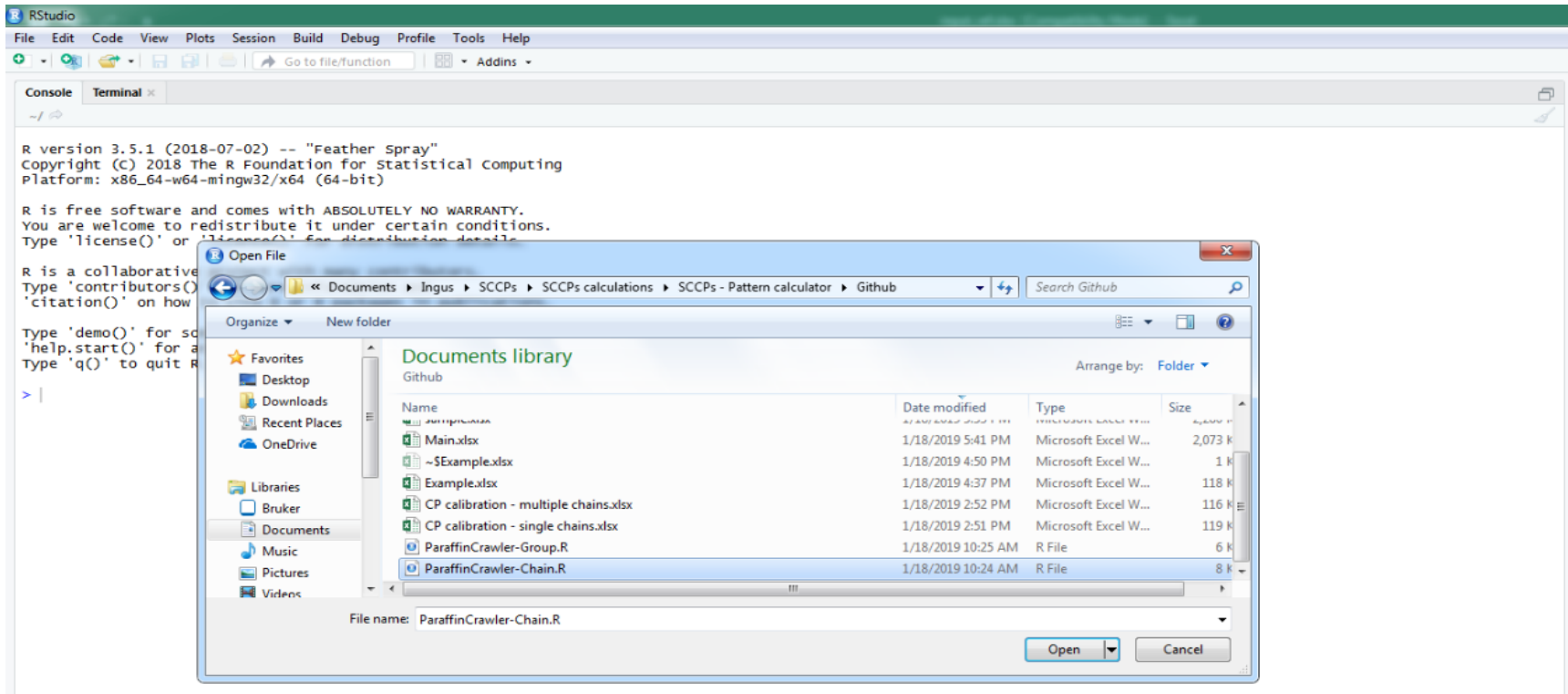
7.) Save “input\_ref.xlsx” file in desired directory. Open “sample.xlsx” file to enter results for sample measurement.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1	Chain	length	Type	Homologue	Area																
2	C10		SCCP	C10H17Ci5	0																
3	C10		SCCP	C10H16Ci6	21600																
4	C10		SCCP	C10H15Ci7	112000																
5	C10		SCCP	C10H14Ci8	236800																
6	C10		SCCP	C10H13Ci9	151200																
7	C10		SCCP	C10H12Ci10	80000																
8	C10		SCCP	C10H11Ci11	16000																
9	C11		SCCP	C11H19Ci5	0																
10	C11		SCCP	C11H18Ci6	40000																
11	C11		SCCP	C11H17Ci7	204000																
12	C11		SCCP	C11H16Ci8	208800																
13	C11		SCCP	C11H15Ci9	226400																
14	C11		SCCP	C11H14Ci10	123200																
15	C11		SCCP	C11H13Ci11	19200																
16	C12		SCCP	C12H21Ci5	20000																
17	C12		SCCP	C12H20Ci6	180000																
18	C12		SCCP	C12H19Ci7	172000																
19	C12		SCCP	C12H18Ci8	158400																
20	C12		SCCP	C12H17Ci9	218400																
21	C12		SCCP	C12H16Ci10	155200																
22	C12		SCCP	C12H15Ci11	68800																
23	C13		SCCP	C13H23Ci5	0																
24	C13		SCCP	C13H22Ci6	48000																
25	C13		SCCP	C13H21Ci7	273600																
26	C13		SCCP	C13H20Ci8	212000																
27	C13		SCCP	C13H19Ci9	224000																
28	C13		SCCP	C13H18Ci10	180000																
29	C13		SCCP	C13H17Ci11	48000																
30																					

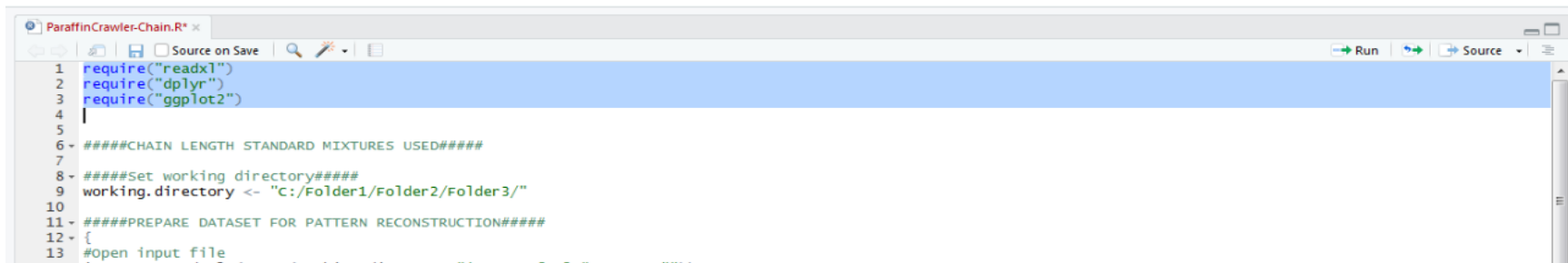
8.) If using MCCPs or LCCPs instead of SCCPs, replace columns A, B, and C with corresponding information (Chain\_length, Type and Homologue) from calibration sheets.

9.) Save “sample.xlsx” file in desired directory.

10.) Go to RStudio software and open “ParaffinCrawler-Chain.R”. Open “ParaffinCrawler-Group.R” if using multiple chain length standard mixtures.



11.) Select first three lines and execute code with "Ctrl+Enter" to load required libraries.



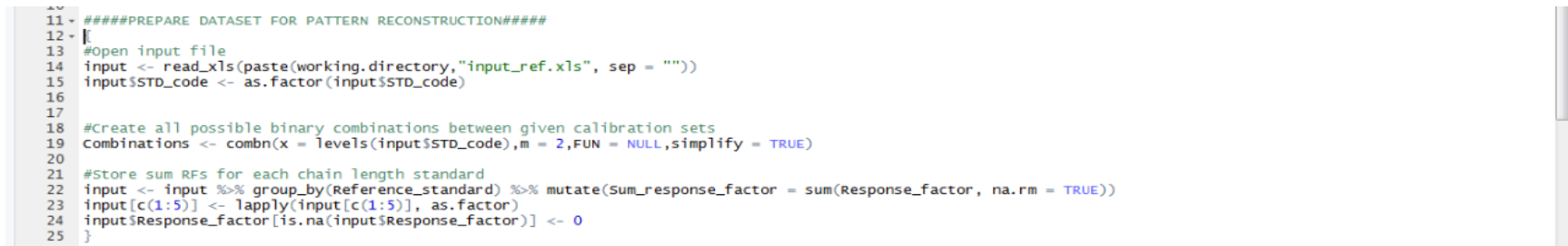
```
ParaffinCrawler-Chain.R* x
1 require("readxl")
2 require("dplyr")
3 require("ggplot2")
4
5
6 #####CHAIN LENGTH STANDARD MIXTURES USED#####
7
8 #####Set working directory#####
9 working.directory <- "C:/Folder1/Folder2/Folder3/"
10
11 #####PREPARE DATASET FOR PATTERN RECONSTRUCTION#####
12 {
13 #Open input file
14 #input <- read_xls(paste(working.directory, "input_ref.xls", sep = ""))
```

12.) In line 9, edit the **working.directory** to the location of "input\_ref.xlsx" and "sample.xlsx". Folders must be separated with "/", not "\"!



```
5
6 #####CHAIN LENGTH STANDARD MIXTURES USED#####
7
8 #####Set working directory#####
9 working.directory <- "C:/Folder1/Folder2/Folder3/"
10
11 #####PREPARE DATASET FOR PATTERN RECONSTRUCTION#####
12 {
```

13.) Click in line 12 on the left side before curly bracket "{". Press "Ctrl+Enter" to run the first part of the code.



```
11 #####PREPARE DATASET FOR PATTERN RECONSTRUCTION#####
12 {
13 #Open input file
14 input <- read_xls(paste(working.directory, "input_ref.xls", sep = ""))
15 input$STD_code <- as.factor(input$STD_code)
16
17
18 #Create all possible binary combinations between given calibration sets
19 combinations <- combn(x = levels(input$STD_code), m = 2, FUN = NULL, simplify = TRUE)
20
21 #Store sum RfS for each chain length standard
22 input <- input %>% group_by(Reference_standard) %>% mutate(Sum_response_factor = sum(Response_factor, na.rm = TRUE))
23 input[c(1:5)] <- lapply(input[c(1:5)], as.factor)
24 input$Response_factor[is.na(input$Response_factor)] <- 0
25 }
```

14.) You do not have to repeat steps 10. - 13. for each sample. Once they have been run, there is no need to do that for each sample unless new Rstudio session (or restart) has occurred.

15.) Enter sample name in line 34.



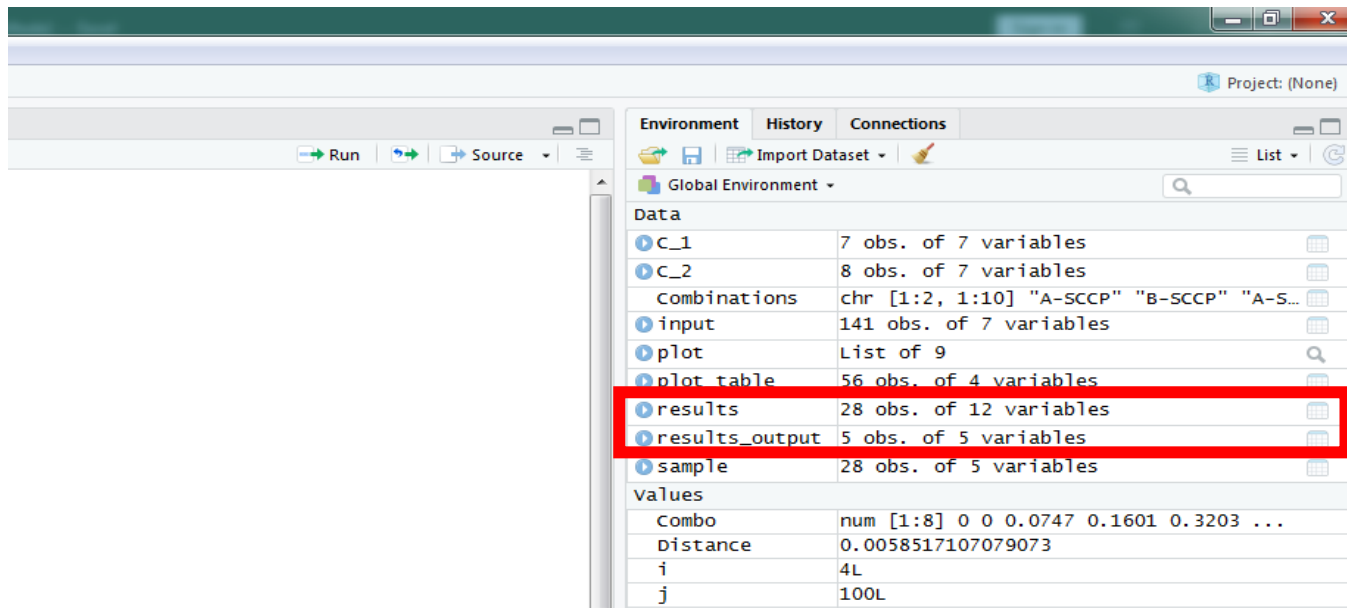
```
31 #####Open sample data####
32 sample <- read_xls(paste(working.directory, "sample.xls", sep = ""))
33 #####Set sample name#####
34 sample.name <- "generic example"
35 #####RUN PATTERN RECONSTRUCTION F as.factor(x) TED (LOADED) SAMPLE####
```

16.) Click in line 32 on the left side before curly bracket "{". Press "Ctrl+Enter" to run the second part of the code.

```
31 - ####Open sample data####
32 - {
33   sample <- read_xls(paste(working.directory,"sample.xls", sep = ""))
34 - ####Set sample name####
35   sample.name <- "Generic example"
36 - ####RUN PATTERN RECONSTRUCTION FOR SELECTED (LOADED) SAMPLE####
37 - {
38   sample$chain_length <- as.factor(sample$chain_length)
39   sample$Area <- as.numeric(sample$Area)
```

17.) Step 16 executed pattern reconstruction procedure and quantification. Now you can see and save the results.

18.) To see results summary and full data table open data frames on the right side panel. Click "play" button on "results\_output" to see the summary, click "results" to see the full data.frame.



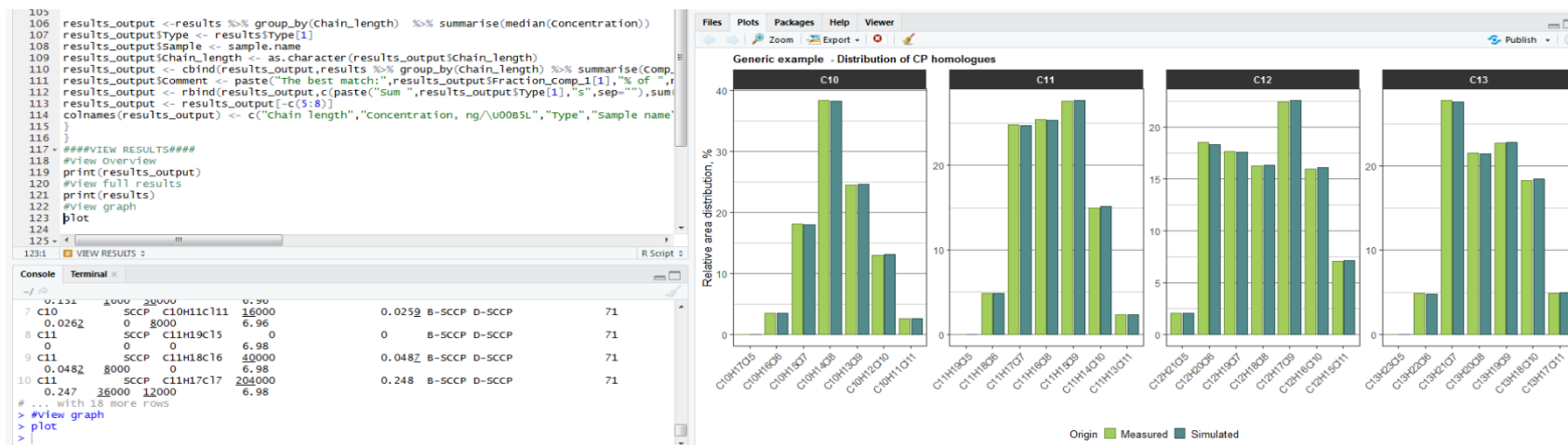
The screenshot shows the RStudio Environment pane with the following data frames listed:

Object	Description
C_1	7 obs. of 7 variables
C_2	8 obs. of 7 variables
Combinations	chr [1:2, 1:10] "A-SCCP" "B-SCCP" "A-S...
input	141 obs. of 7 variables
plot	List of 9
plot table	56 obs. of 4 variables
results	28 obs. of 12 variables
results_output	5 obs. of 5 variables
sample	28 obs. of 5 variables

The 'results' and 'results\_output' objects are highlighted with a red box. Below the data frames, the 'Values' section shows the following information:

Variable	Value
Combo	num [1:8] 0 0 0.0747 0.1601 0.3203 ...
Distance	0.0058517107079073
i	4L
j	100L

19.) To visualize the calculated patterns click in line 123 and execute it by pressing "Ctrl+Enter". The plots will be visualized in right panel ("Plots").



20.) To save all files go to line 127, edit save.directory and execute lines 130, 132, and 134 by clicking to each line and pressing "Ctrl+Enter" to save summary of results (.txt separated by TAB), full results (.txt separated by TAB) and relative distribution plot (.tiff), respectively. All these files will be named by sample.name, which was defined in step 15 and can be located in save.directory.

```
125 #####SAVE RESULTS#####
126 #Set save directory
127 save.directory <- "E:/folder1/folder2/folder3/"
128
129 #Save Overview
130 write.table(results_output, paste(save.directory,sample.name,"-overview", ".txt", sep = ""), s
131 #Save full results
132 write.table(results, paste(save.directory,sample.name,"-full_results", ".txt", sep = ""), sep=
133 #Save distribution plot
134 ggsave(filename = paste(sample.name,"-CP_distribution_plot", ".tiff", sep = ""),device = "tiff",
135
```

21.) Repeat the procedure from step 15 to 20 for each sample. Remember to replace data in "sample.xlsx" file when running a different sample.

## Acknowledgments

The backbone for this approach was largely inspired/adapted from two publications:

[Schinkel, L., Lehner, S., Knobloch, M., Lienemann, P., Bogdal, C., McNeill, K., & Heeb, N. V. \(2018\). Transformation of chlorinated paraffins to olefins during metal work and thermal exposure – Deconvolution of mass spectra and kinetics. Chemosphere, 194, 803–811. https://doi.org/10.1016/j.chemosphere.2017.11.168](https://doi.org/10.1016/j.chemosphere.2017.11.168)

[Bogdal, C., Alsberg, T., Diefenbacher, P. S., Macleod, M., & Berger, U. \(2015\). Fast quantification of chlorinated paraffins in environmental samples by direct injection high-resolution mass spectrometry with pattern deconvolution. Analytical Chemistry, 87\(5\), 2852–2860. https://doi.org/10.1021/ac504444d](https://doi.org/10.1021/ac504444d)

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