



EPA PMF v5.0

Receptor model for source apportionment studies

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ENV/ES/000584



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What is?

- Free Program to solve Positive Matrix Factorization (PMF)
- Available at <https://www.epa.gov/air-research/positive-matrix-factorization-model-environmental-data-analyses>



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New features? compared to v3

- Constraints on source profiles and contributions (**pulling**)
- 2 more output **error estimate** (DISP, BS-DISP)

Alternatives?

	Pulling	Errors of output	User-friendly
EPA PMF v5	Green	Green	Green
EPA PMF v3	Orange	Light Green	Green
PMF2	Yellow	Orange	Yellow
ME-2 scripting	Green	Light Green	Orange



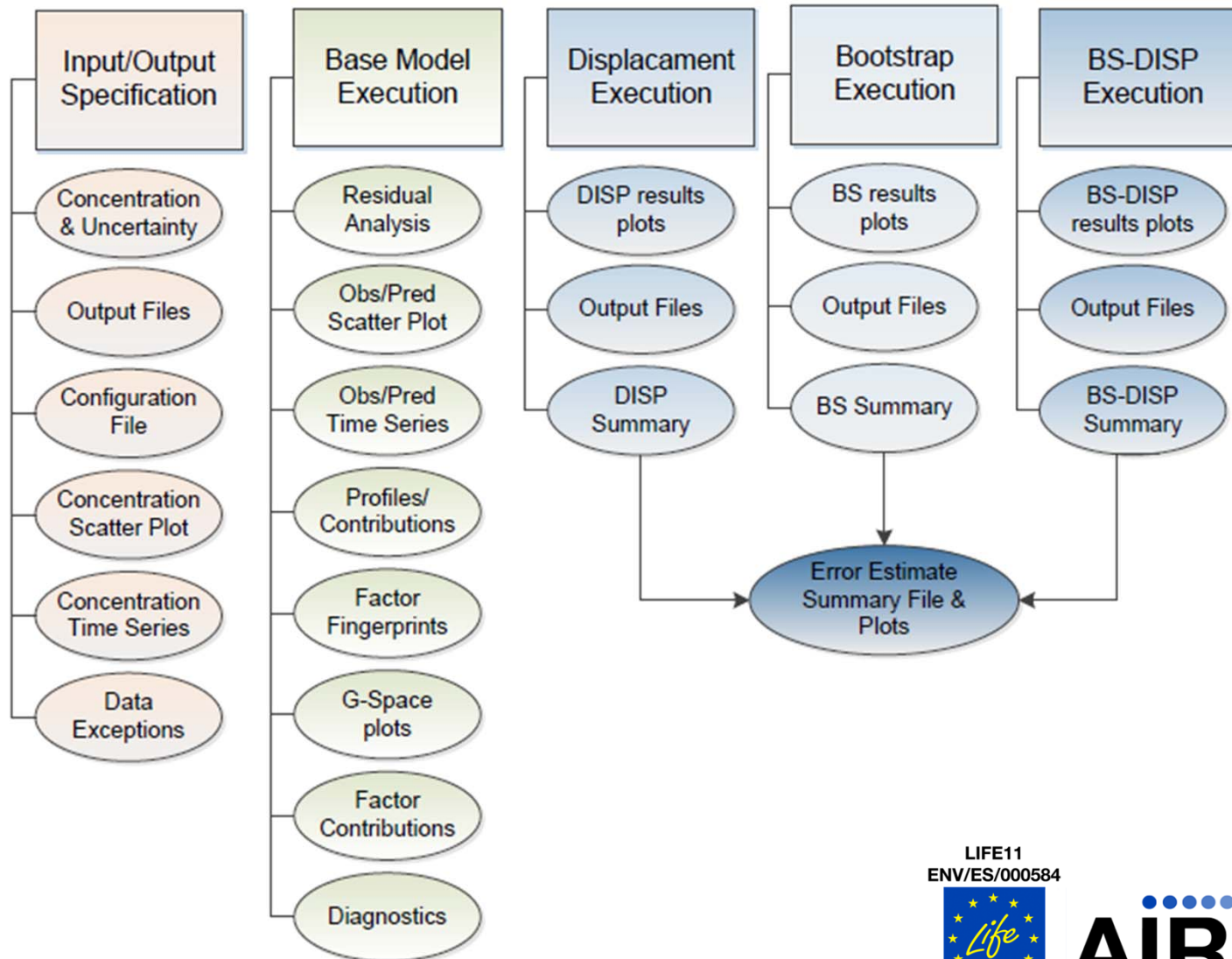
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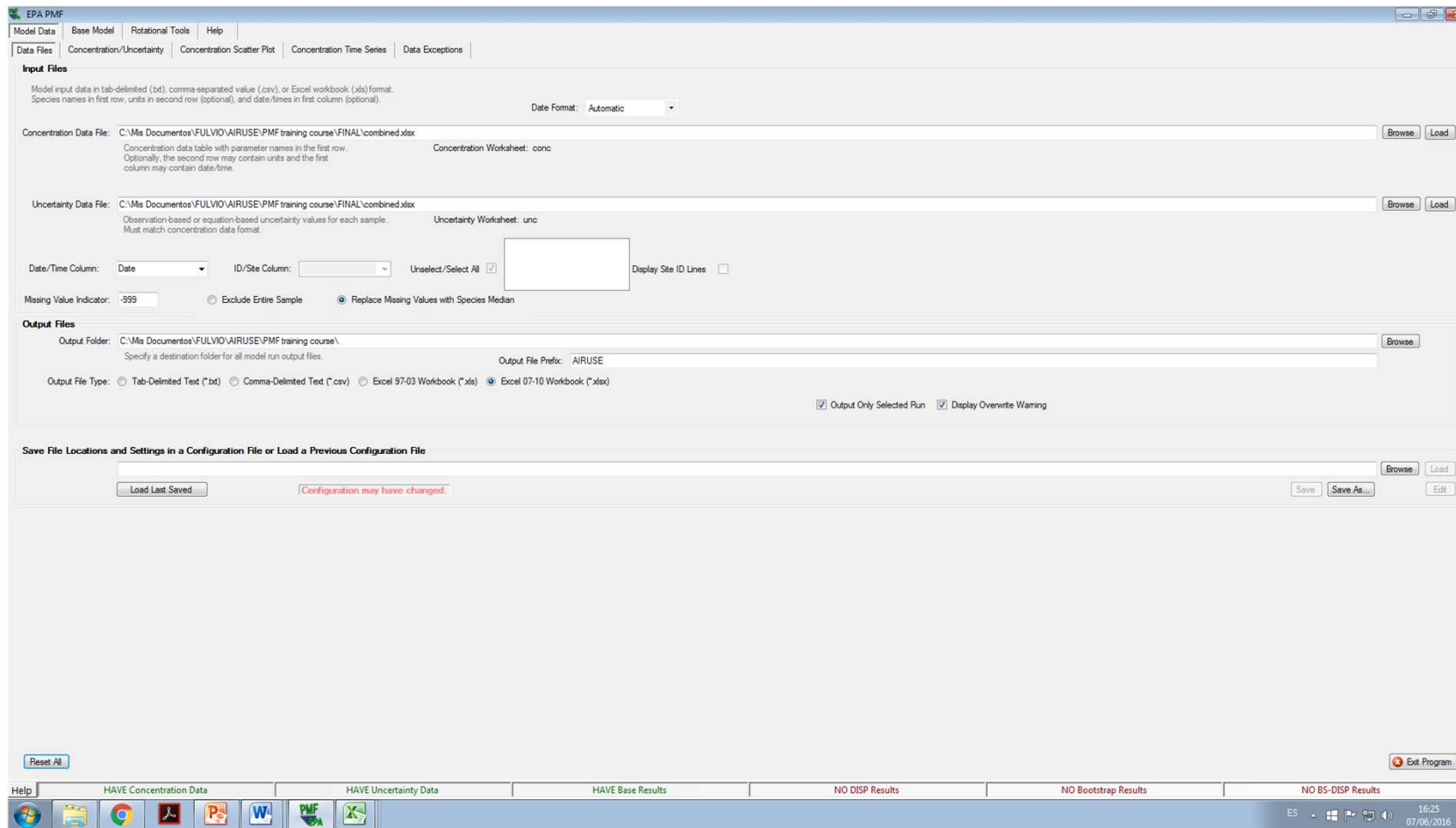
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Structure



Example



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Input files

- .txt .csv .xls
- Date/time, **ID column** or none
- One file/sheet for concentrations (can include units), one for uncertainties (>0, no units)
- Full uncertainties or equation based file
- Missing data
- Save configuration. Does not save results!

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	F
1	DATE	Aluminum µg/m3	Ammonia µg/m3	Bromine µg/m3	Calcium µg/m3	Chlorine µg/m3	Copper µg/m3	EC µg/m3	Iron µg/m3	Lead µg/m3	Manganese µg/m3	Nickel µg/m3	Nitrate µg/m3	OC µg/m3	
3	2/9/2000	0.0021	3.8020	0.0107	0.0076	0.0047	0.0059	3.1230	0.1497	0.0157	0.0043	0.0077	5.3700	7.3930	
4	2/15/2000	0.0057	1.3740	0.0005	0.0325	0.0016	0.0019	1.0710	0.0673	0.0055	0.0004	0.0285	0.8785	3.3310	
5	2/27/2000	0.0029	2.1890	0.0028	0.0422	0.0286	0.0028	0.6732	0.0727	0.0073	0.0002	0.0215	3.8820	5.2030	
6	3/4/2000	0.0011	0.4901	0.0014	0.0329	0.0024	0.0010	0.5503	0.0483	0.0061	0.0004	0.0188	0.4962	3.6160	
7	3/10/2000	0.0075	0.3099	0.0006	0.0247	0.0039	0.0003	0.2669	0.0665	0.0002	0.0016	0.0083	0.6763	2.8140	
8	3/22/2000	0.0006	1.1570	0.0033	0.0285	0.0015	0.0029	0.9487	0.0621	0.0044	0.0012	0.0107	1.0670	2.4190	
9	4/6/2000	0.0296	1.3520	0.0025	0.0863	0.0006	0.0041	2.1990	0.1492	0.0089	0.0034	0.0254	1.4860	4.7350	
10	4/9/2000	0.0165	0.2800	0.0011	0.0263	0.0016	0.0003	0.6535	0.0396	0.0017	0.0019	0.0257	0.2515	1.6790	
11	4/12/2000	0.0108	1.1290	0.0026	0.0304	0.0000	0.0046	0.9983	0.0959	0.0042	0.0001	0.0344	1.1900	2.6390	
12	4/15/2000	0.0065	1.9540	0.0037	0.1075	0.0236	0.0099	3.1430	0.1976	0.0110	0.0025	0.0437	4.3040	6.9490	
13	4/18/2000	0.0072	0.1993	0.0028	0.0261	0.0073	0.0017	0.6603	0.0639	0.0004	0.0027	0.0082	0.6816	1.9990	
14	4/21/2000	0.0092	0.1432	0.0022	0.0250	0.0042	0.0023	0.7096	0.0765	0.0003	0.0009	0.0126	0.6017	1.7230	
15	4/24/2000	0.0289	0.4066	0.0000	0.0337	0.0007	0.0006	1.1100	0.0630	0.0067	0.0005	0.0256	0.2174	2.4420	
16	4/27/2000	0.0033	1.9030	0.0031	0.0329	0.0010	0.0024	1.4970	0.0640	0.0082	0.0013	0.0247	3.3670	3.5390	
17	4/30/2000	0.0120	0.5734	0.0021	0.0442	0.0097	0.0022	0.6726	0.0741	0.0025	0.0041	0.0153	0.5117	3.3610	
18	5/3/2000	0.0098	1.3300	0.0014	0.0385	0.0039	0.0015	1.1210	0.0735	0.0077	0.0000	0.0065	1.3980	4.2570	
19	5/12/2000	0.0009	0.1049	0.0013	0.0284	0.0009	0.0033	1.2070	0.1106	0.0046	0.0000	0.0114	0.6438	3.8490	
20	5/15/2000	0.0096	1.1600	0.0010	0.0337	0.0023	0.0002	0.6730	0.0902	0.0061	0.0004	0.0167	0.3547	3.1960	
21	5/18/2000	0.0348	2.9830	0.0037	0.1068	0.0083	0.0096	1.9910	0.1519	0.0064	0.0031	0.0166	3.3460	6.1610	
22	5/21/2000	0.0008	1.9910	0.0014	0.0409	0.0011	0.0025	0.4828	0.0449	0.0008	0.0018	0.0089	2.0880	2.5760	
23	5/24/2000	0.0067	1.8460	0.0010	0.0786	0.0013	0.0005	1.4190	0.0967	0.0006	0.0007	0.0063	1.3960	0.7990	

Input data uncertainties

Several sources of uncertainty:

- analytical determination (the largest)
- air volume sampled
- deviation from the sampling convention
- ...

Input data uncertainties

Several sources:

Table 1. Methods of calculating uncertainties for PMF analyses of PM data.

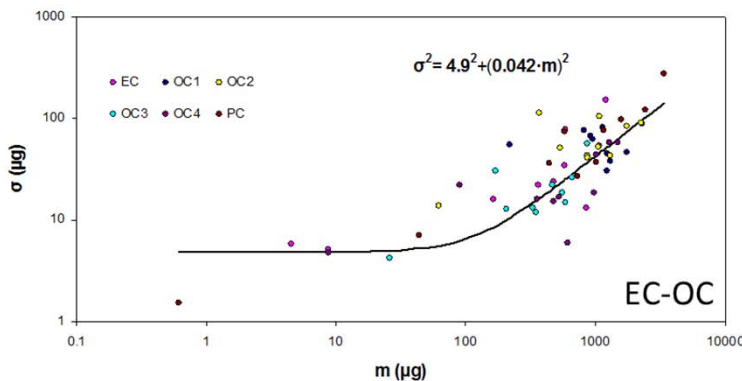
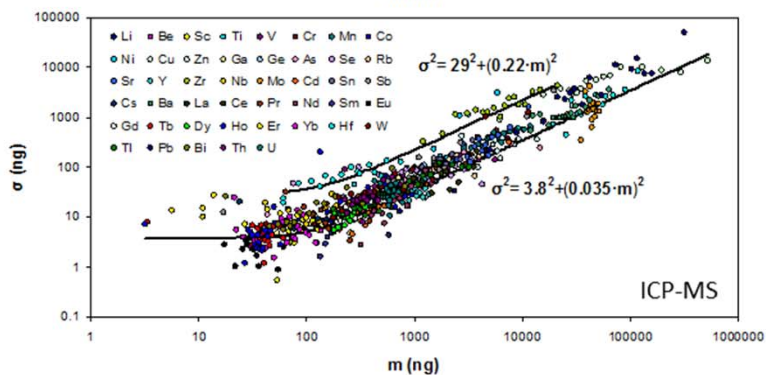
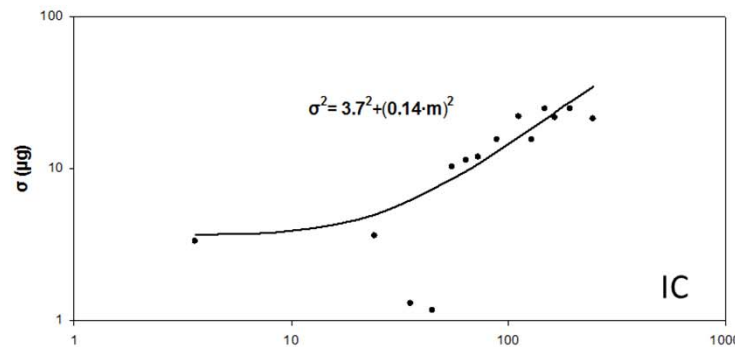
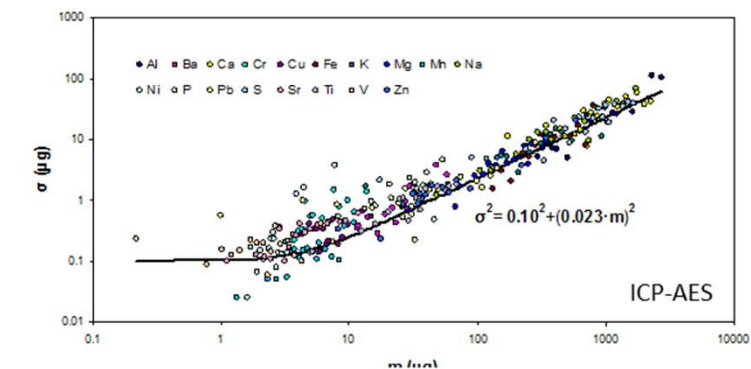
Formula for PMF Uncertainty (σ_{ij})	References
$s_{ij} + C_3 \cdot x_{ij} $ $(0.05 \cdot x_{ij}) + DL_{ij}$	27 Chueinta et al., 2000 10 Ito et al., 2004
$s_{ij} + \frac{DL_{ij}}{3}$	7, 11, 12, 13, 15, 20, 23, 24, 54
$\bar{s}_j + \frac{\overline{DL}_j}{3}$	46 Polissar et al., 1996
$s_{ij} + 0.2 \cdot DL_{ij}$	6 Ramadan et al., 2000
$0.3 + DL_{ij}$	71 Xie et al., 1999
$k_i \cdot x_{ij} + \frac{DL_{ij}}{3}$	47 Kim et al., 2005
$\sqrt{a_1 s_{ij}^2 + b_1 DL_{ij}^2}$	19 Polissar et al., 2001
$\sqrt{(rep)^2 + (0.05 \cdot x_{ij})^2}$	39 Prendes et al., 1999
$\sqrt{3 \cdot (s_{ij})^2 + DL_{ij}^2}$	52 Song et al., 2001

where x_{ij} is the concentration of species j measured on sample i

Notes: s_{ij} = analytical uncertainty; DL_{ij} = method detection limit; C_3 = value between 0.1 and 0.2; rep = reproducibility; k = fraction developed for each species by analyzing uncertainty vs. concentration plots; a_1, b_1 = scaling factors; overbar = average.

(Reff et al., 2007)

Uncertainty in Barcelona dataset



$$\sigma_a^2 = \sigma_0^2 + (\alpha \cdot m)^2$$

$$\sigma_A^2 = \sigma_a^2 + \sigma_{BLK}^2$$

$$\sigma_{ij}^2 = \sqrt{\frac{\sigma_A^2}{V_i^2} + (\beta \cdot x_{ij})^2}$$

Analytical technique	# of samples	# of repetitions
ICP - AES	30 + 2 blanks	4
ICP - MS	30 + 2 blanks	4
OC - EC	8 + 2 blanks	6
HPLC	57 + 6 blanks	2
Selective electrode (NH ₄ ⁺)	57 + 6 blanks	2

Escrig et al., (2009)

Thompson & Howarth (1976), Anttila et al, (1995)

Uncertainty- input

- Calculated individually
- Equation based

	A	B	C	D	E	F	G	H
1	unc	Aluminum	Ammonium	Arsenic	Barium	Bromine	Calcium	Chlorine
2	2	0.00419	0.0125	0.00098	0.0068	0.0016	0.0038	0.002635
3	10	10	10	10	10	10	10	10
4								

$$Unc = \sqrt{(Error\ Fraction \times concentration)^2 + (0.5 \times MDL)^2}$$



Missing data

- Delete row or
- Substitute with median but check that scaled residual is less than 1.
- You can improve solution by substituting PMF fitted values (Brown et al., 2015)

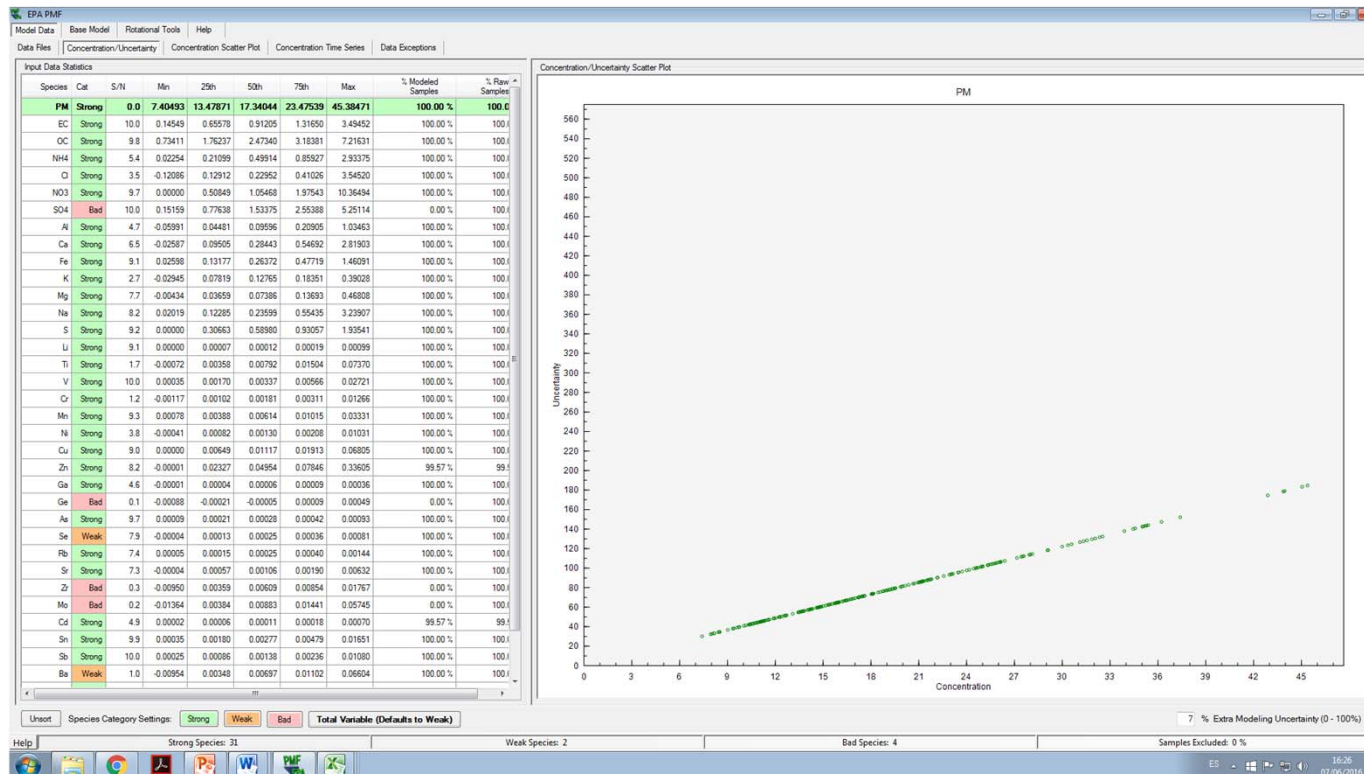


Below Detection Limit values

- Censoring BDL data (e.g. $DL/2$) does not help and generate modelling errors which complicates output error analysis.

Species selection

- Total variable
- Extra-uncertainty
- %ADL missing



Signal to Noise (S/N)

- Artificial high (some peaks) and low (missing values) S/N were common in PMF v3
- This new S/N calculation is that species with concentrations always below their uncertainty have a S/N of 0. Species with concentrations that are twice the uncertainty value have a S/N of 1. **S/N greater than 1** may often indicate a species with “good” signal. “Weak” if the S/N ratio is greater than 0.5 but less than 1

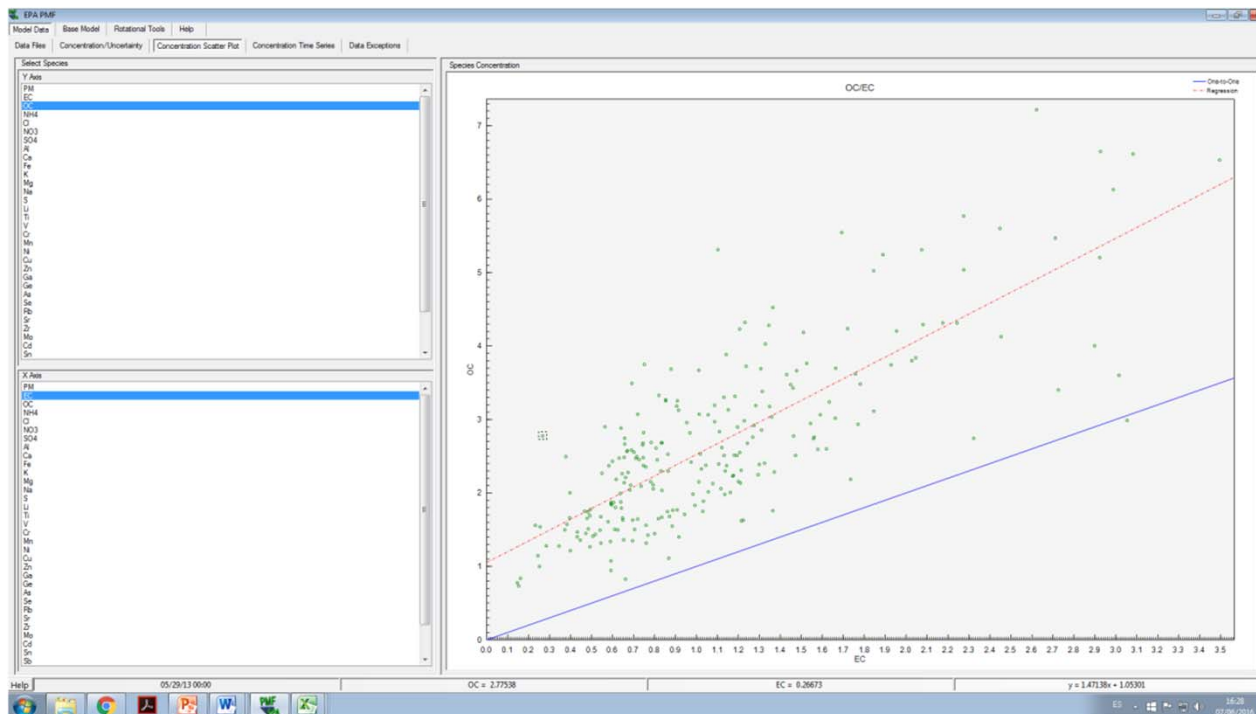
$$d_{ij} = \left(\frac{x_{ij} - s_{ij}}{s_{ij}} \right) \text{ if } x_{ij} > s_{ij}$$
$$d_{ij} = 0 \quad \text{if } x_{ij} \leq s_{ij} \quad (5-3)$$

S/N is then calculated using Equation 5-4:

$$\left(\frac{S}{N} \right)_j = 1/n \sum_{i=1}^n d_{ij} \quad (5-4)$$

Data analysis 1.

- Scatter plots
- Excluding samples...



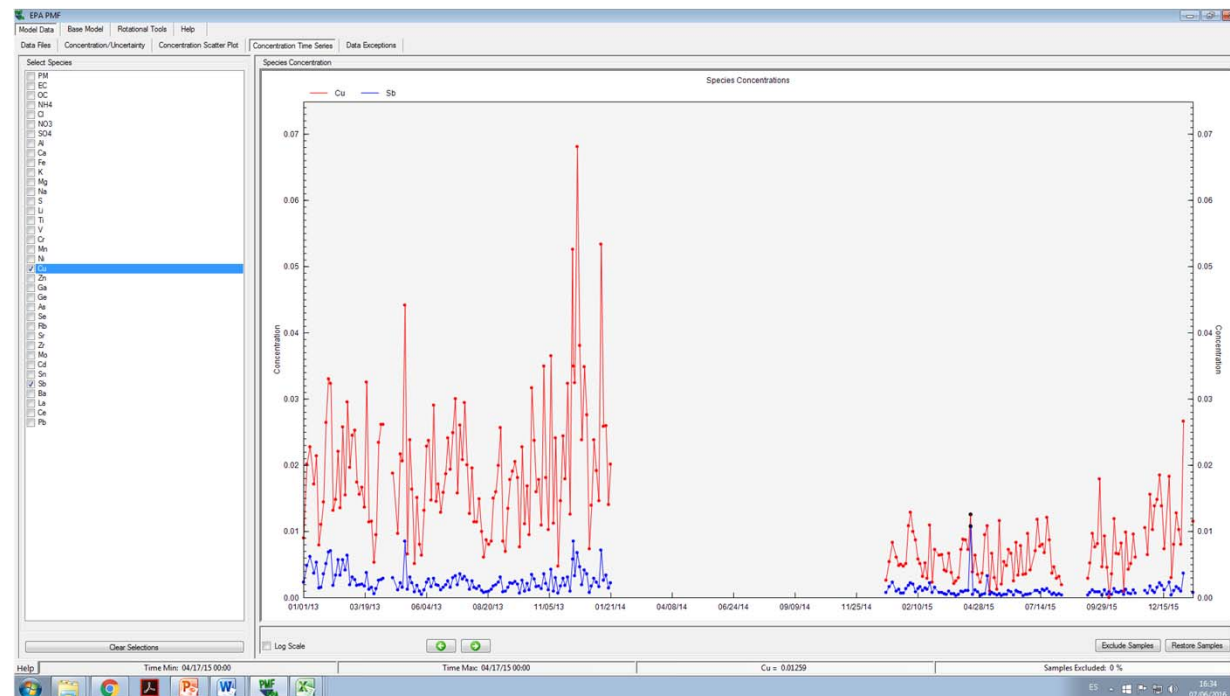
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Data analysis 2

- Time series
- Summary of data exception



Run the model

EPA PMF

Model Data | Base Model | Rotational Tools | Help

Base Model Runs | Base Model Results

Base Model Runs

Number of Runs: 30 Number of Factors: 8

Random Start Seed Number: 33

Error Estimation

Base Model Displacement Method

Selected Base Run: 29

Base Model Bootstrap Method

Selected Base Run: 29

Block Size: 43

Number of Bootstraps: 20

Min. Correlation R-Value: 0.6

Base Model BS-DISP Method

Displacement	Species	Cat	S/N
<input checked="" type="checkbox"/>	PM	Strong	0.0
<input type="checkbox"/>	EC	Strong	10.0
<input type="checkbox"/>	OC	Strong	9.8
<input type="checkbox"/>	NH4	Strong	5.4
<input type="checkbox"/>	Cl	Strong	3.5
<input type="checkbox"/>	NO3	Strong	9.7
<input type="checkbox"/>	SO4	Bad	10.0
<input type="checkbox"/>	Al	Strong	4.7
<input type="checkbox"/>	Ca	Strong	6.5
<input type="checkbox"/>	Fe	Strong	9.1
<input type="checkbox"/>	K	Strong	2.7
<input type="checkbox"/>	Mg	Strong	7.7
<input type="checkbox"/>	Na	Strong	8.2
<input type="checkbox"/>	S	Strong	9.2
<input type="checkbox"/>	Li	Strong	9.1
<input type="checkbox"/>	Tl	Strong	1.7

Base Model Run Summary

Run Number	Q (Robust)	Q (True)	Converged
1	7030.6	7141.5	Yes
2	7030.5	7141.6	Yes
3	7030.5	7141.6	Yes
4	7030.5	7141.6	Yes
5	7030.5	7141.6	Yes
6	7030.6	7141.6	Yes
7	7030.6	7141.6	Yes
8	7030.6	7141.6	Yes
9	7030.6	7141.6	Yes
10	7030.5	7141.6	Yes
11	7030.6	7141.6	Yes
12	7030.5	7141.6	Yes
13	7030.6	7141.6	Yes
14	7030.5	7141.6	Yes
15	7030.5	7141.6	Yes
16	7030.5	7141.6	Yes
17	7030.6	7141.6	Yes
18	7030.5	7141.6	Yes
19	7030.5	7141.6	Yes
20	7030.6	7141.6	Yes
21	7030.5	7141.6	Yes
22	7030.5	7141.6	Yes
23	7030.6	7141.6	Yes
24	7030.6	7141.6	Yes
25	7030.5	7141.6	Yes
26	7030.6	7141.6	Yes
27	7030.5	7141.6	Yes
28	7030.6	7141.6	Yes
29	7030.5	7141.6	Yes
30	7030.6	7141.6	Yes

Factor Names

Run	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8
Run 29	Heavy oil	Non-exhaust	Mineral	Industrial	Aged sea salt	Exhaust	Nitrate	Sulfate
Run 30	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8

Run Progress

Help HAVE Concentration Data HAVE Uncertainty Data HAVE Base Results NO DISP Results NO Bootstrap Results NO BS-DISP Results

ES 16:36 07/06/2016

Q values

- Min Qrobust is highlighted

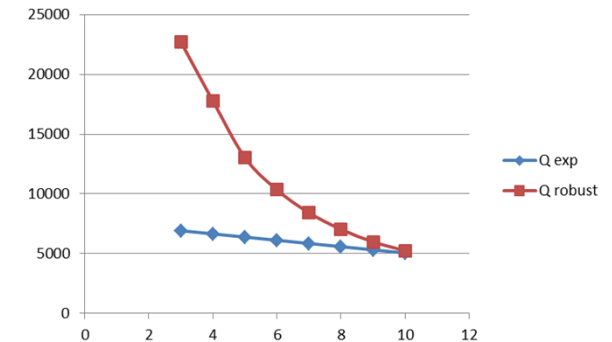
$$Q_{\text{Robust}} = \sum_{i=1}^n \sum_{j=1}^m \left(\frac{e_{ij}}{h_{ij}\sigma_{ij}} \right)^2 \quad (4)$$

where

$$h_{ij} = 1 \quad \text{for} \quad |e_{ij}/\sigma_{ij}| \leq \alpha \quad (5a)$$

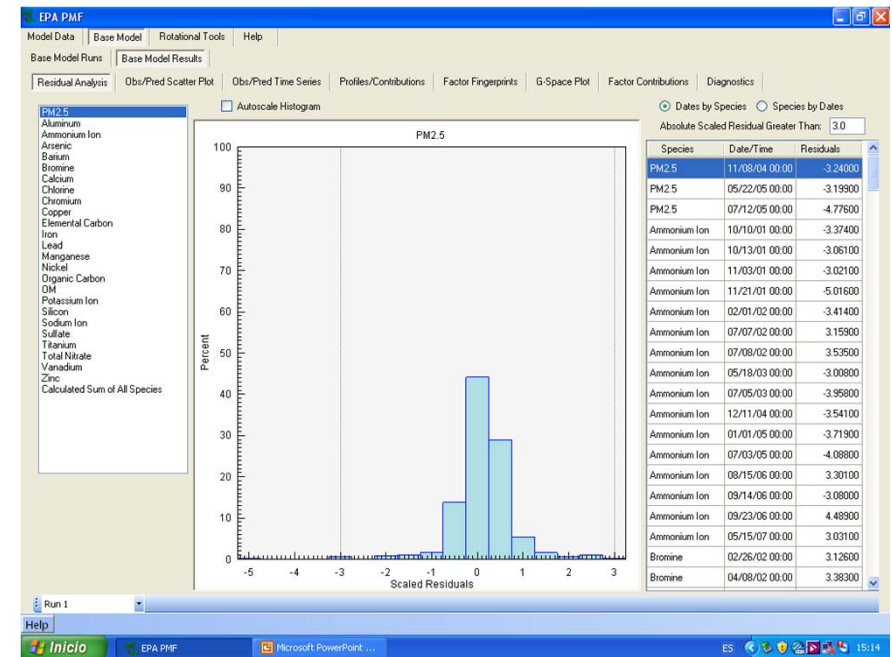
$$h_{ij} = |e_{ij}/\sigma_{ij}|/\alpha \quad \text{for} \quad |e_{ij}/\sigma_{ij}| > \alpha \quad (5b)$$

In robust mode, the PMF algorithm attempts to minimize Q_{Robust} rather than Q as defined in eq 2 (hereafter, the latter is referred to as Q_{True}).



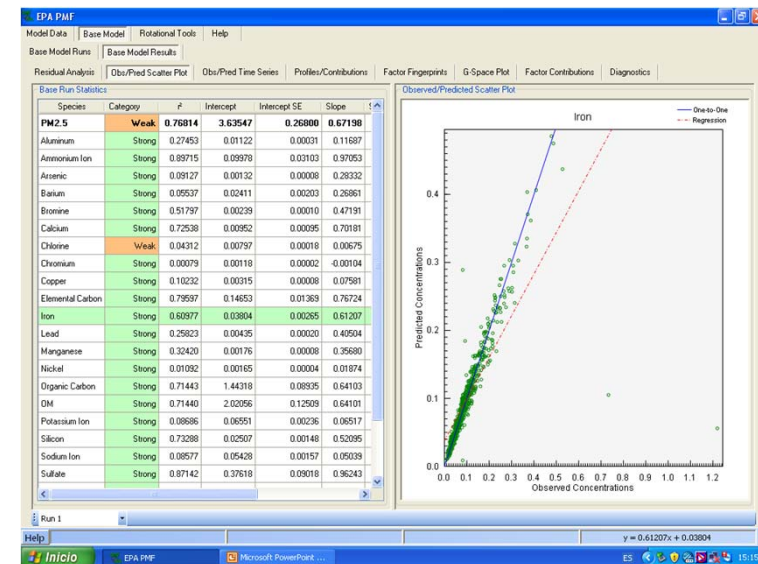
Results and diagnostics 1

- Residual analysis
- Autoscale
- High residual samples



Results and diagnostics 2

- Obs/Pred
- Revisit specie selection?



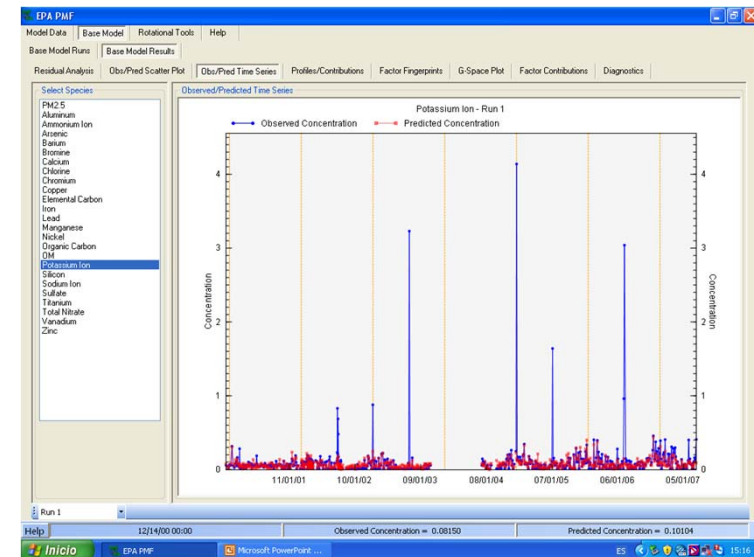
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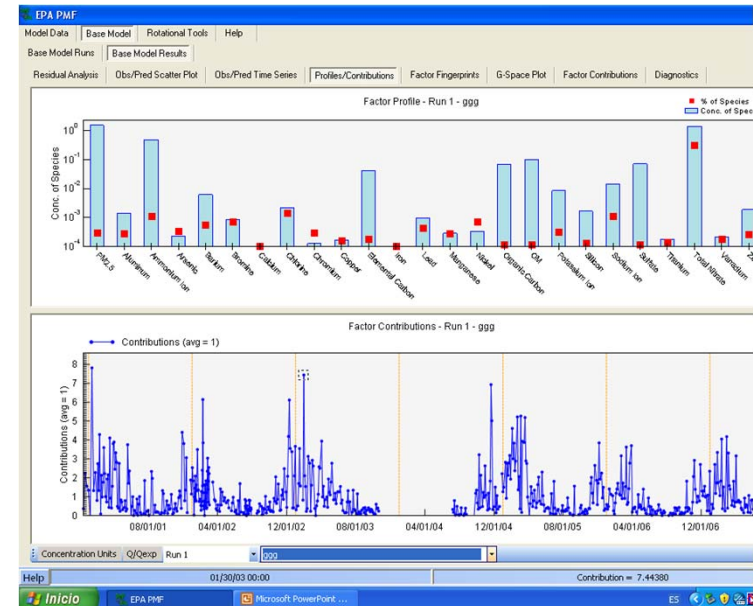
Results and diagnostics 3

- Obs/Pred time series
- Revisit sample selection?
- Missing sources?

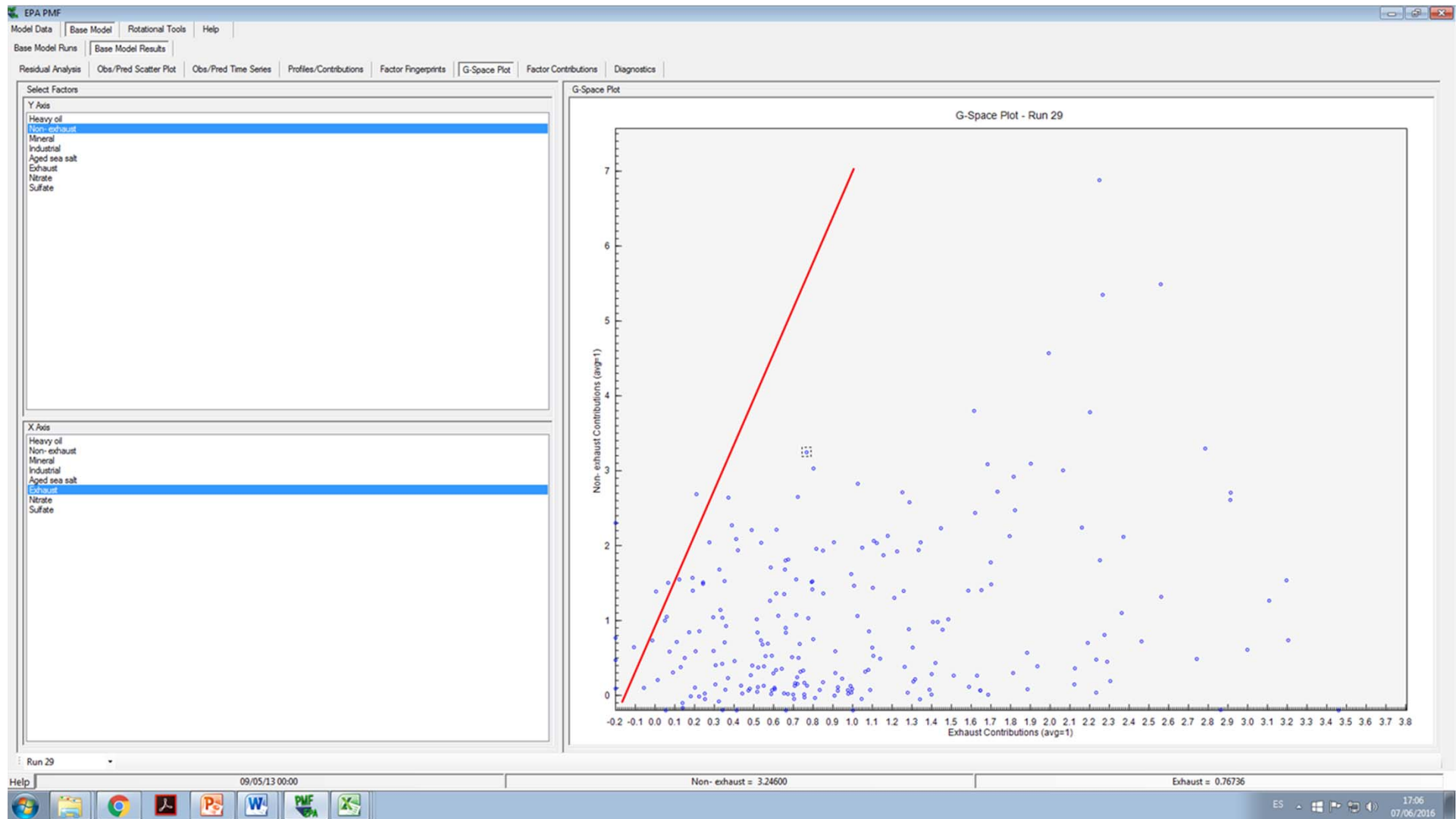


Results and diagnostics 4

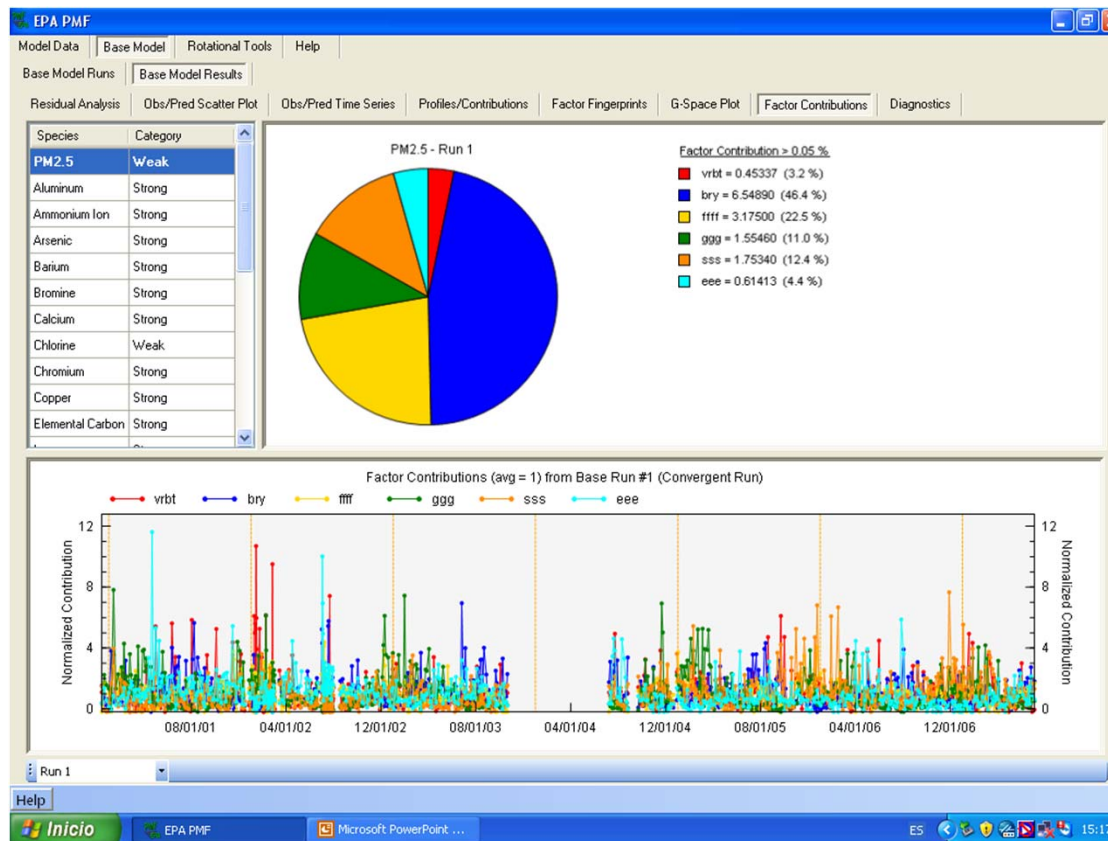
- Concentration unit
- Q/Qexp
- 3 matrices in the output file
 - $\mu\text{g}/\text{m}^3$
 - % of species
 - % of total variable



G-space plots



Contributions

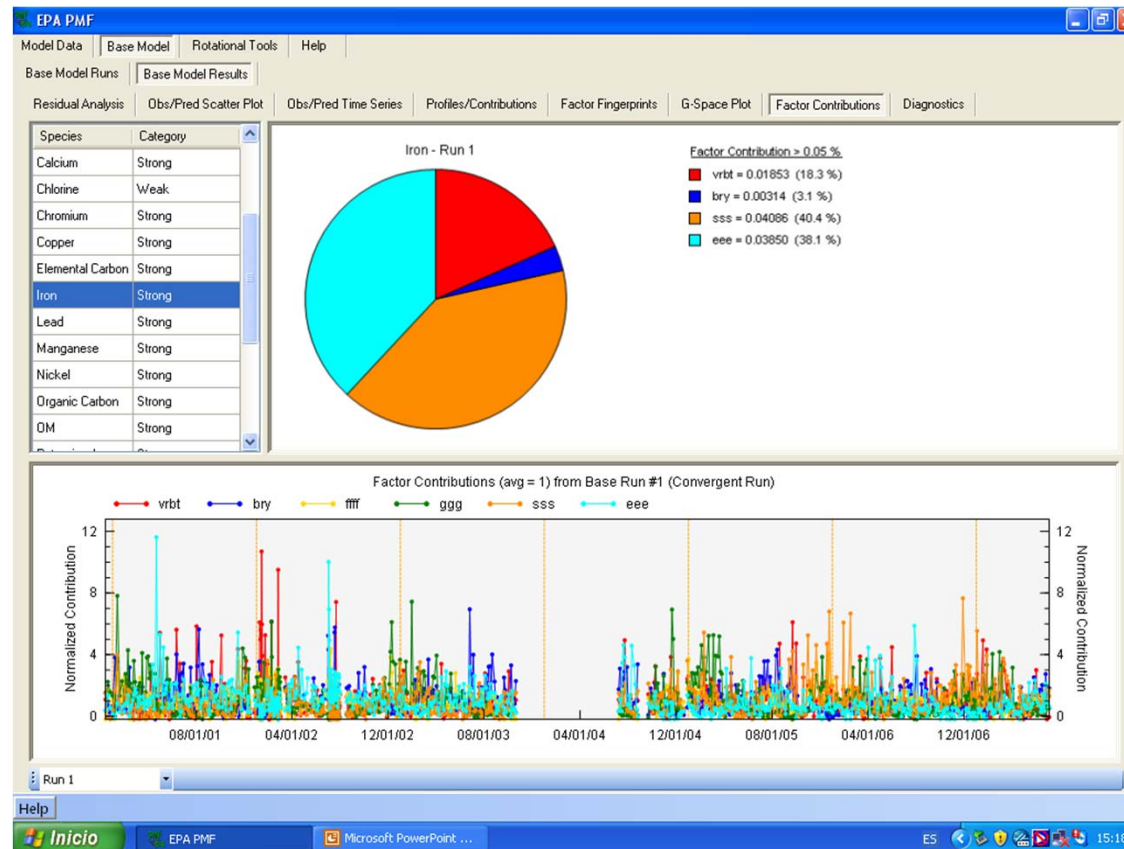


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For single species





Output error estimate

1. Random errors (Bootstrapping).
2. Rotational errors (Displacement)
3. Both (BS-DISP)

Modelling errors difficult to estimate, and they are not minimized by large datasets

If uncertainties are not well specified, use only BS-DISP or BS

Zíková et al (2016) Atmospheric Environment, 134, pp. 84-95.

Brown, et al (2015) Science of the Total Environment, 518-519, pp. 626-635.

Paatero et al (2014) Atmospheric Measurement Techniques, 7 (3), pp. 781-797.

Xie et al., 2012, 2014; Kioumourtzoglou et al., 2014

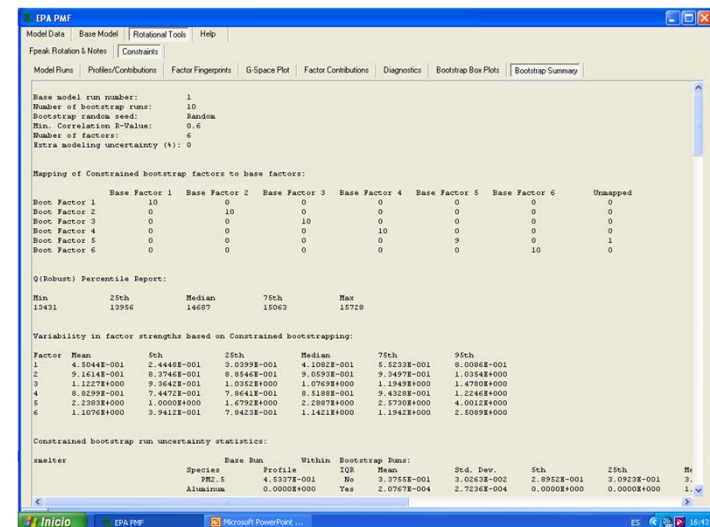


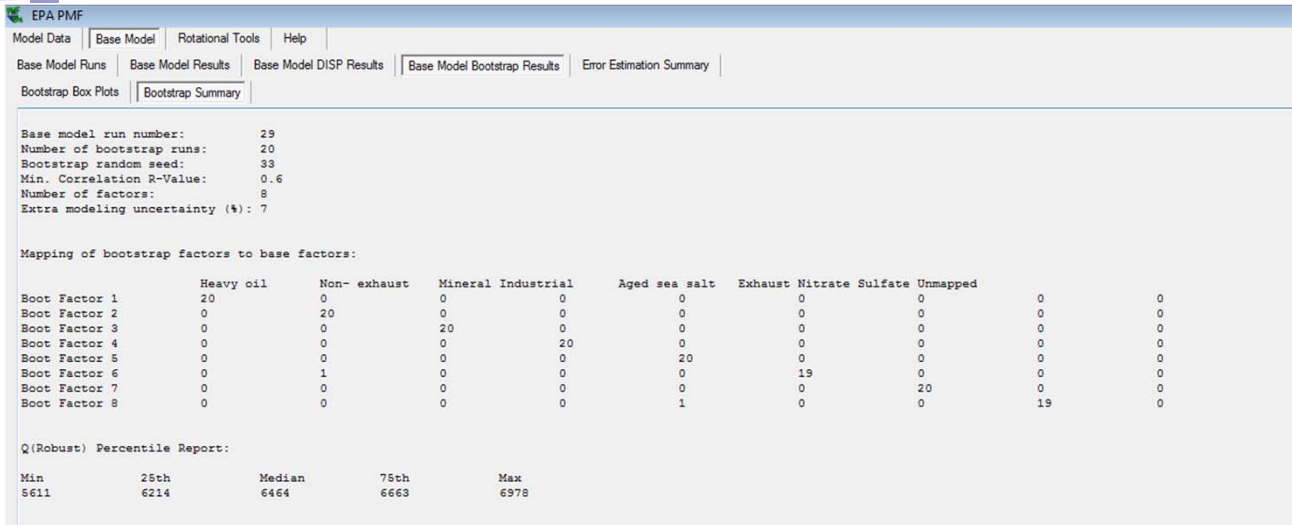
The screenshot displays the EPA PMF software interface. The 'Base Model Runs' section shows 30 runs with 8 factors. The 'Error Estimation' section is set to 'Base Model Displacement Method' with a selected base run of 29. The 'Base Model Bootstrap Method' section shows a selected base run of 29, a block size of 43, and 20 bootstraps. The 'Base Model BS-DISP Method' section shows a table of displacement, species, category, and S/N values for various species like PM, EC, OC, NH4, O3, NO3, SO4, Al, Ca, Fe, K, Mg, Na, S, U, and Ti. The 'Factor Names' section shows 8 factors: Factor 1 (Heavy oil), Factor 2 (Non-exhaust), Factor 3 (Mineral), Factor 4 (Industrial), Factor 5 (Aged sea soil), Factor 6 (Exhaust), Factor 7 (Nitrate), and Factor 8 (Sulfate). The 'Run Progress' bar is visible at the bottom.



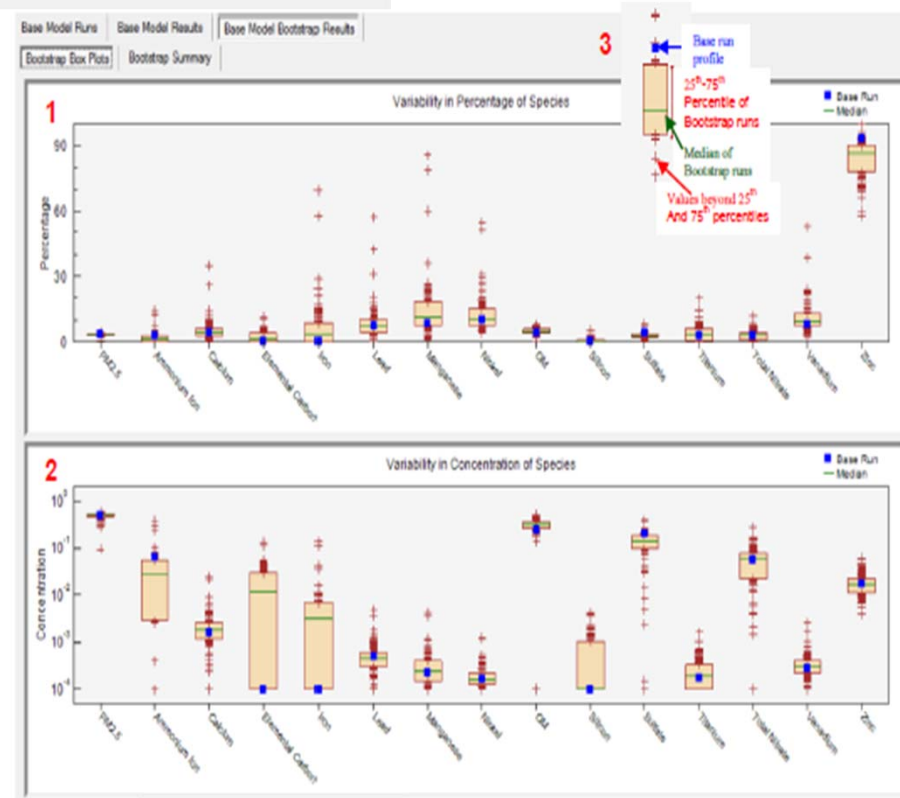
Bootstrapping diagnostic

- Random errors, partially evaluates the rotational ambiguity
- not influenced by the user-specified sample uncertainties.
- >80% mapped factors





- Species with base run outside the IQR need evaluation





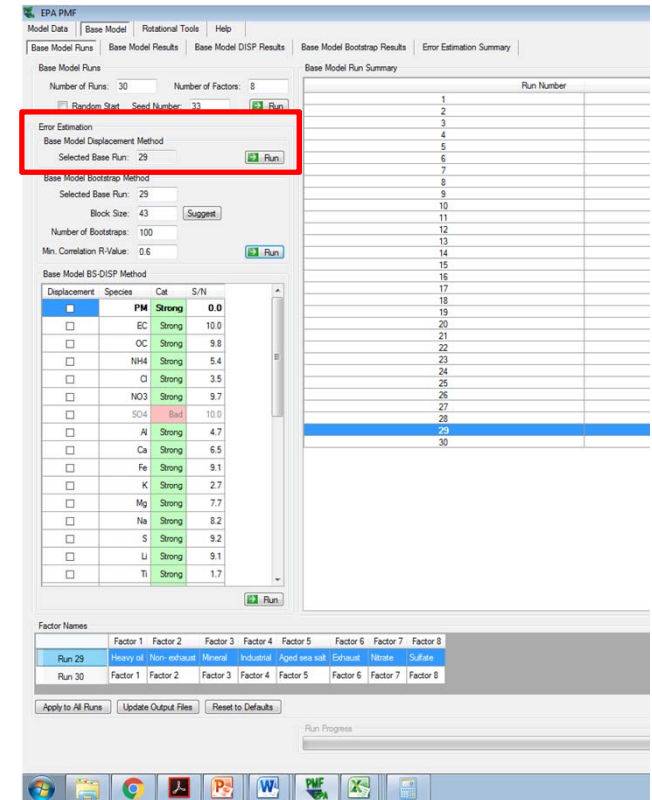
DISP

Only on strong/tracer species.
Valid only if data uncertainties
are reliable

Invalid if $Q/Q_{exp} > 10$

Diagnostics:

- Error code: 0
- Second value < 1%
- Number of swaps



Case 1. Small Errors	Case 2. Realistic Errors	Case 3. Simple Errors + 1 extra factor modeled
0 -0.111	0 0.000	0 -2.557
<u>0 0 0 0</u>	<u>0 0 0 0</u>	<u>6 5 3 0 14</u>
0 0 0 0	0 0 0 0	8 6 4 1 19
0 0 0 0	0 0 0 0	8 7 4 1 20
0 0 0 0	0 0 0 0	8 8 5 1 22





BS-DISP

- Only key and major species
- Long computation times
 1. Each DISP defines the span of rotationally accessible space.
 2. Each BS resample moves this space around, randomly in different directions.
 3. Taken together, all the replications of the rotationally accessible space, in random locations, represent both the random uncertainty and the rotational uncertainty.

Model Data | Base Model | Rotational Tools | Help

Base Model Runs

Number of Runs: 20 Seed: random Run

Number of Factors: 6

Error Estimation

Base Model Bootstrap Method

Selected Base Run: 10 Seed: random

Block Size: 22 Suggest

Number of Bootstraps: 100

Min. Correlation R-Value: 0.6 Run

Base Model BS-DISP Method

Displacement	Species	Cat	S/N
<input type="checkbox"/>	Titanium	Strong	1.4
<input checked="" type="checkbox"/>	Total Nitrate	Strong	1.9
<input type="checkbox"/>	Vanadium	Weak	0.9
<input checked="" type="checkbox"/>	Zinc	Strong	2.0

Run

Base Model Displacement Method

Selected Base Run: 10 Run

Factor Names

	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6
Run 10	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6
Run 11	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6
Run 12	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6

Apply to All Runs Update Output Files Reset to Defaults

Run Progress

Help HAVE Concentration Data HAVE Uncertainty Data HAVE Base Results HA



BS-DISP diagnostic

Ideally

- **N° of runs+1**
- **<1% (>0.5% could indicate a local minimum)**
- **Zero values**
- **0 in first row**

The screenshot shows the 'Base Model BS-DISP Results' window. The 'BS-DISP Summary' tab is active, displaying a table with the following data:

101	-0.190	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0

The five values in the first line are:

- (1) $k = \#$ of cases in the file (includes both the full-data case and the accepted (not rejected) resamples). If no cases were excluded, k should be equal to the number of bootstraps * number of factors * number of species selected for BS-DISP.
- (2) Largest decrease of Q . A large value is not alarming in itself, it only says that there was at least one resample where a deeper minimum appeared.
- (3,4,5) $\#$ of cases with: /drop of Q / swap in best fit / swap in DISP/

Below the first line is a table (four lines) which contains swap counts for factors (columns) for each dQ_{max} level (rows), which are in descending order $dQ_{max}=0.5, 1, 2, 4$. If swaps are present in the first line for the lowest dQ_{max} , it indicates the solution is not well constrained, and should not be used.

Detailed BS-DISP results are included in the *_BSDISPresi-4.txt files (corresponding to the four dQ_{max} levels) in the output folder.

Note: BS-DISP intervals include effects of random errors and rotational ambiguity. For modeling errors, if user misspecifies standard deviation of data, BS-DISP results are more robust than for DISP since the DISP phase of BS-DISP does not displace as strongly as DISP by itself.



BS-DISP: three examples

51 -0.209 0 0 0	39 -21.149 8 0 4	11 -0.461 0 0 135
0 0 0 0	0 0 0 0	7 40 27 1 54
0 0 0 0	1 0 2 1	9 52 44 1 71
0 0 0 0	1 0 2 1	18 59 53 1 93
0 0 0 0	2 1 4 1	26 67 66 1 113





Rotational tools

- FPEAK (similar to previous version, Paatero 2000)

- Constraints

- Expr.builder
- From Base run

The screenshot shows the EPA PMF software interface. The 'Expressions Builder' section is highlighted with a red box, showing a 'Ratio' expression being built. The 'Constraints' section is highlighted with a blue box, showing a table for adding constraints.

Expressions Builder

Ratio

Factor	Species (numerator)	Species (denominator)
smelter	PM2.5	PM2.5
soil	Aluminum	Aluminum
secondary	Ammonium Ion	Ammonium Ion
traffic	Arsenic	Arsenic
marine	Barium	Barium
heavy oil	Bromine	Bromine
	Calcium	Calcium
	Chlorine	Chlorine
	Chromium	Chromium
	Copper	Copper
	Elemental Carbon	Elemental Carbon

Value: 1

Expression: $[\text{traffic}|\text{Copper}] - 1 * [\text{traffic}|\text{Zinc}] = 0$

dQ: 69.41 % dQ: 0.50

Constraints

Factor	Element	Type	Value	dQ	% dQ
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Constrained Model Run

Selected Base Run: 1

dQ (Robust)	Q (Robust)	% dQ (Robust)	Q (Aux)	Q (True)	Converged
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Error Estimation

Constrained Model Bootstrap Method

Number of Bootstraps: 20 Seed: Random

Minimum Correlation R-Value: 0.6 Block Size: 22

Constrained Model BS-DISP Method

Displacement	Species	Cat	S/N
<input checked="" type="checkbox"/>	PM2.5	Weak	9.0
<input type="checkbox"/>	Aluminum	Strong	0.7
<input type="checkbox"/>	Ammonium Ion	Strong	1.4
<input type="checkbox"/>	Arsenic	Strong	0.5

Constrained Model Displacement Method

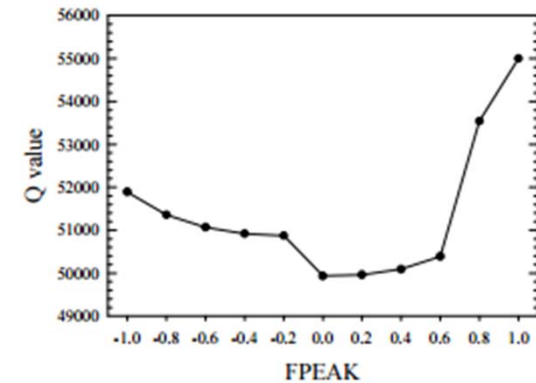
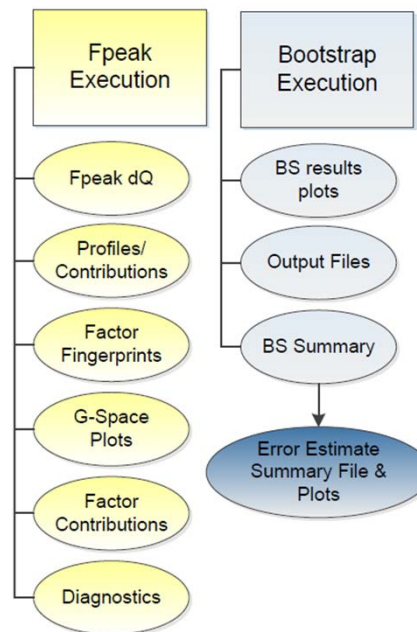
Selected Base Run: 1

Fpeak

The screenshot shows the EPA PMF software interface. The 'Fpeak Model Run Summary' table is as follows:

Strength	dQ (Robust)	Q (Robust)	% dQ (Robust)	Q (Aux)	Q (True)	Converged
-0.5	81.9	7112.4	1.15	66.8	7155.3	Yes
-0.3	23.7	7054.2	0.34	17.8	7147.0	Yes
0.3	29.5	7060.0	0.42	24.7	7146.8	Yes
0.5	124.6	7155.1	1.74	111.3	7155.2	Yes
1.0	510.9	7541.4	6.77	483.2	7169.7	Yes

Control panels include 'Fpeak Model Runs' (Selected Base Run: 29, Selected Fpeak Runs: -0.5, -0.2, 0.25, 0.5, 1.0) and 'Fpeak Model Bootstrap Method' (Number of Bootstraps: 20, Minimum Correlation R-Value: 0.6, Block Size: 43).





■ Expression builder

- Ratio (elements of same factors)
- Mass balance (elements of different factors)
- Custom (also on contributions)

The screenshot displays the EPA PMF software interface. The 'Expressions' panel is highlighted with a red box, showing the 'Expression Builder' section. It includes a 'Ratio' tab, a list of factors (smelter, soil, secondary, traffic, marine, heavy oil), and two lists of species (numerator and denominator). A table below shows the expression: $[\text{trafficCopper}] - 1 * [\text{trafficZinc}] = 0$ with a dQ value of 63.41 and a % dQ value of 0.50. The 'Constrained Model Run' panel is also visible, showing a table of species and their displacement values.

dQ (Robust)	Q (Robust)	% dQ (Robust)	Q (Aux)	Q (True)	Converged

Displacement	Species	Cat	S/N
■	PM2.5	Weak	9.0
□	Aluminum	Strong	0.7
□	Ammonium Ion	Strong	1.4
□	Arsenic	Strong	0.5



■ Expression builder

- Ratio (elements of same factors)
- Mass balance (elements of different factors)
- Custom (also on contributions)

Expression Builder

Mass Balance

Expression: $[soil]Aluminum - 10 * [traffic]Aluminum = 0$

Expression	dQ	% dQ
$[soil]Aluminum - 10 * [traffic]Aluminum = 0$	63.411	0.50

Constrained Model Run

dQ (Robust)	Q (Robust)	% dQ (Robust)	Q (Aux)	Q (True)	Converged
308.7	14190.9	2.18	202.8	16312.8	Yes

Constrained Model BS-DISP Method

Displacement	Species	Cat	S/N
<input type="checkbox"/>	PM2.5	Weak	9.0
<input checked="" type="checkbox"/>	Aluminum	Strong	0.7
<input type="checkbox"/>	Ammonium Ion	Strong	1.4
<input type="checkbox"/>	Arsenic	Strong	0.5

Expression Builder

Custom

Expression: $[smelter]Aluminum - 0.1 * [smelter]PM2.5 = 0$

Expression	dQ	% dQ
$[smelter]Aluminum - 0.1 * [smelter]PM2.5 = 0$	63.411	0.50

Constrained Model Run

dQ (Robust)	Q (Robust)	% dQ (Robust)	Q (Aux)	Q (True)	Converged
308.7	14190.9	2.18	202.8	16312.8	Yes

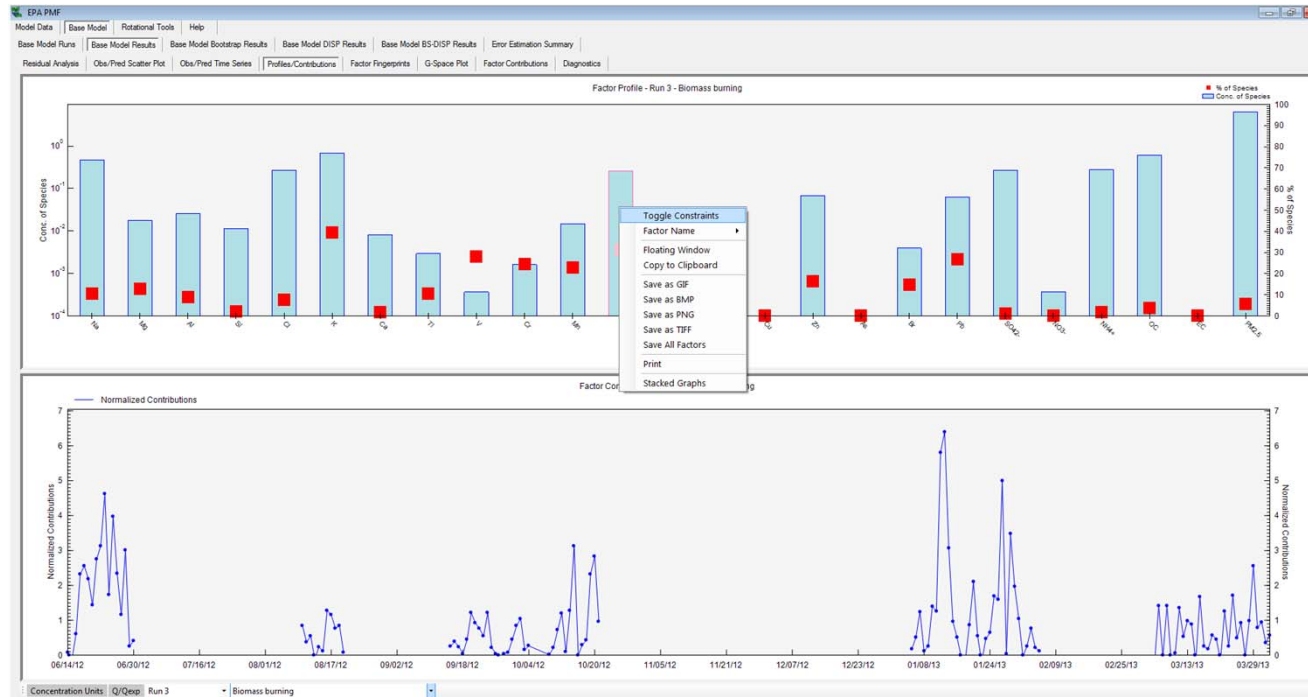
Constrained Model BS-DISP Method

Displacement	Species	Cat	S/N
<input type="checkbox"/>	PM2.5	Weak	9.0
<input checked="" type="checkbox"/>	Aluminum	Strong	0.7
<input type="checkbox"/>	Ammonium Ion	Strong	1.4
<input type="checkbox"/>	Arsenic	Strong	0.5



From the base run

- Pulling existing factor profile
- Pulling existing contributions
- Pulling G space plots





Strength of pulling

Soft options (with maximum dQ):

- Pull down maximally
- Pull up maximally
- Pull to value

Hard options (regardless of dQ):

- Forced to zero
- Forced to original value
- Forced to Upper/lower limits

The screenshot displays the EPA PMF software interface. The 'Constraints' tab is active, showing a table of constraints for various elements. The 'Constraints' table is highlighted with a pink box:

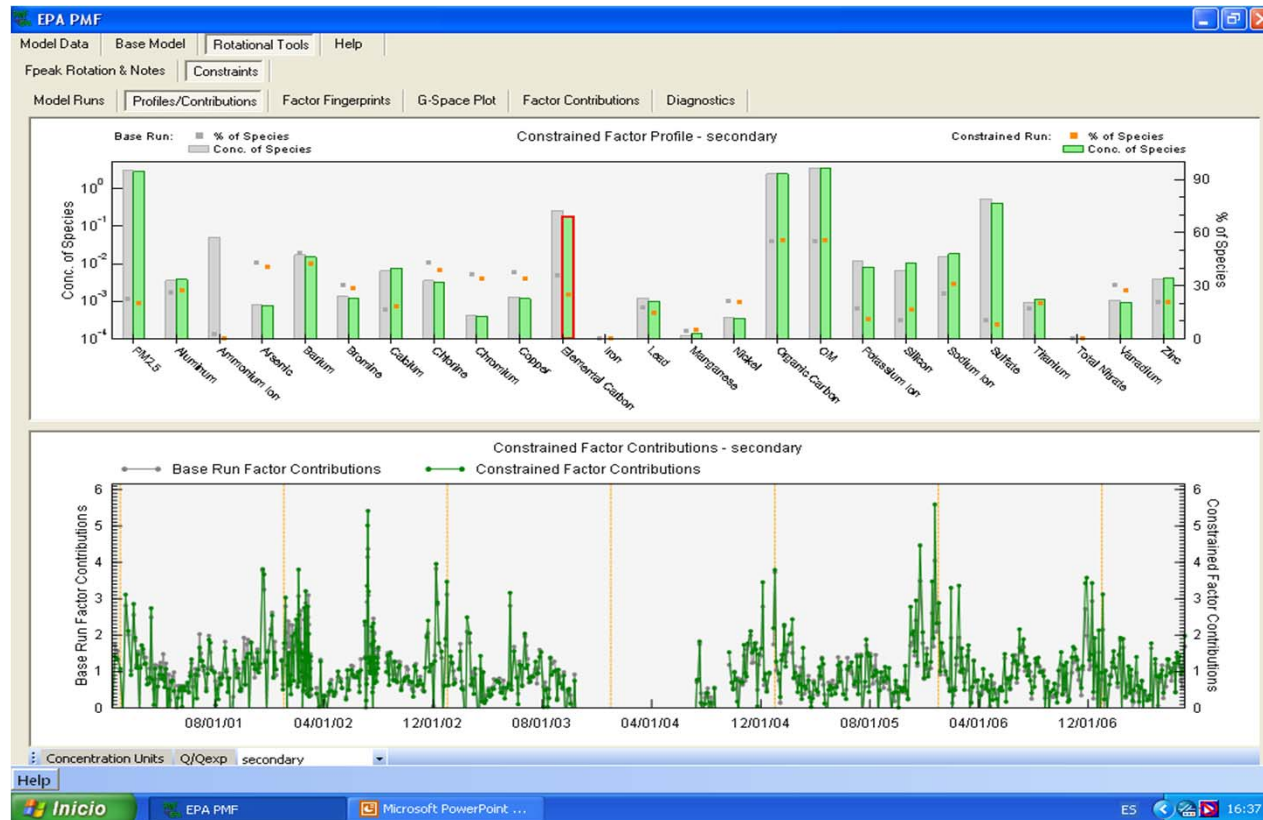
Element	Type	Value	dQ	% dQ
Sodium Ion	Pull Down Maximally	NA	694.11	5
OM	Set to Zero	0	NA	NA
Elemental Carbon	Pull to Value	0.01	138.82	1

The 'Error Estimation' section shows a table of displacement results:

Displacement	Species	Cat	S/N
<input type="checkbox"/>	PM2.5	Weak	9.0
<input type="checkbox"/>	Aluminum	Strong	0.7
<input type="checkbox"/>	Ammonium Ion	Strong	1.4
<input type="checkbox"/>	Arsenic	Strong	0.5



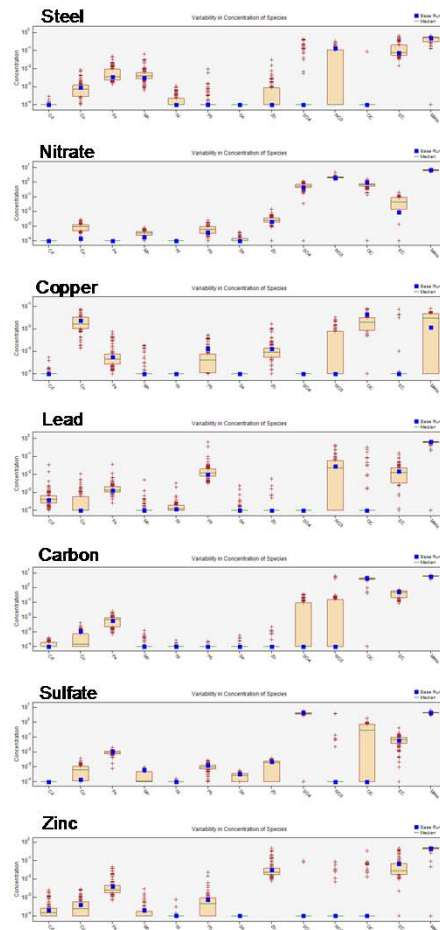
Results of constrained PMF



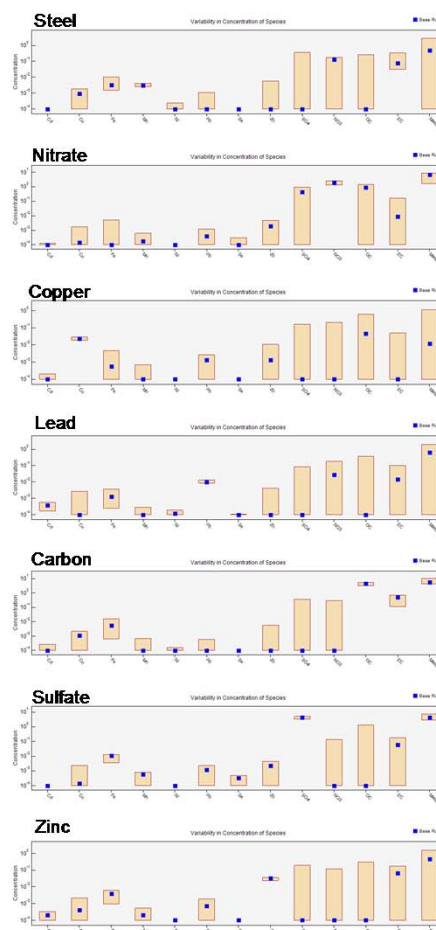


All error estimates can be applied also on Constrained PMF

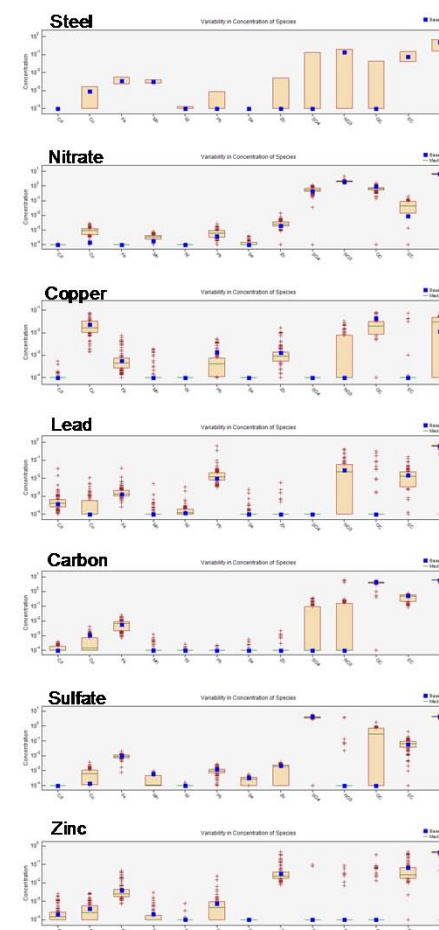
BS



BS-DISP



DISP



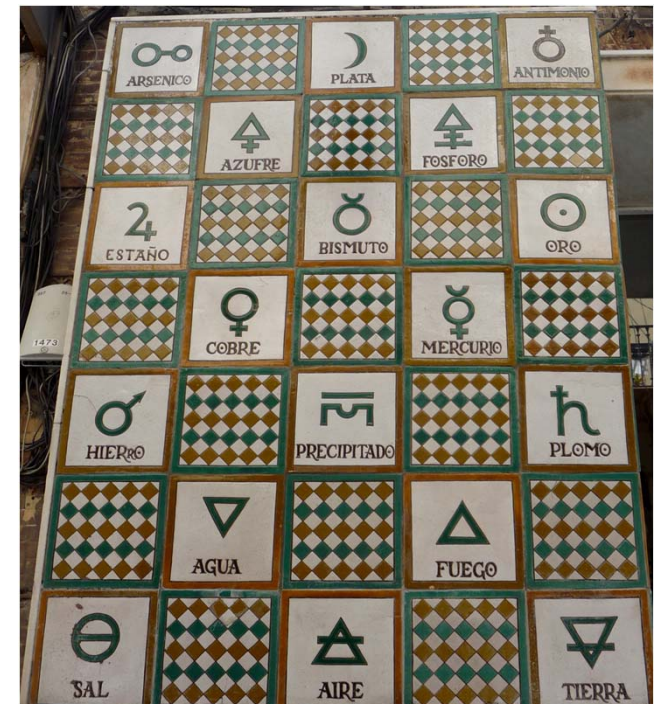


Thank you for your attention!

.....in some cases a satisfactory analysis cannot be performed with any number of factors

.....we did not reach a full understanding of Error Estimates, more studies are Needed

Brown et al., 2015 (STOTEN)





What to report

- Uncertainty estimate method
- Weak species
- Q values , Q exp
- Missing/BDL values treatment
- BS mapping
- DISP swaps and dQ