

REGIONAL TRAINING COURSE ON METHODS AND TOOLS TO IDENTIFY SOURCES OF AIR POLLUTION

IAEA RER 1013: Supporting Air Quality Management

Source apportionment by Positive Matrix Factorization

Marta Almeida

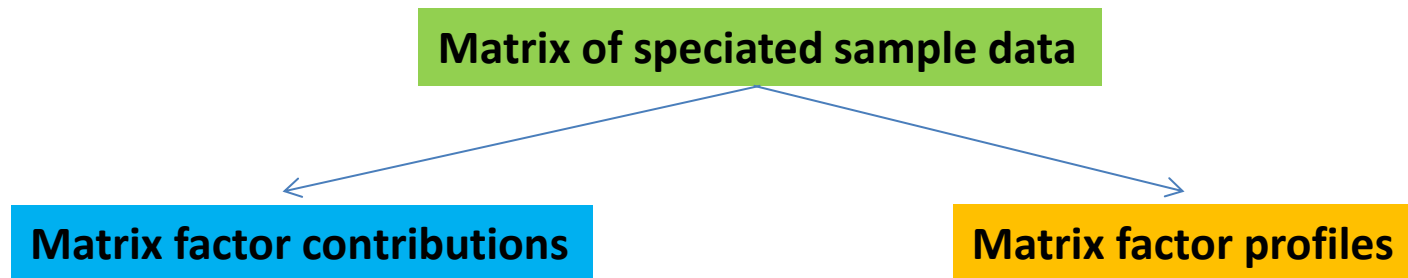
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Sacavém, Portugal
02 –06 June, 2014

Concept

Objective:

- Identify number of factors – p
- The species profile of each source – f
- Amount of mass contributed by each factor to each individual sample – g



j →

	Al	As	Br
09-01-2011 12:00	6.4609	0.0008	0.0108
12-01-2011 12:25	7.0842	0.0009	0.0093
14-01-2011 12:45	3.3487	0.0004	0.0053
18-01-2011 13:45	12.2642	0.0017	0.0087
24-01-2011 12:40	0.1984	0.0010	0.0028
26-01-2011 13:20	0.2612	0.0003	0.0023

↓ i

$$x_{ij} = \sum_{k=1}^p g_{ik} f_{kj} + e_{ij}$$

Residual for each sample/species

Object function Q

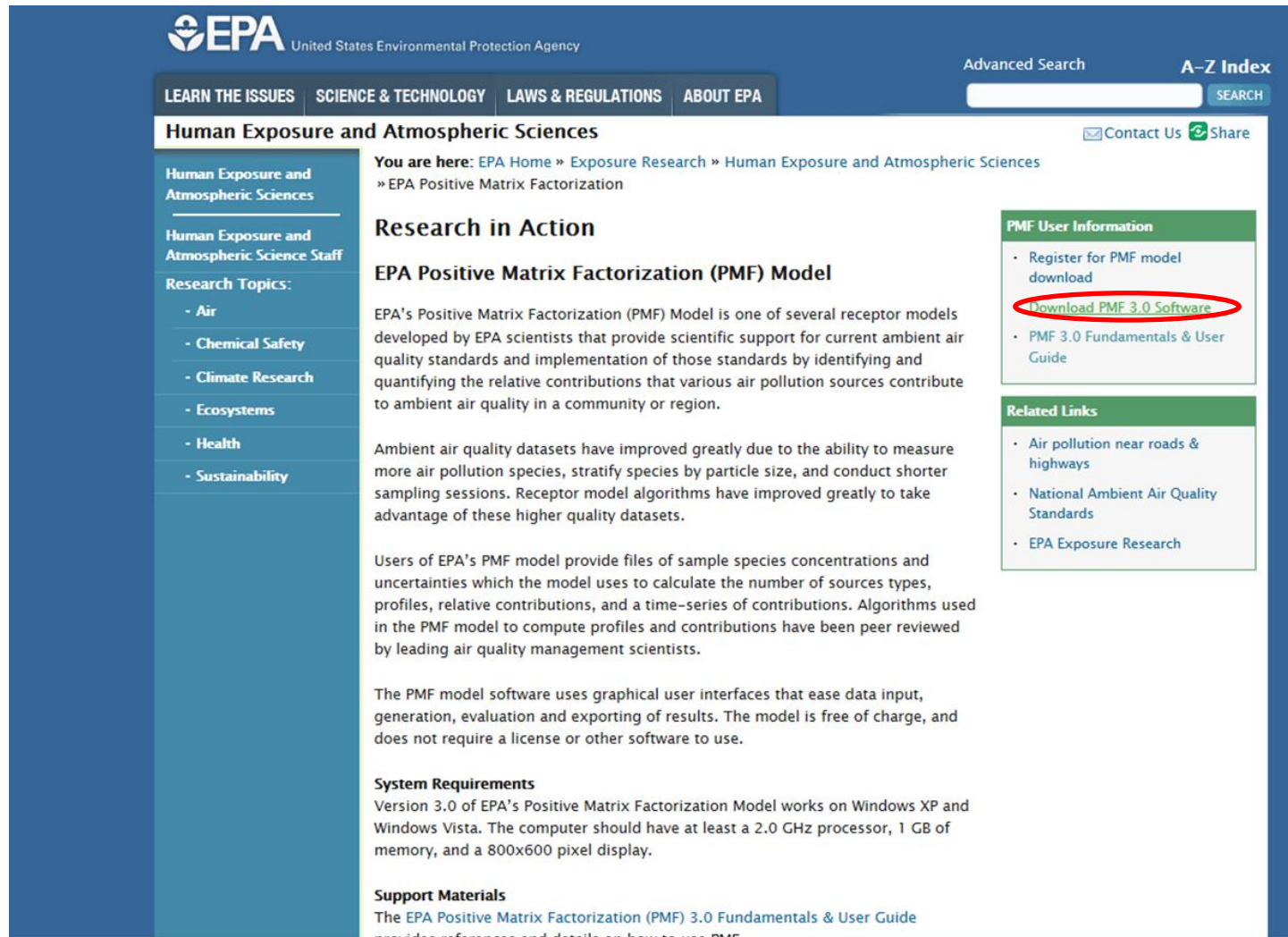
- Results are constrained so that no sample can have negative source contribution;
- PMF allows each data point to be individually weighed;
- The PMF solution minimizes the object function Q, based upon the data uncertainties (u).

$$Q = \sum_{i=1}^n \sum_{j=1}^m \left[\frac{x_{ij} - \sum_{k=1}^p g_{ik} f_{kj}}{u_{ij}} \right]^2$$

Getting started

Download the programme

<http://www.epa.gov/head/research/pmf.html>



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» EPA Positive Matrix Factorization

Research in Action

EPA Positive Matrix Factorization (PMF) Model

EPA's Positive Matrix Factorization (PMF) Model is one of several receptor models developed by EPA scientists that provide scientific support for current ambient air quality standards and implementation of those standards by identifying and quantifying the relative contributions that various air pollution sources contribute to ambient air quality in a community or region.

Ambient air quality datasets have improved greatly due to the ability to measure more air pollution species, stratify species by particle size, and conduct shorter sampling sessions. Receptor model algorithms have improved greatly to take advantage of these higher quality datasets.

Users of EPA's PMF model provide files of sample species concentrations and uncertainties which the model uses to calculate the number of sources types, profiles, relative contributions, and a time-series of contributions. Algorithms used in the PMF model to compute profiles and contributions have been peer reviewed by leading air quality management scientists.

The PMF model software uses graphical user interfaces that ease data input, generation, evaluation and exporting of results. The model is free of charge, and does not require a license or other software to use.

System Requirements

Version 3.0 of EPA's Positive Matrix Factorization Model works on Windows XP and Windows Vista. The computer should have at least a 2.0 GHz processor, 1 GB of memory, and a 800x600 pixel display.

Support Materials

The [EPA Positive Matrix Factorization \(PMF\) 3.0 Fundamentals & User Guide](#) provides references and details on how to use PMF.

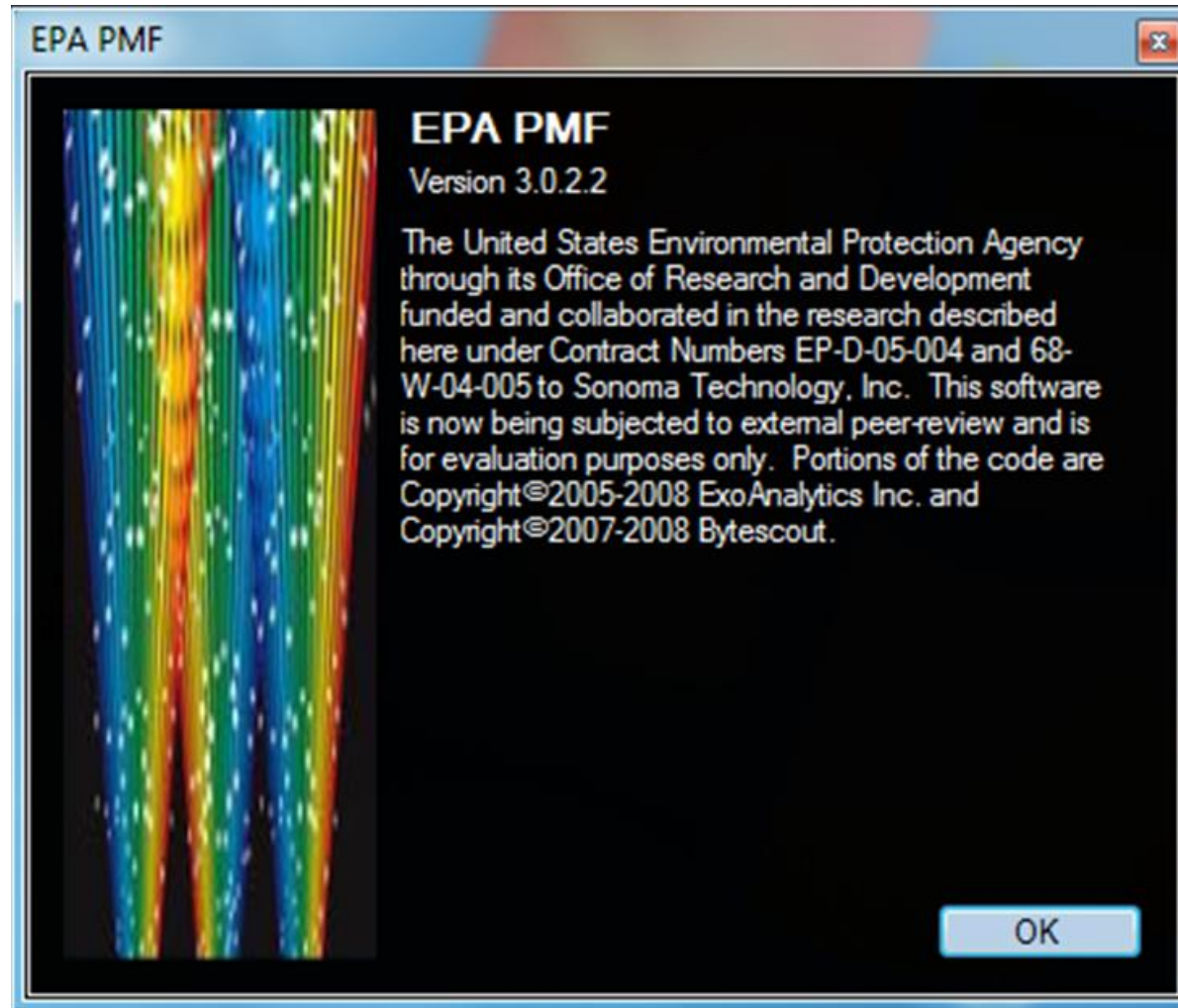
PMF User Information

- Register for PMF model download
- Download PMF 3.0 Software**
- PMF 3.0 Fundamentals & User Guide

Related Links

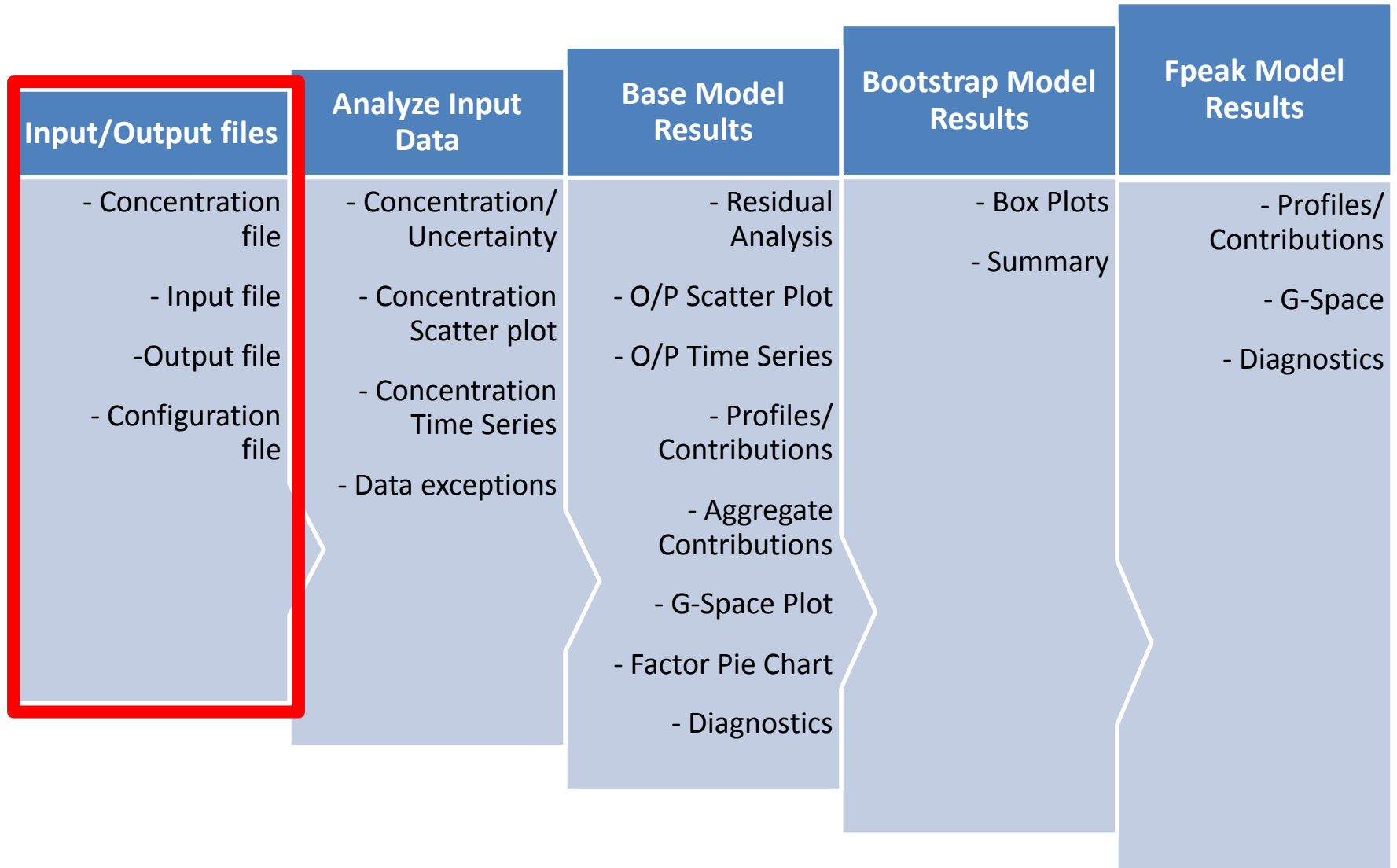
- Air pollution near roads & highways
- National Ambient Air Quality Standards
- EPA Exposure Research

Getting started



run as administrator

Order of the operations



Input/Output Files

EPA PMF v3.0.2.2

File View Action Help

Input/Output Files | Analyze Input Data | Model Execution | Base Model Results | Bootstrap Model Results | Fpeak Model Results

Input Files

Model input data in tab-delimited (.txt), comma-separated value (.csv), or Excel workbook (.xls) format. Species names in first row, units in second row (optional), and date/times in first column (optional).

Concentration Data File: C:\PMF workshop\DatabaseCVDust.xlsx Browse

Concentration data table with parameter names in the first row. Optionally, the second row may contain units and the first column may contain date/time.

Uncertainty Data File: C:\PMF workshop\DatabaseCVDust.xlsx Browse

Observation-based or equation-based uncertainty values for each sample. Must match concentration data format.

Missing Value Indicator: -999 ☒ Exclude Entire Sample ☐ Replace Missing Values with Species Median

Output Files

Output Folder: C:\PMF workshop Browse

Specify a destination folder for all model run output files.

Output File Type: ☒ Tab-Delimited Text (*.txt) ☐ Comma-Delimited Text (*.csv) ☐ Excel Workbook (*.xls)

Program Configuration:

Configuration File: C:\PMF workshop\EPAPMF.cfg Browse

Enter or browse to a configuration file.

Load Configuration Save Configuration Exit

HAVE Concentration Data **HAVE Uncertainty Data** **NEED Base Results** **NEED Bootstrap Results**

Input/Output Files

Input files

1. Concentration of chemical species
2. Uncertainties

Accepted formats

1. Tab-delimited (.txt)
2. Comma-separated value (.csv)
3. MS Excel (.xls)



Blank cells are not accepted



Factor analysis technique provides a robust solution when the number of samples minus the number of variable is at least 30 (Henry, 1991)

Concentration file

A		B	C	D	E	F	G
1	SAMPLE	Al	As	Br	Ce	Cr	Cu
2	09-01-2011 12:00	6.4608686	0.0007851	0.0107995	0.0084138	0.0059733	
3	12-01-2011 12:25	7.0841526	0.0008773	0.0092972	0.0123250	0.0076864	
4	14-01-2011 12:45	3.3487461	0.0004447	0.0053121	0.0044104	0.0027498	
5	18-01-2011 13:45	12.2641534	0.0016797	0.0087070	0.0165186	0.0097598	
6	24-01-2011 12:40	0.1984172	0.0010497	0.0028407	0.0014837	0.0000040	
7	26-01-2011 13:20	0.2612301	0.0003027	0.0023261	0.0008012	0.0000040	
8	31-01-2011 13:25	0.8072121	0.0001354	0.0068794	0.0019740	0.0000040	
9	02-02-2011 13:40	3.7180185	0.0005623	0.0187804	0.0035270	0.0060591	
10	03-02-2011 14:00	33.9842892	0.0034903	0.0281858	0.0321722	0.0213273	
11	04-02-2011 14:00	54.0052522	0.0032138	0.0287018	0.0358654	0.0271958	
12	05-02-2011 12:00	56.6012609	0.0046405	0.0209047	0.0256021	0.0216202	
13	05-02-2011 19:10	33.6179915	0.0030329	0.0169174	0.0230384	0.0171064	
14	06-02-2011 12:00	52.0479121	0.0034749	0.0221730	0.0245887	0.0161911	
15	07-02-2011 09:25	32.7112158	0.0028426	0.0152159	0.0195285	0.0124952	
16	08-02-2011 08:45	10.7573965	0.0010036	0.0064979	0.0090763	0.0050988	
17	09-02-2011 08:30	3.3180070	0.0005160	0.0101554	0.0033347	0.0031442	
18	11-02-2011 08:20	1.9854946	0.0001963	0.0103436	0.0015092	0.0000076	
19	13-02-2011 12:45	2.4681021	0.0005101	0.0197646	0.0011780	0.0007477	
20	15-02-2011 13:00	0.5497766	0.0005101	0.0084447	0.0005602	0.0000040	
21	17-02-2011 13:20	1.2933946	0.0005101	0.0095033	0.0006169	0.0000153	
22	19-02-2011 13:35	1.4006697	0.0001313	0.0119213	0.0012829	0.0004312	
23	21-02-2011 13:50	3.7123976	0.0003954	0.0116682	0.0033004	0.0020265	
24	23-02-2011 14:10	7.3253142	0.0007366	0.0141350	0.0057125	0.0034139	
25	24-02-2011 14:30	15.5569509	0.0009783	0.0146358	0.0098247	0.0065134	
26	27-02-2011 18:15	52.9080878	0.0033424	0.0229199	0.0328968	0.0252674	
27	28-02-2011 08:35	27.8334643	0.0021360	0.0138742	0.0215295	0.0151400	
28	28-02-2011 18:50	14.0098193	0.0010812	0.0121890	0.0108934	0.0066902	
29	01-03-2011 14:30	3.7418556	0.0003387	0.0131845	0.0019734	0.0015361	
30	03-03-2011 14:50	1.2940722	0.0005101	0.0074997	0.0004380	0.0000047	
31	08-03-2011 08:10	0.7963118	0.0005101	0.0044267	0.0014140	0.0000040	
32	13-03-2011 11:45	0.4869752	0.0001125	0.0059196	0.0004656	0.0002421	
33	16-03-2011 13:00	1.6784129	0.0005101	0.0137418	0.0010122	0.0004989	
34	18-03-2011 13:10	1.6455298	0.0005101	0.0075600	0.0004380	0.0014823	
35	21-03-2011 14:00	0.8301145	0.0005101	0.0091647	0.0004380	0.0005765	
36	23-03-2011 14:30	4.8377170	0.0007050	0.0118048	0.0041565	0.0039638	
37	28-03-2011 09:00	4.4095921	0.0003631	0.0104453	0.0000915	0.0035963	
38	30-03-2011 13:30	1.5942125	0.0003941	0.0099768	0.0000770	0.0016625	
39	02-04-2011 17:20	1.6785513	0.0003725	0.0121507	0.0001575	0.0014170	
40	05-04-2011 14:45	1.0001000	0.0001000	0.0100000	0.0001000	0.0001000	

Samples

Parameters

Input/Output Files

Types of Uncertainties files

1. Sample specific – Uncertainty file provides an estimate of the uncertainty for each sample of each species;
2. Equation-based – file provides species-specific parameters that PMF uses to calculate uncertainties for each sample.

1. Sample specific
Uncertainty file

		B	C	D	E
		Al	As	Br	Ce
1	01-2011 12:00	0.323043	0.000384	0.000841	0.00061
2	01-2011 12:25	0.354208	0.000135	0.000894	0.00051
3	14-01-2011 12:45	0.167437	7.82E-05	0.000426	0.00011
4	18-01-2011 13:45	0.613208	0.000504	0.001086	0.00221
5	24-01-2011 12:40	0.009921	7.17E-05	0.000431	0.00021
6	26-01-2011 13:20	0.013062	0.00013	0.000223	7.85E-05
7	31-01-2011 13:25	0.040361	5.12E-05	0.000494	0.0031
8	02-02-2011 13:40	0.185901	0.000125	0.001243	0.0058
9	03-02-2011 14:00	1.699214	0.000395	0.004335	0.00631
10	04-02-2011 14:00	2.700263	0.000274	0.002741	0.01211

2. Equation based
Uncertainty file

	A	B	C	D
	Al	As	Br	Ce
2	0.006021	0.002	0.004	0.0005
3	4	9	6	9
4				
5				

← Method Detection Limit (MDL)

← Error fraction (in percentage)

If concentration \leq Detection limit $\Rightarrow Unc = \frac{5}{6} \times MDL$

If concentration \leq Detection limit $\Rightarrow Unc = \sqrt{((Error\ Fraction \times concentration)^2 + (MDL)^2)}$

Input/Output Files

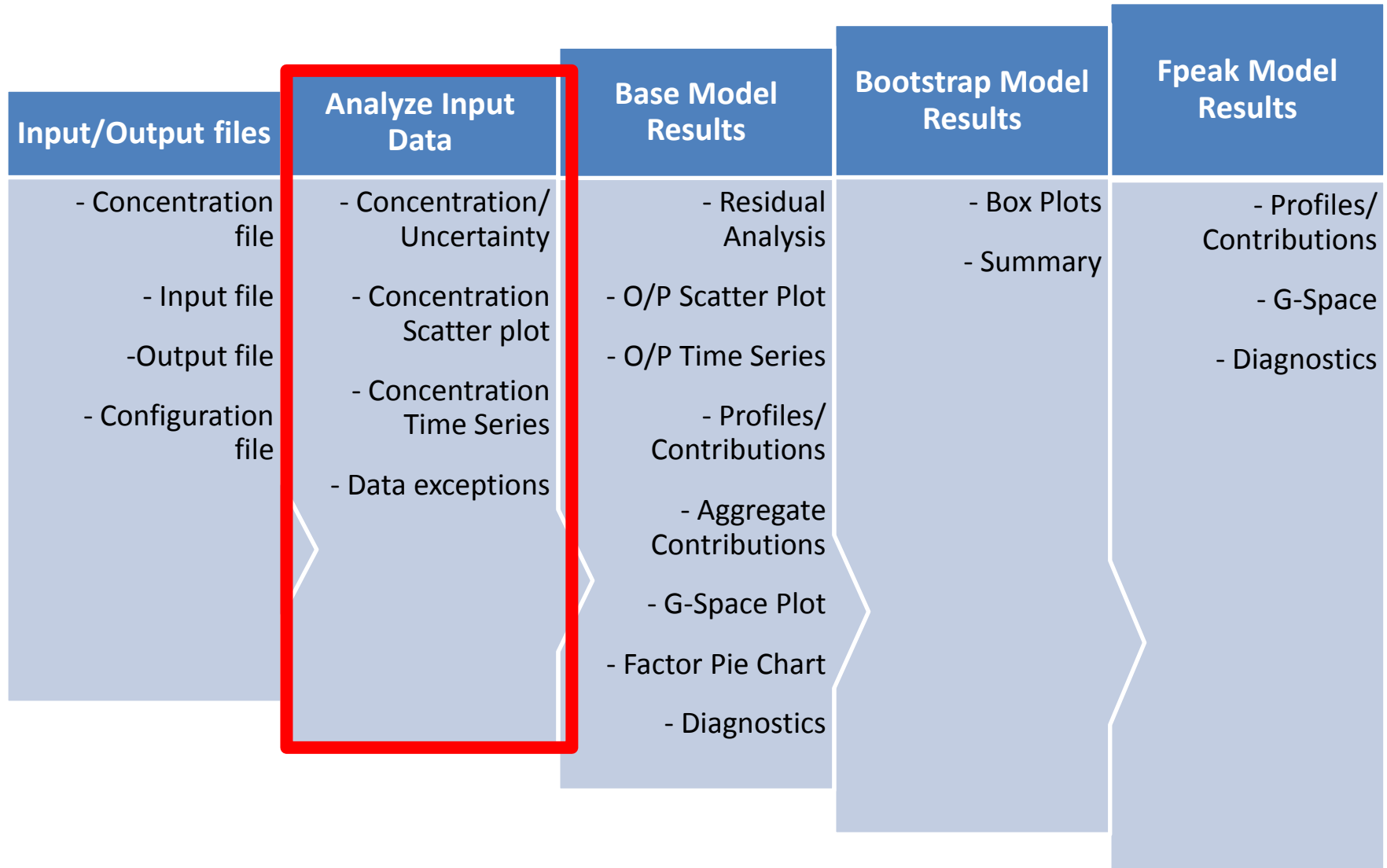
Missing values in the data base

	Concentration	Uncertainty
Concentration < MDL	$\frac{1}{2}$ MDL	$\frac{5}{6}$ MDL
Missing values	Geometric Mean	$4 \times$ Geometric Mean

Input/Output Files

Output Files	
*_diag	Contains a record of the user inputs and model diagnostic information
*_contrib	Contains the contributions for each base run
*_profile	Contains the profiles for each base run
*_resid	Contains the residuals for each base run
*_strength	Contains the factor strength for each base run
*_profile_boot	Contains the number of bootstrap runs mapped to each base run, each bootstrap profile that was mapped to the base profile and all bootstrap statistics
*_fpeak	Contains the profiles and contributions of each fpeak run

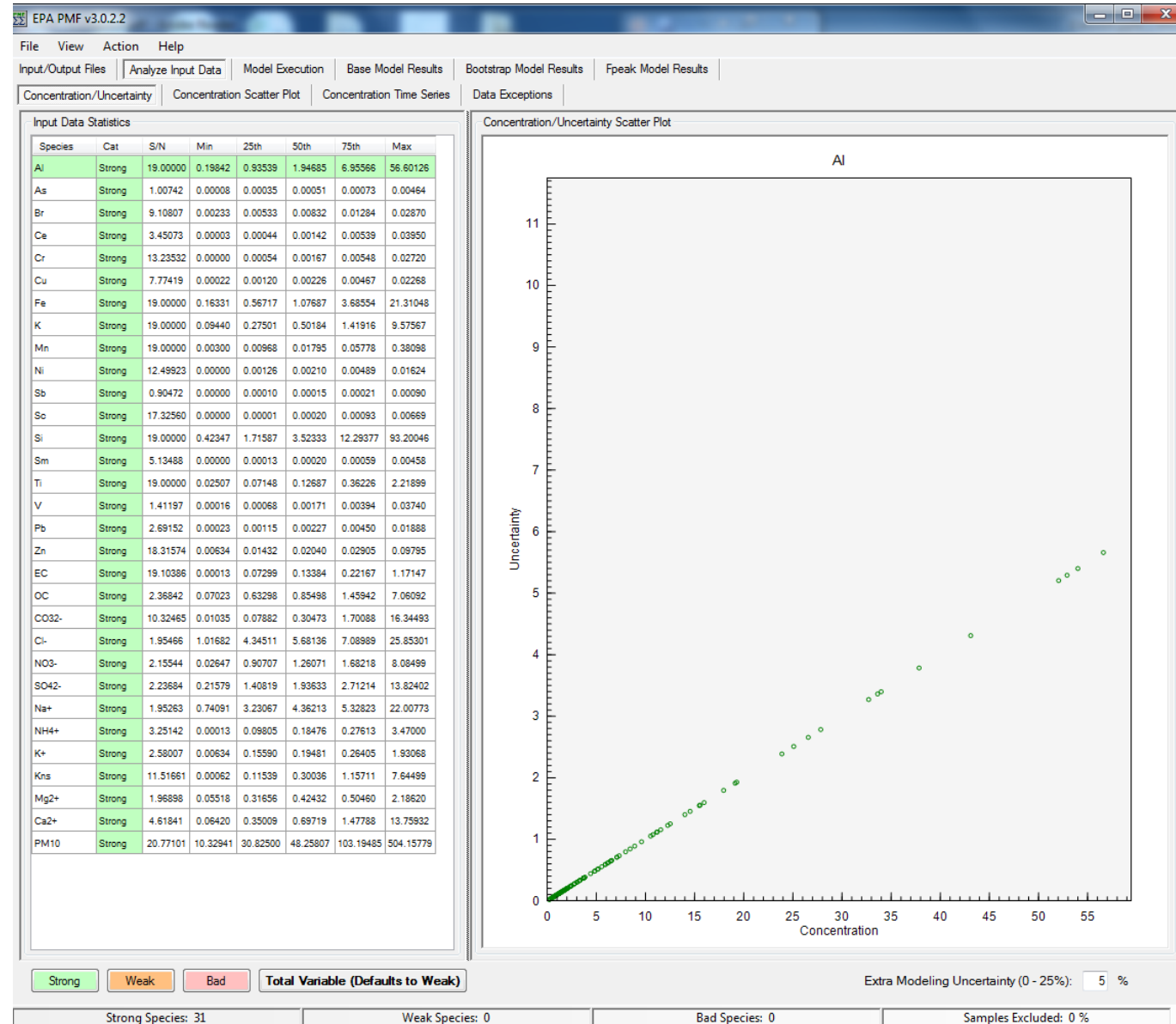
Order of the operations



Analyze input data

Objective:

- To analyze the **concentration and uncertainty** data before running the model;
- Help the user decide whether **certain species should be excluded or down-weighted**;
- Help the user decide whether **certain samples should be excluded**.



Analyze input data

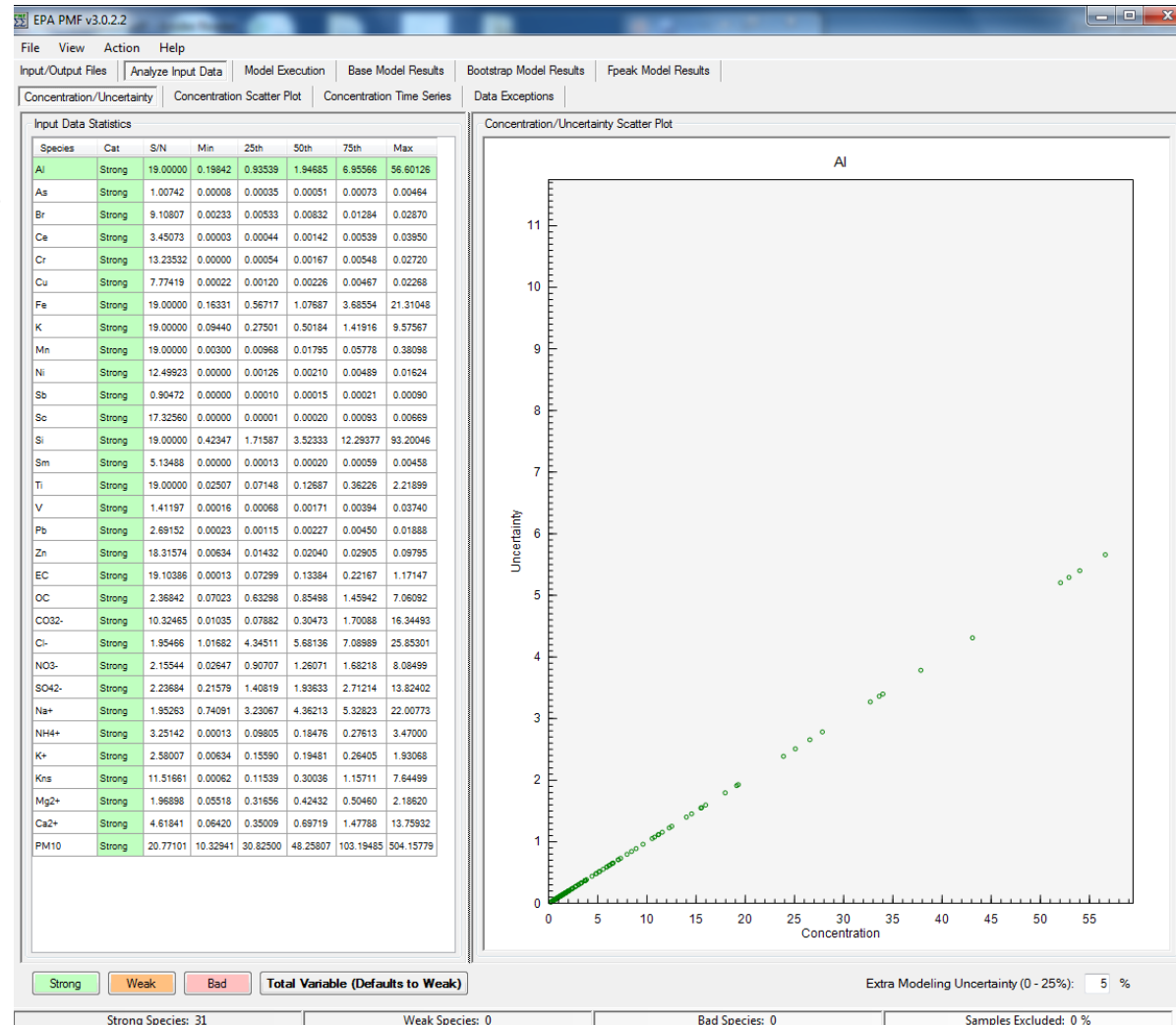
Concentration/Uncertainty

The following statistics are calculated for each species:

- Signal-to-noise ratio (S/N)

$$\left(\frac{S}{N}\right)_j = \sqrt{\frac{\sum_{i=1}^n (x_{ij} - s_{ij})^2}{\sum_{i=1}^n s_{ij}^2}}$$

- Minimum concentration value
- 25th percentile
- Median
- 75th percentile
- Maximum concentration value

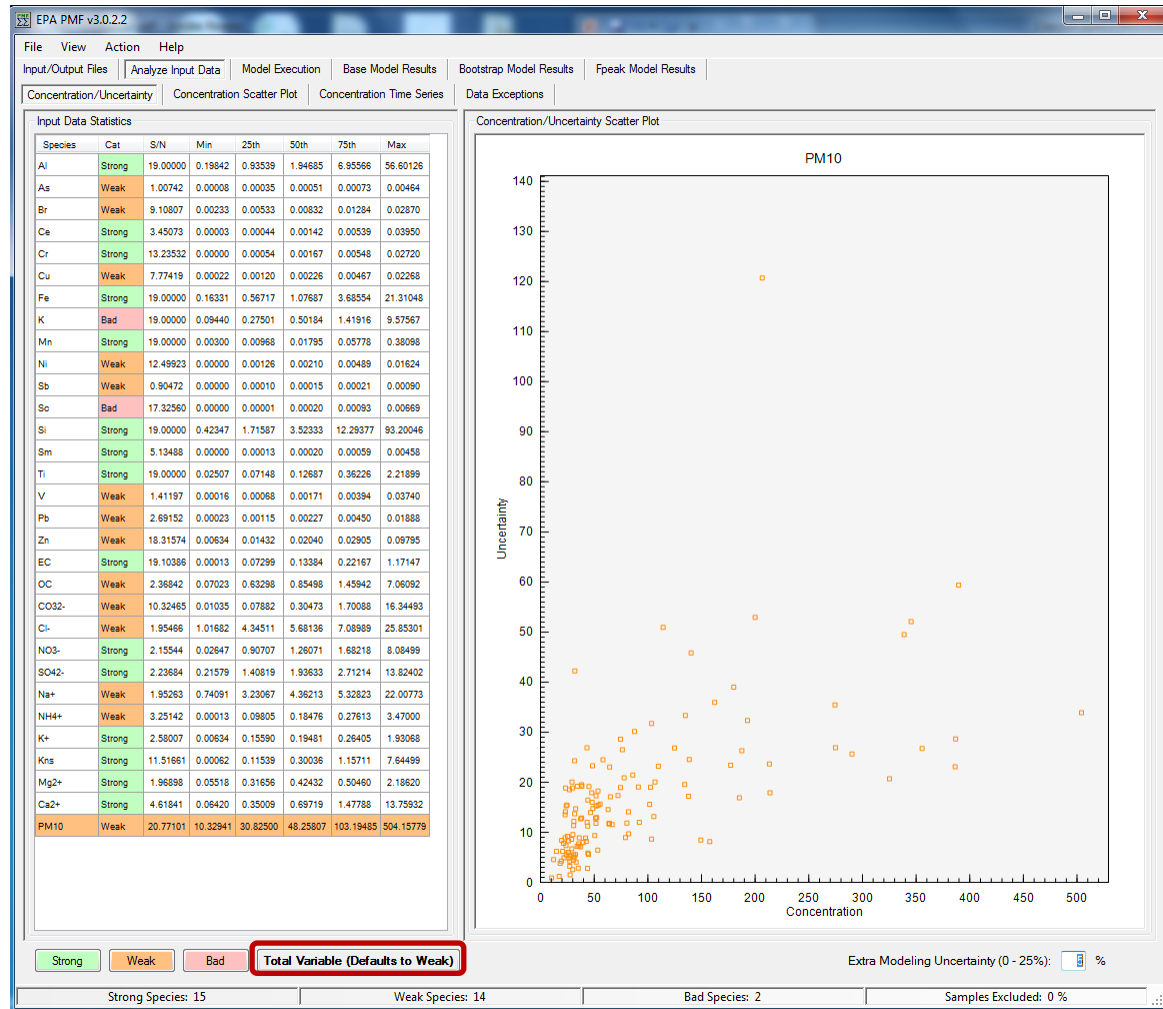


Analyze input data

Concentration/Uncertainty

Based on these statistics + knowledge of the data set the user can categorise a specie as:

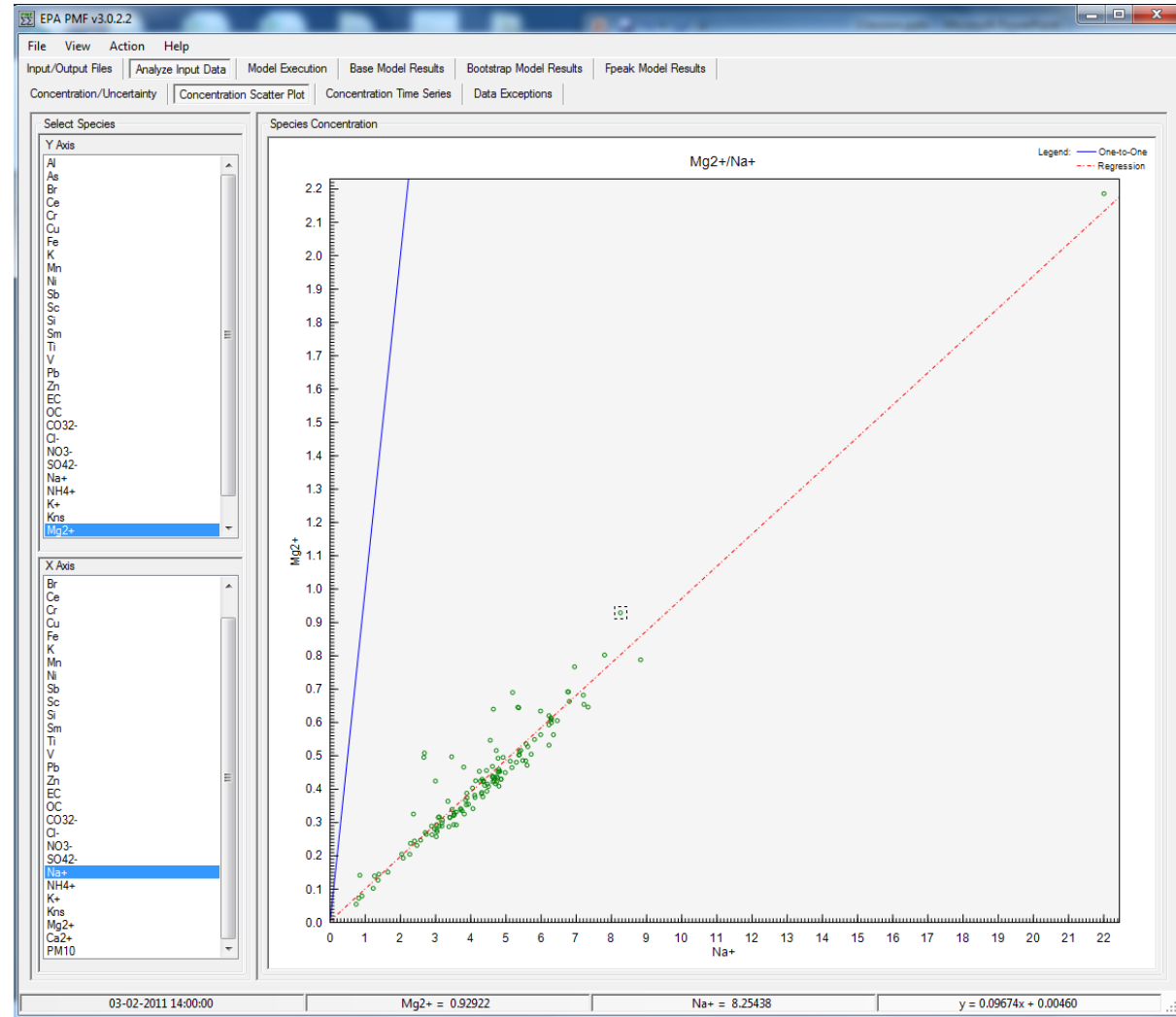
$S/N > 2$	STRONG	-
$0.2 < S/N < 2$	WEEK	uncertainty is tripled
$S/N < 0.2$	BAD	Specie is excluded



Analyze input data

Scatter plots

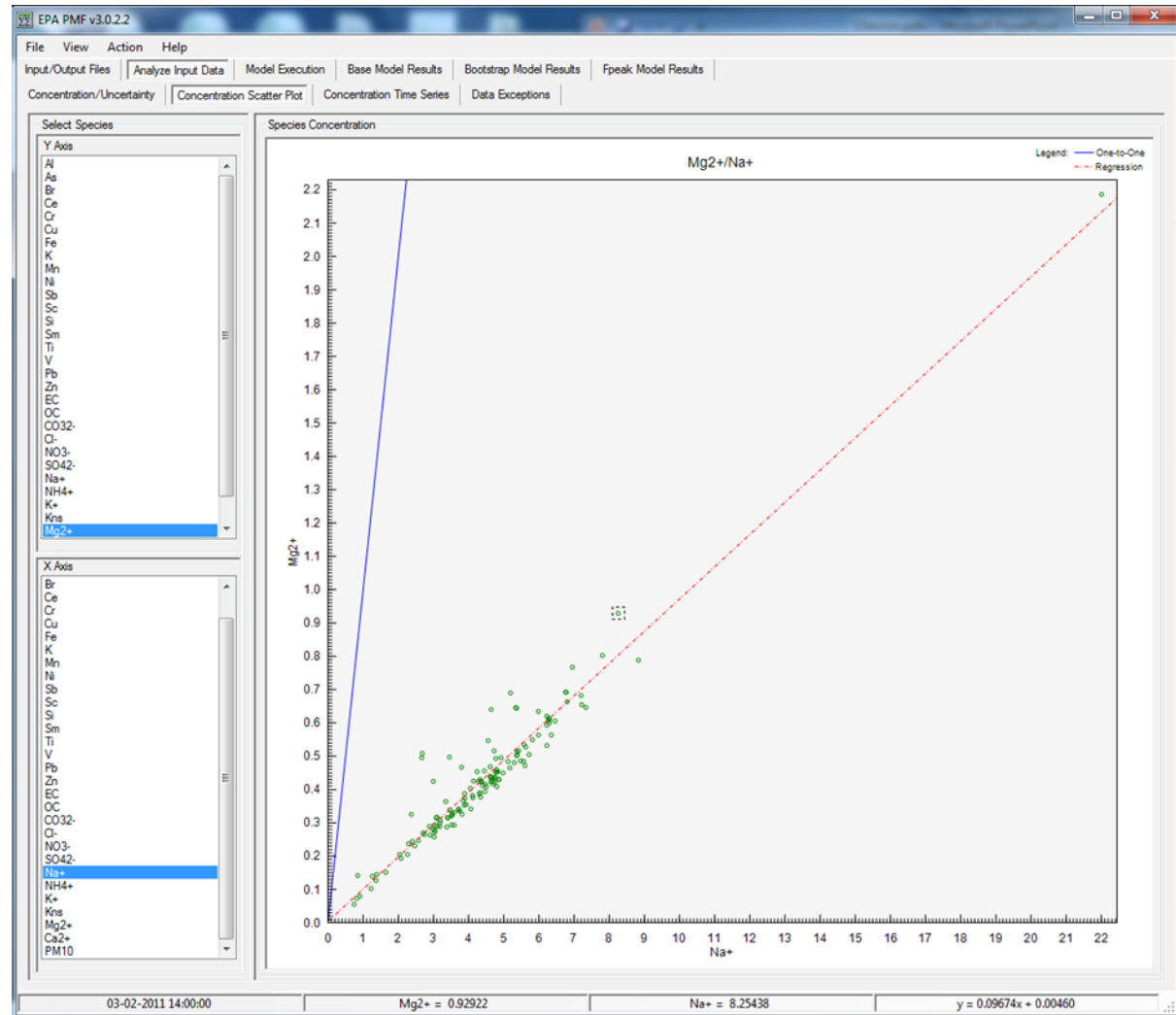
- Useful pre-PMF analysis tool;
- The user should examine scatter plots to look for expected relations



Analyze input data

Scatter plots

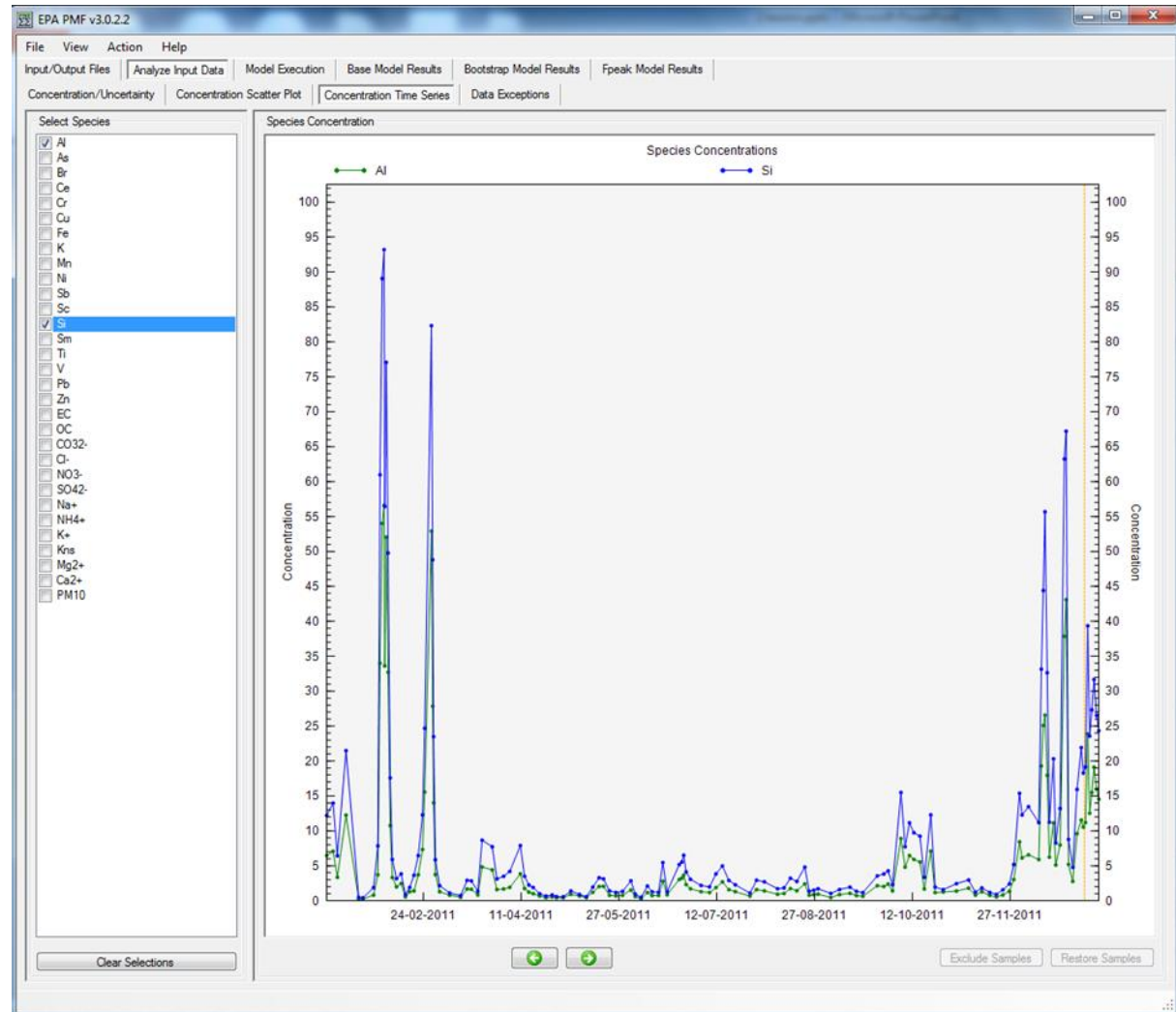
- Useful pre-PMF analysis tool;
- The user should examine scatter plots to look for expected relations



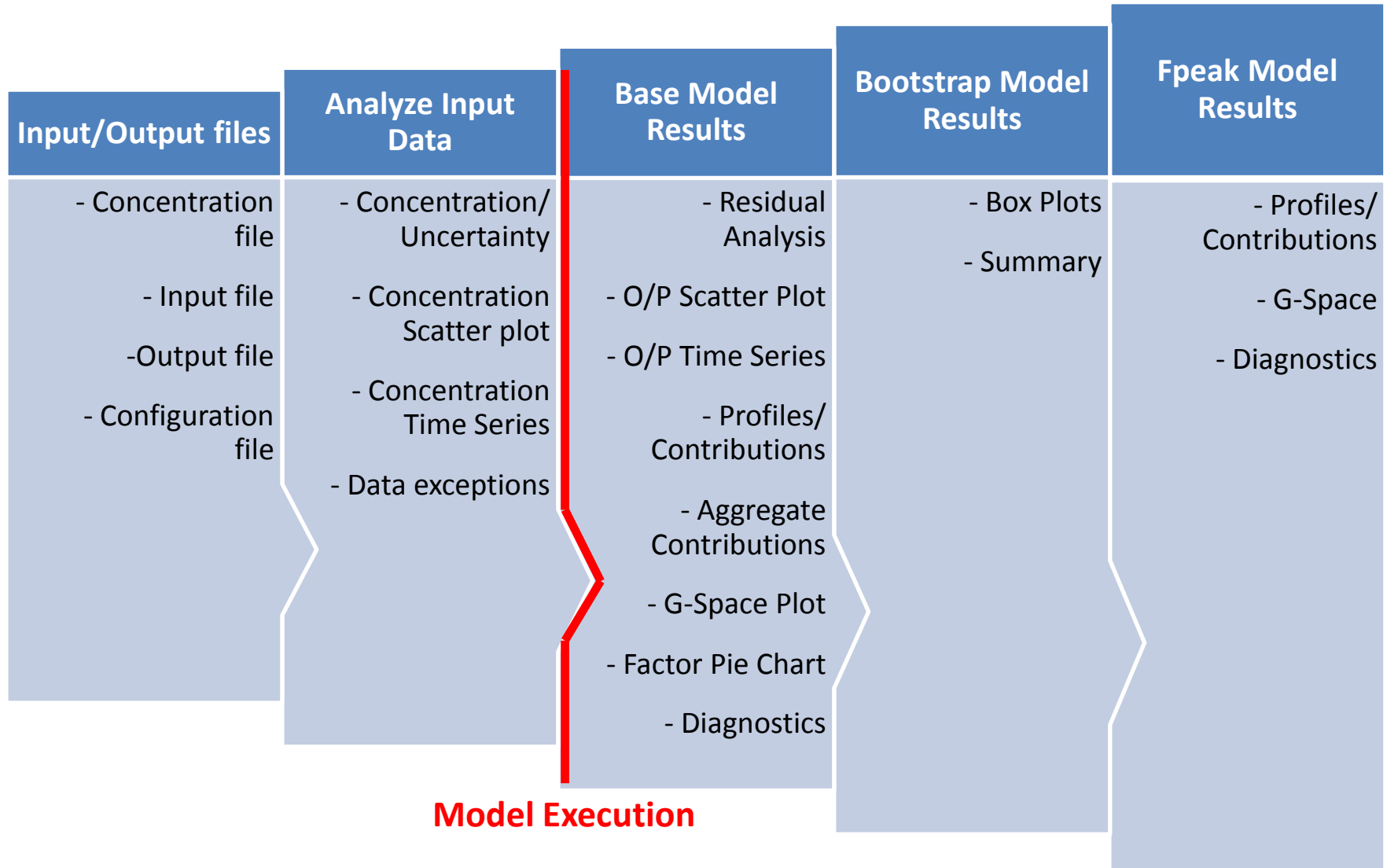
Analyze input data

Concentration Time Series

- Useful to detect unusual events;
- Help to exclude extreme events from the model.



Order of the operations



Model execution

2.

EPA PMF v3.0.2.2

File View Action Help

Input/Output Files Analyze Input Data **Model Execution** Base Model Results Bootstrap Model Results Fpeak Model Results

Base Model Run Summary

Run Number	Q (Robust)	Q (True)	Converged
1	8155.9	9462.5	Yes
2	8154.8	9462.2	Yes
3	8151.5	9472.9	Yes
4	8287.7	9334.5	Yes
5	8137.1	9487.4	No
6	8155.0	9462.1	Yes
7	8151.4	9473.0	Yes
8	8625.4	9668.9	Yes
9	8152.6	9473.4	Yes
10	8471.5	9815.8	No
11	8589.7	9379.7	Yes
12	8138.4	9483.2	Yes
13	8150.4	9461.9	No
14	8154.8	9462.5	Yes
15	8155.8	9462.9	Yes
16	8353.0	9485.3	No
17	8589.5	9379.1	Yes
18	8150.4	9473.0	Yes
19	8155.8	9463.4	Yes
20	8152.5	9473.3	Yes


Fpeak Model Run Summary

Strength	dQ(Robust)	Q (Robust)	Q (True)	Converged
----------	------------	------------	----------	-----------

Base Model Runs


Number of Runs: 20 Seed: 4


Number of Factors: 5

Output File Prefix: CV5sources 

Bootstrap Model Runs

Selected Base Run: 12 Seed: 25

Number of Bootstraps: 100 

Minimum Correlation R-Value: 0.6 Block Size: 7 

Fpeak Model Runs


Selected Fpeak Runs:

☒ Strength of Fpeak 1: -0.2

☒ Strength of Fpeak 2: -0.4

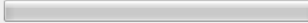

☒ Strength of Fpeak 3: 0.2

☒ Strength of Fpeak 4: 0.4

☒ Strength of Fpeak 5: 0.6 

Selected Base Run: 12

Run Progress

HAVE Concentration Data HAVE Uncertainty Data HAVE Base Results **NEED Bootstrap Results**

1.

Model execution

Base run summary

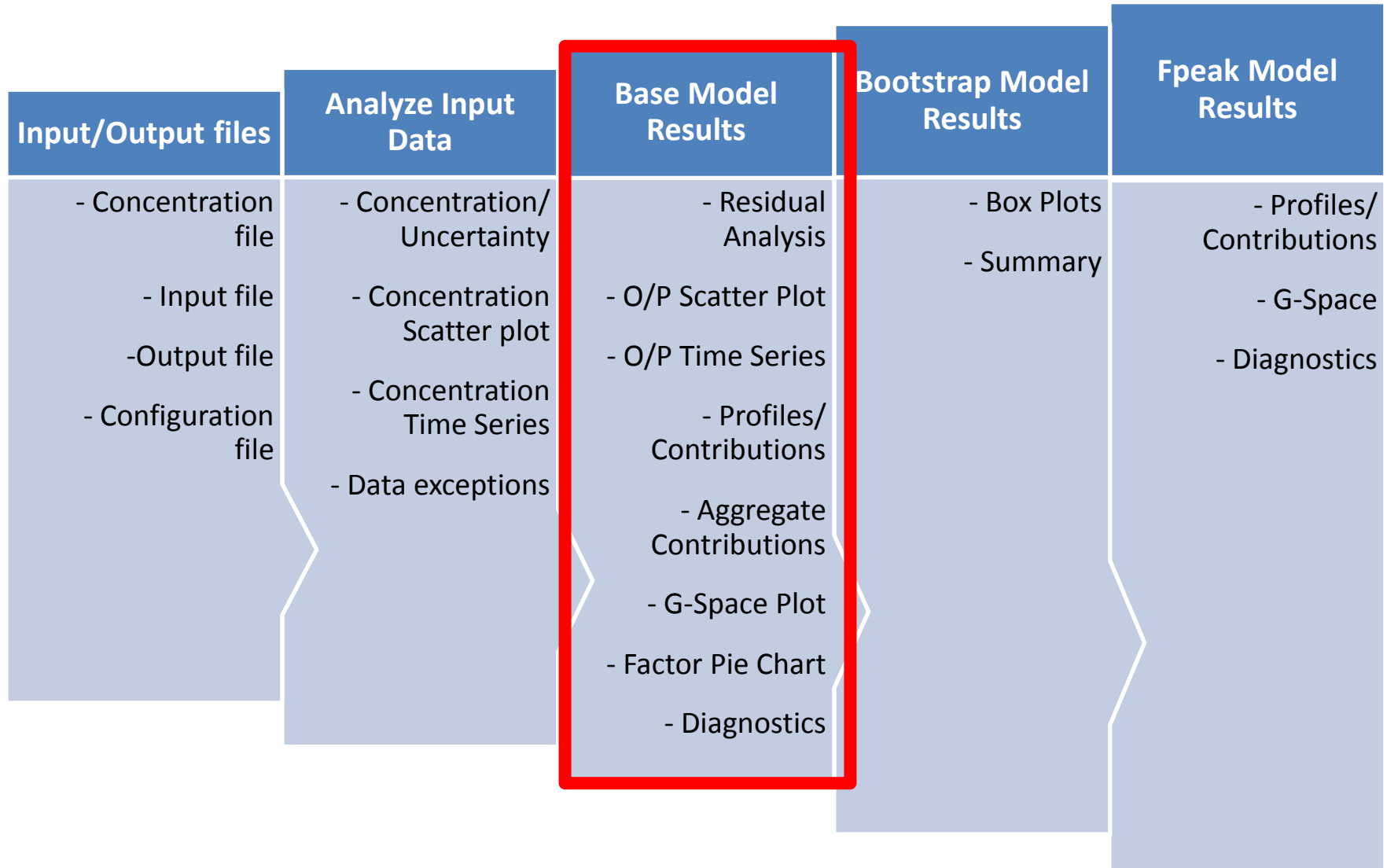
Q values - assessment of how well the model fit the input data

- Q (robust) – calculated excluding outliers
- Q (true) – calculated including all points
- Theoretical $Q \approx nm - p(n+m)$ (n - no. of species; m – no. of samples; p - no. of factors)
- ✓ $Q(\text{true}) > 1.5 Q(\text{robust}) \Rightarrow$ indicate that peak events may be disproportionately influencing the model ;
- ✓ Theoretical $Q \approx Q(\text{true})$ and $Q(\text{robust})$

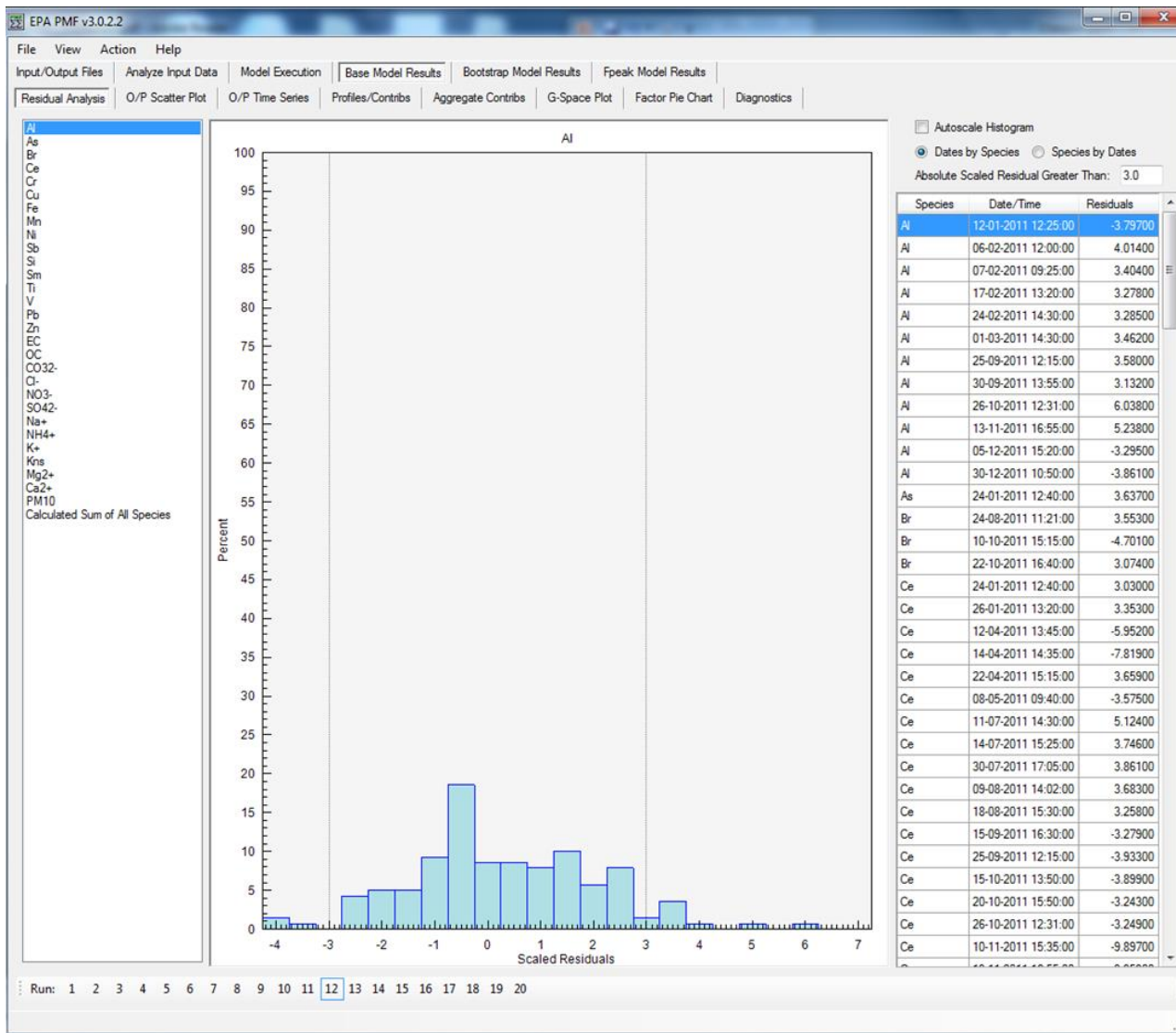
Only converged solutions should be investigated further

(Causes for non-convergence - Uncertainties too low, specified incorrectly or inappropriate input parameters)

Order of the operations



Base model results



Residuals

Objective:

- To determine how well the model fit each species
- Poor fit when:
 - large residuals ($|r| > 3$)
 - Non-normal curve

Base model results

CV5sources_diag.txt

Run #	1	2	3	4	5	6	7	8
81	2	0.00821						
82	3	259.8379	260.1555					
83	4	2849.994	2849.279	2726.793				
84	5	53.03933	53.12823	228.6654	2752.602			
85	6	0.02843	0.0168	260.6482	2849.56	53.27601		
86	7	259.8587	260.1769	0.00243	2726.958	228.6735	260.6648	
87	8	3833.837	3833.224	3823.323	4064.099	3813.02	3833.068	3823.676
88	9	260.4854	260.8184	0.01706	2726.222	229.1004	261.3315	0.01905
89	10	2327.9	2327.974	2565.518	4446.691	2395.004	2327.952	2565.553
90	11	4519.633	4519.98	4419.528	3682.418	4459.516	4520.757	4419.734
91	12	45.32126	45.402	227.842	2757.037	0.30816	45.54358	227.8531
92	13	3.98219	4.01865	241.7509	2817.844	28.00605	4.07842	241.7695
93	14	0.02214	0.01463	260.6825	2848.512	53.26383	0.01509	260.7019
94	15	0.01462	0.02633	260.0799	2848.74	53.02029	0.05808	260.1049
95	16	3639.825	3639.17	3597.748	583.7556	3588.288	3639.783	3597.843
96	17	4521.896	4522.243	4421.643	3685.414	4461.709	4523.026	4421.85
97	18	259.4781	259.7885	0.01021	2728.496	228.4843	260.2604	0.0078
98	19	0.13329	0.12151	258.9462	2846.328	52.77469	0.11694	258.9596
99	20	260.7893	261.1235	0.04384	2724.585	229.1965	261.6548	0.04959

Computer > Local Disk (C:) > PMF workshop

Organize Include in library Share with Burn New folder

★ Favorites

- Desktop
- Downloads
- Recent Places
- Dropbox

Libraries

- Documents

Name	Type
CV5sources_contrib.txt	Text Document
CV5sources_diag.txt	Text Document
CV5sources_profile.txt	Text Document
CV5sources_resid.txt	Text Document
CV5sources_strength.txt	Text Document
DatabaseCVDust.xlsx	Folha de Cálculo ...
EPAPMF.cfg	CFG File

$$d_{jkl} = \sum_i (r_{ijk} - r_{ijl})^2$$

Sum of d across all species for each base run pair (D)

Run #	Run #	Run	#	Al	As	Br	Ce	Cr	Cu	Fe	Mn	Ni	Sb	Si	Sm	Ti	V	Pb	Zn	EC
103	2	1	0.00022	0.00001	0.00006	0.00064	0.00077	0.00004	0.00008	0.0005	0.00005	0.00012	0.00022	0.00011	0.00002	0.00001	0.0001	0.00055	0.00004	
104	3	1	1.56054	0.00688	1.38919	13.6333	45.53774	1.58126	3.30895	0.82247	3.53419	0.05241	1.49753	58.41959	0.95316	0.10767	0.07127	1.78711	94.70732	1.88618
105	3	2	1.56612	0.00691	1.38955	13.65378	45.58625	1.57917	3.3137	0.82352	3.52274	0.05184	1.50383	58.51976	0.95605	0.10712	0.07098	1.78854	94.77009	1.88608
106	4	1	137.2596	0.38293	14.58692	434.1233	120.2832	8.35829	20.29624	16.48825	49.3341	1.0591	100.9746	480.7712	28.93016	3.0131	0.3546	20.98657	158.1019	17.88321
107	4	2	137.1478	0.38237	14.56936	433.9725	120.2951	8.35292	20.29538	16.50423	49.40058	1.05596	100.921	480.7954	28.94103	3.01589	0.35466	20.99235	158.0467	17.87637
108	4	3	132.6391	0.41546	13.16562	358.2067	75.82526	10.88516	15.20979	16.43151	45.36695	1.01639	98.19128	425.5995	28.38158	3.24943	0.35516	18.01001	317.5494	20.93921
109	5	1	0.4552	0.00033	0.15311	1.03112	3.42159	0.04953	0.29177	0.13685	0.63709	0.00998	0.24916	42.33177	0.21478	0.01197	0.00735	0.16106	0.23423	0.01395
110	5	2	0.45581	0.00035	0.15249	1.03306	3.44015	0.04893	0.29181	0.13718	0.63622	0.01008	0.25085	42.3696	0.21519	0.012	0.00728	0.16068	0.23198	0.01388
111	5	3	0.85709	0.00546	0.66641	7.60717	24.23784	1.57411	1.83762	0.40588	1.26928	0.03536	1.05975	79.3885	0.65222	0.08779	0.03765	0.94792	91.83623	1.70671
112	5	4	135.1217	0.38511	13.8325	408.9375	97.79378	7.69669	17.74662	16.46028	47.78758	1.01129	100.1253	495.216	28.8441	2.89664	0.32657	19.61574	156.4335	17.76484
113	6	1	0.0008	0.00003	0.00026	0.00177	0.00143	0.00011	0.00033	0.00032	0.00083	0.00006	0.00033	0.00091	0.00048	0.00003	0.00003	0.00043	0.00091	0.00016

$$D_{kl} = \sum_j D_{jkl}$$

Base model results

EPA PMF v3.0.0.5

FileViewActionHelp

Input/Output FilesAnalyze Input DataModel ExecutionBase Model ResultsFpeak Model ResultsBootstrap Model Results

Residual AnalysisO/P Scatter PlotO/P Time SeriesProfiles/ContribsAggregate ContribsG-Space PlotFactor Pie ChartDiagnostics

Base run summary table:

Run #	Q(Robust)	Q(True)	Converged	# Steps
1	25620.3	30712.3	Yes	1431
2	25619.9	30709.2	Yes	1327
3	26467.3	32448.2	Yes	821
4	25620.3	30710.3	Yes	2195
5	25620.1	30709.3	Yes	1860

Scaled residual analysis:

Sum of the sum of the squares of the scaled residuals for all species

Run #	1	2	3	4
2	3.37280			
3	15982.80917	15951.67926		
4	1.05658	0.76646	15965.96734	
5	2.60058	0.06986	15955.59931	0.39663

Sum of the squares of the scaled residuals for each species

Run #	Run #	Mass	Ammonium Ion	Arsenic	Barium	Bromine	Calcium	Chromium	Copper
2	1	0.00001	1.69390	0.00731	0.00517	0.00509	0.02168	0.00617	0.02436
3	1	0.01463	2612.85460	62.70325	93.91410	38.93613	466.78244	101.19067	515.0581
3	2	0.01460	2610.69087	62.90646	93.96395	38.85630	465.79330	101.11192	517.0898
4	1	0.00001	0.55809	0.00254	0.00760	0.00193	0.00952	0.00205	0.00874
4	2	0.00000	0.31271	0.00153	0.00304	0.00122	0.00593	0.00147	0.00669
4	3	0.01460	2609.60936	62.76013	93.86382	38.90212	466.60525	101.14724	515.9578
5	1	0.00001	1.33802	0.00580	0.00749	0.00394	0.01480	0.00478	0.01379
5	2	0.00000	0.02195	0.00022	0.00113	0.00021	0.00196	0.00021	0.00088
5	3	0.01460	2610.85831	62.84247	93.91661	38.86575	465.93276	101.13653	516.7463
5	4	0.00000	0.17097	0.00084	0.00082	0.00065	0.00265	0.00080	0.00337

*** Factor Analysis of Base Run #1 ***

Regression diagnostics:

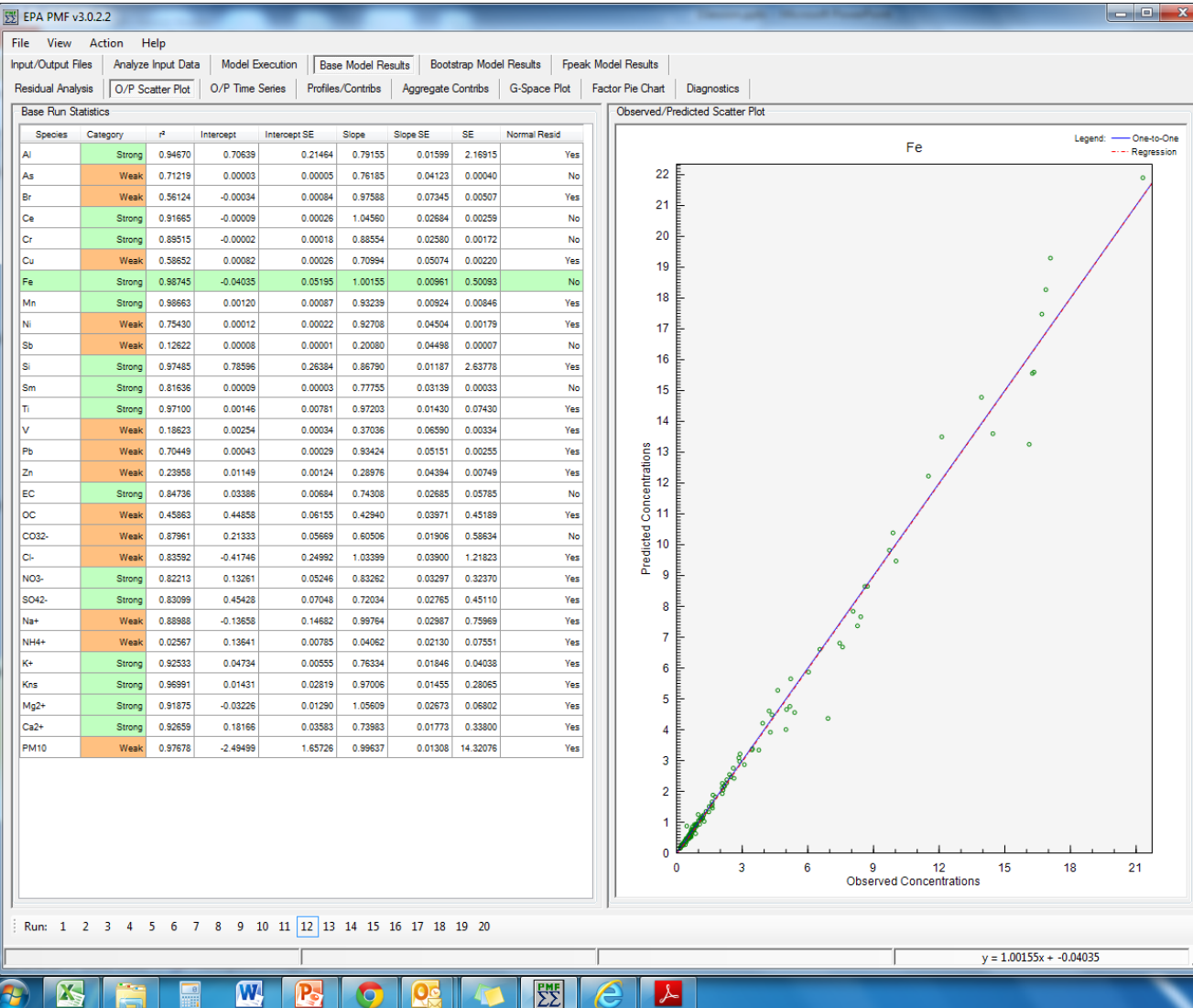
Species	Intercept	Slope	SE	r ²	KS Test Stat	KS Test P Value
Mass	2.74	0.84	4.01	0.82	0.20	0.00
Ammonium Ion	0.03	0.98	0.19	0.99	0.04	0.21
Arsenic	0.00	0.18	0.00	0.09	0.22	0.00
Barium	0.01	0.02	0.01	0.01	0.19	0.00

Base model results

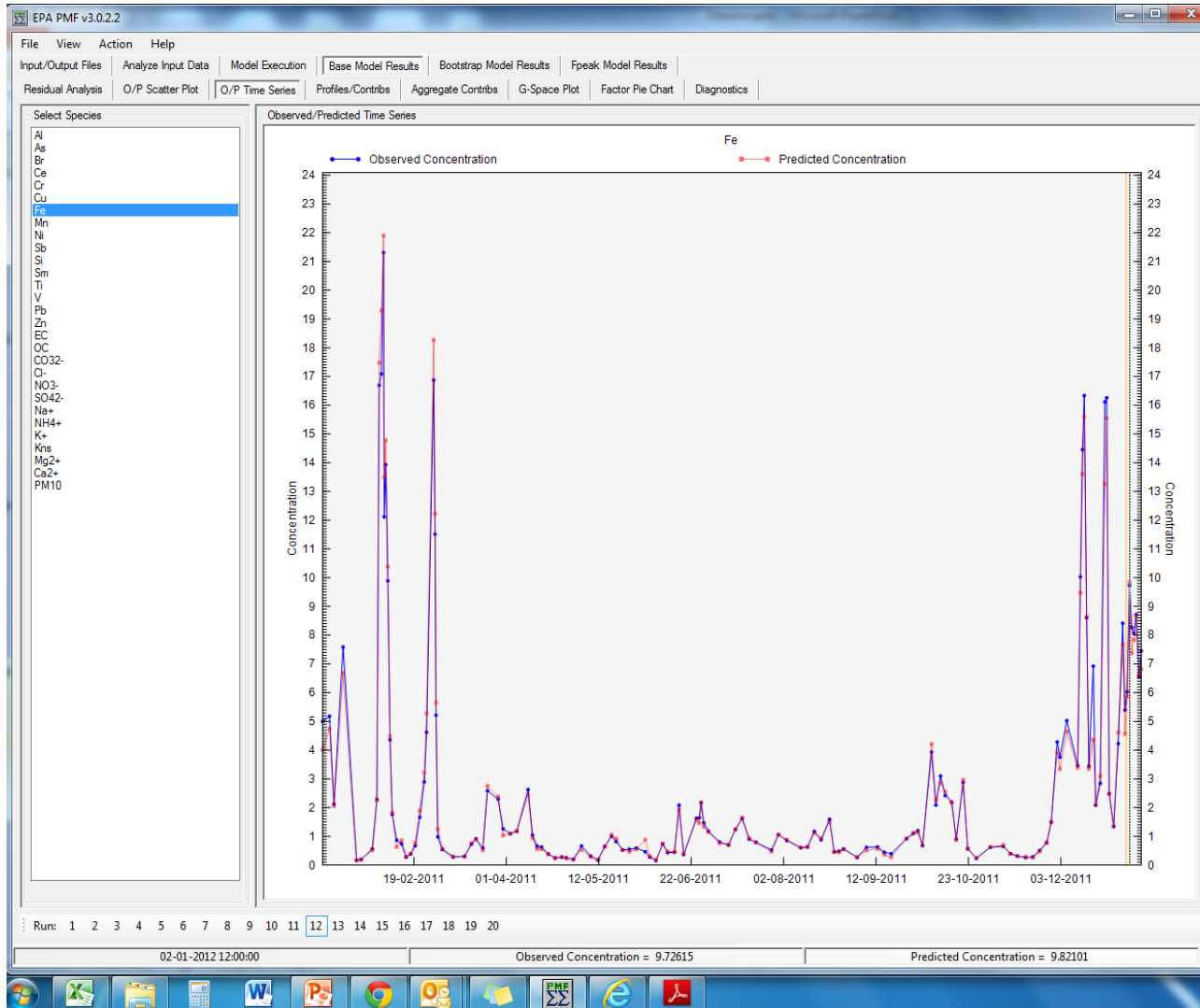
Observed/Predicted scatter plot

Objective:

- To determine how well the model fit each species
- Evaluate if a species should be down weighted or excluded from the model



Base model results

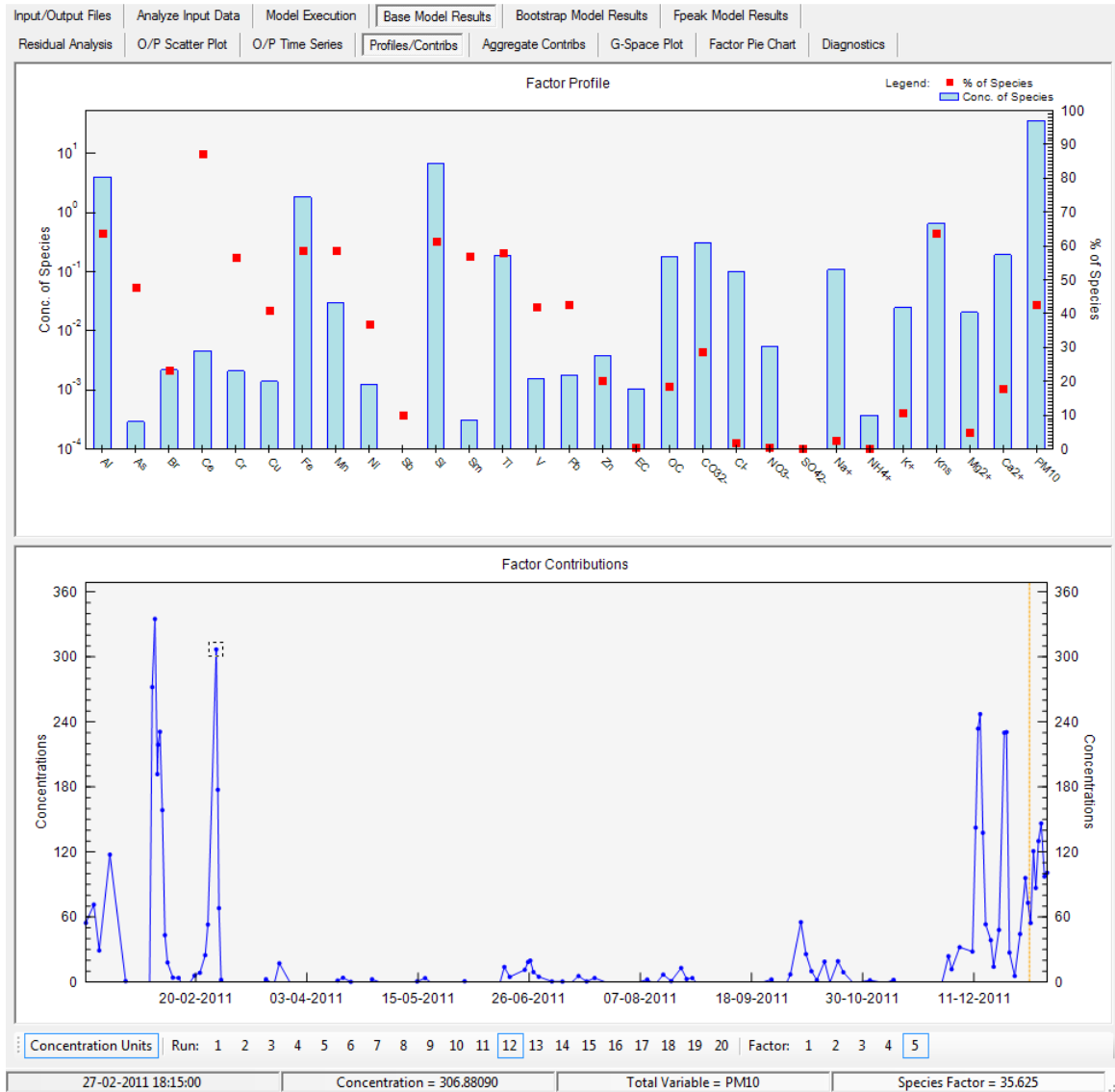


Observed/Predicted time series

Objective:

- To determine how well the model fit each species
- Evaluate if a species should be down weighted or excluded from the model

Base model results



Profiles/Contribs

Objective:

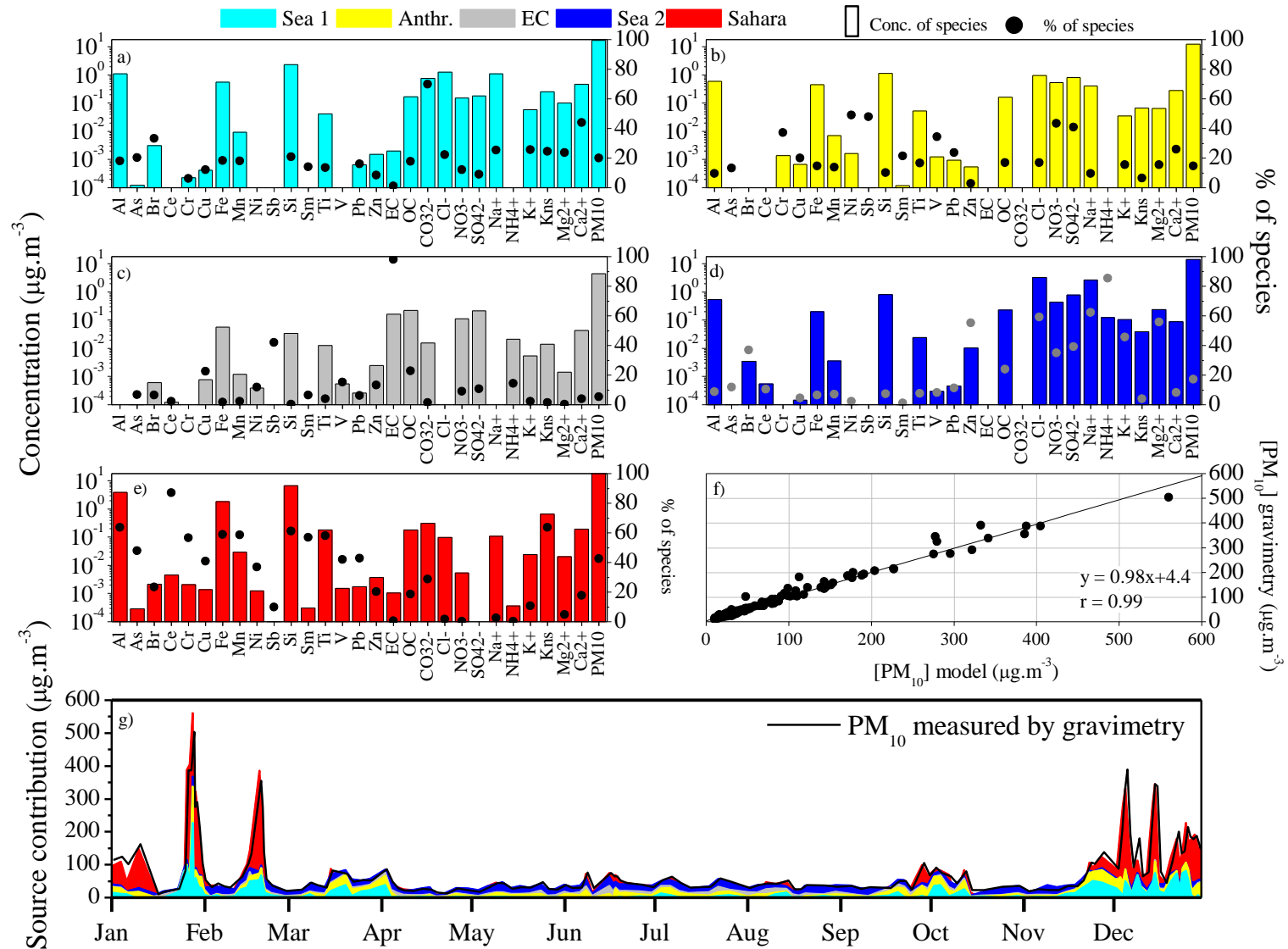
- Display the factors resolved by PMF;
- Two graphs are displayed:
 - Profile graph
 - Mass of each species apportioned to the factor
 - Percent of each species apportioned to the factor
 - Contribution of the factor to the total mass by sample

Name	Type
CV5sources_contrib.txt	Text Document
CV5sources_diag.txt	Text Document
CV5sources_profile.txt	Text Document
CV5sources_resid.txt	Text Document
CV5sources_strength.txt	Text Document
DatabaseCVDust.xlsx	Folha de Cálculo ...
EPAPMF.cfg	CFG File

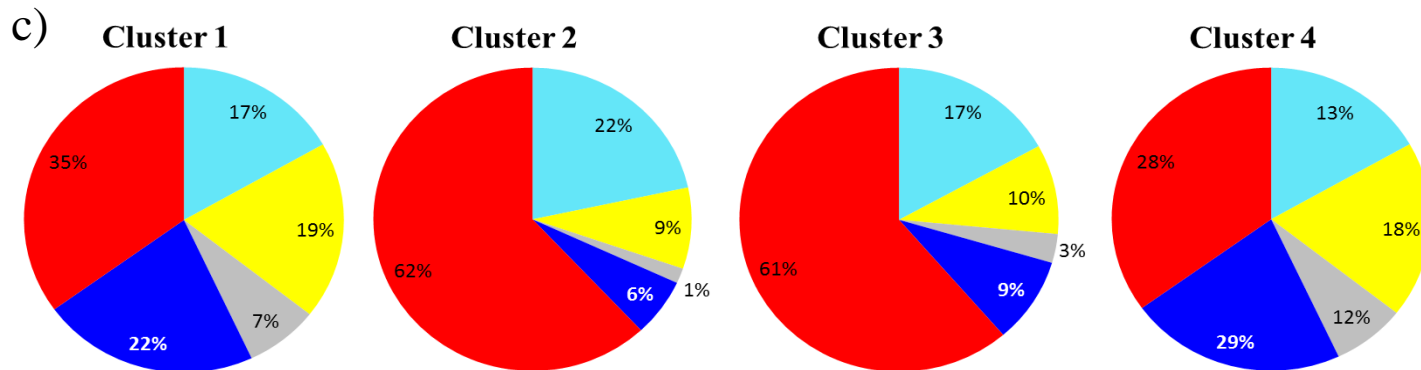
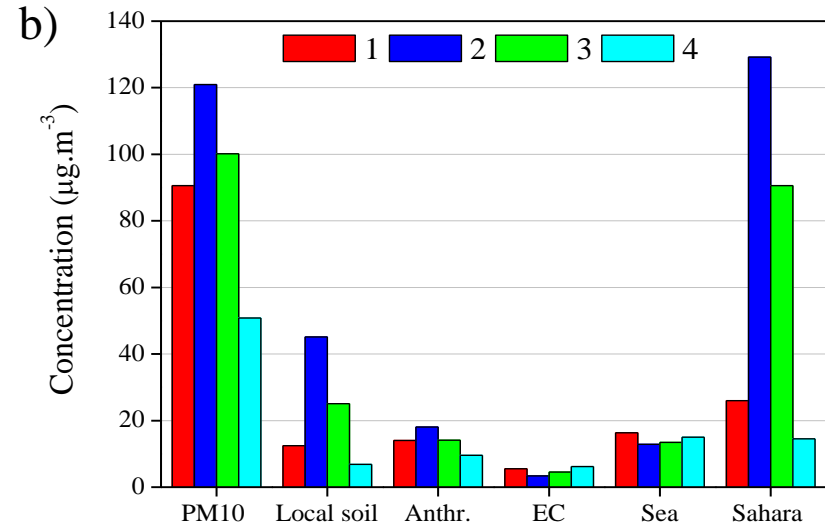
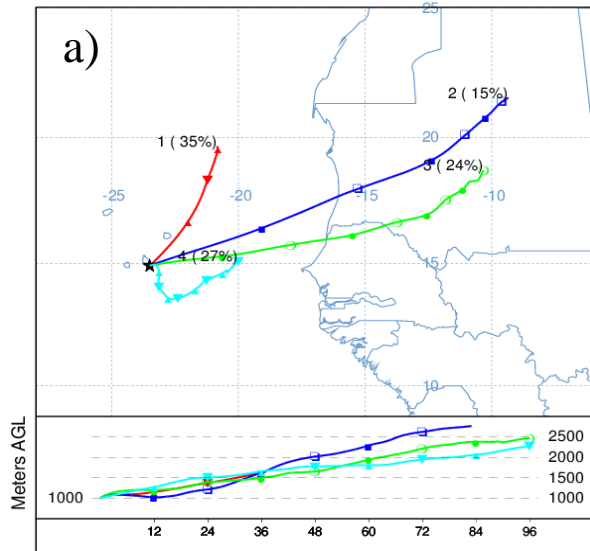
Identifications of sources

	Species	Source
F1	Br, CO_3^{2-} , Ca^{2+}	Local soil
F2	Cr, Ni, Sb, V, NO_3^- , SO_4^{2-}	Anthropogenic source
F3	Sb, EC	Anthropogenic source
F4	Br, Zn, Cl^- , NO_3^- , SO_4^{2-} , Na^+ , NH_4^+ , K^+ , Mg^{2+}	Sea
F5	Al, As, Ce, Cr, Cu, Fe, Mn, Mi, Si, Sm, Ti, V, Pb, Kns	Sahara dust

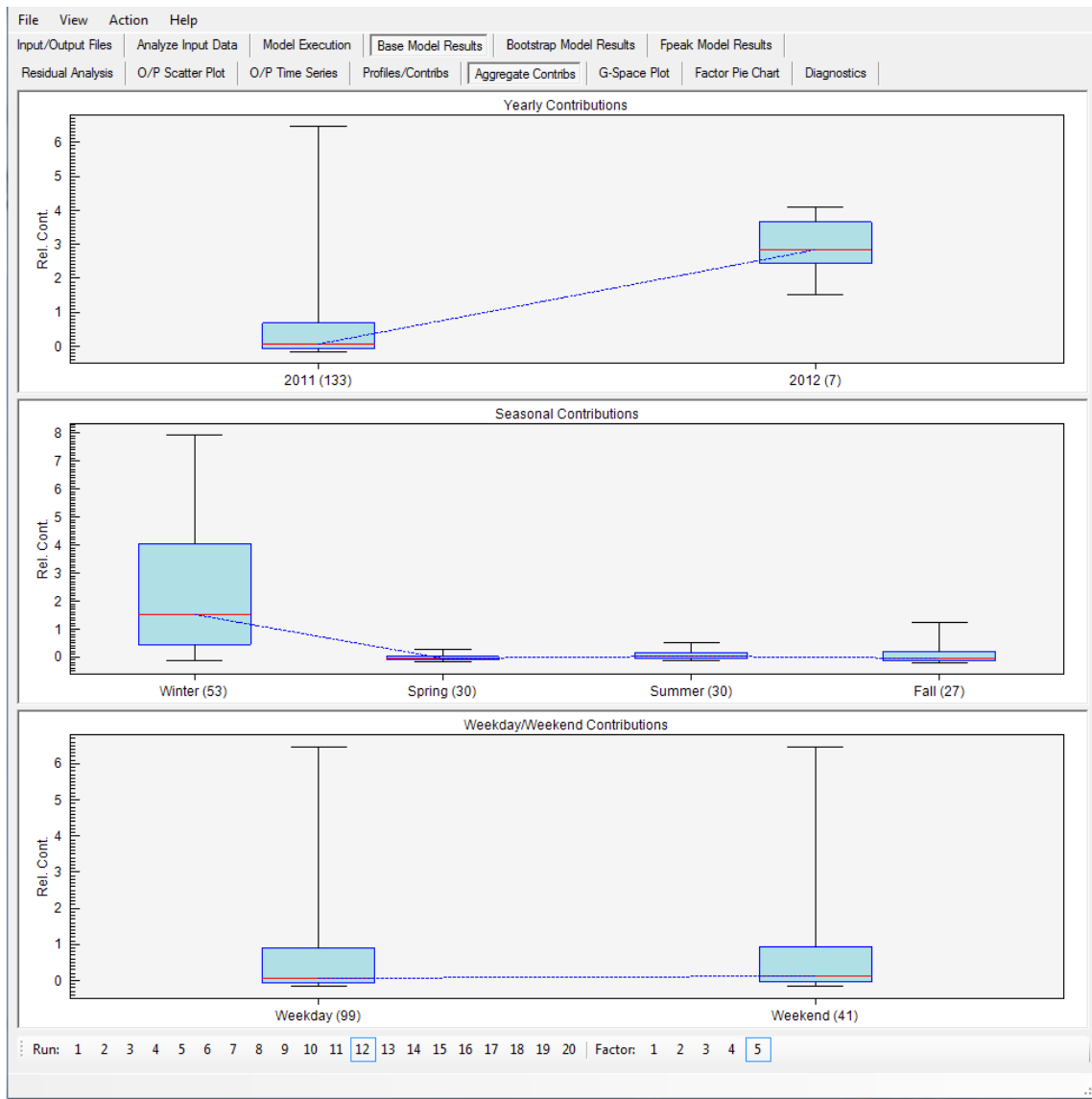
Base model results



Base model results



Base model results

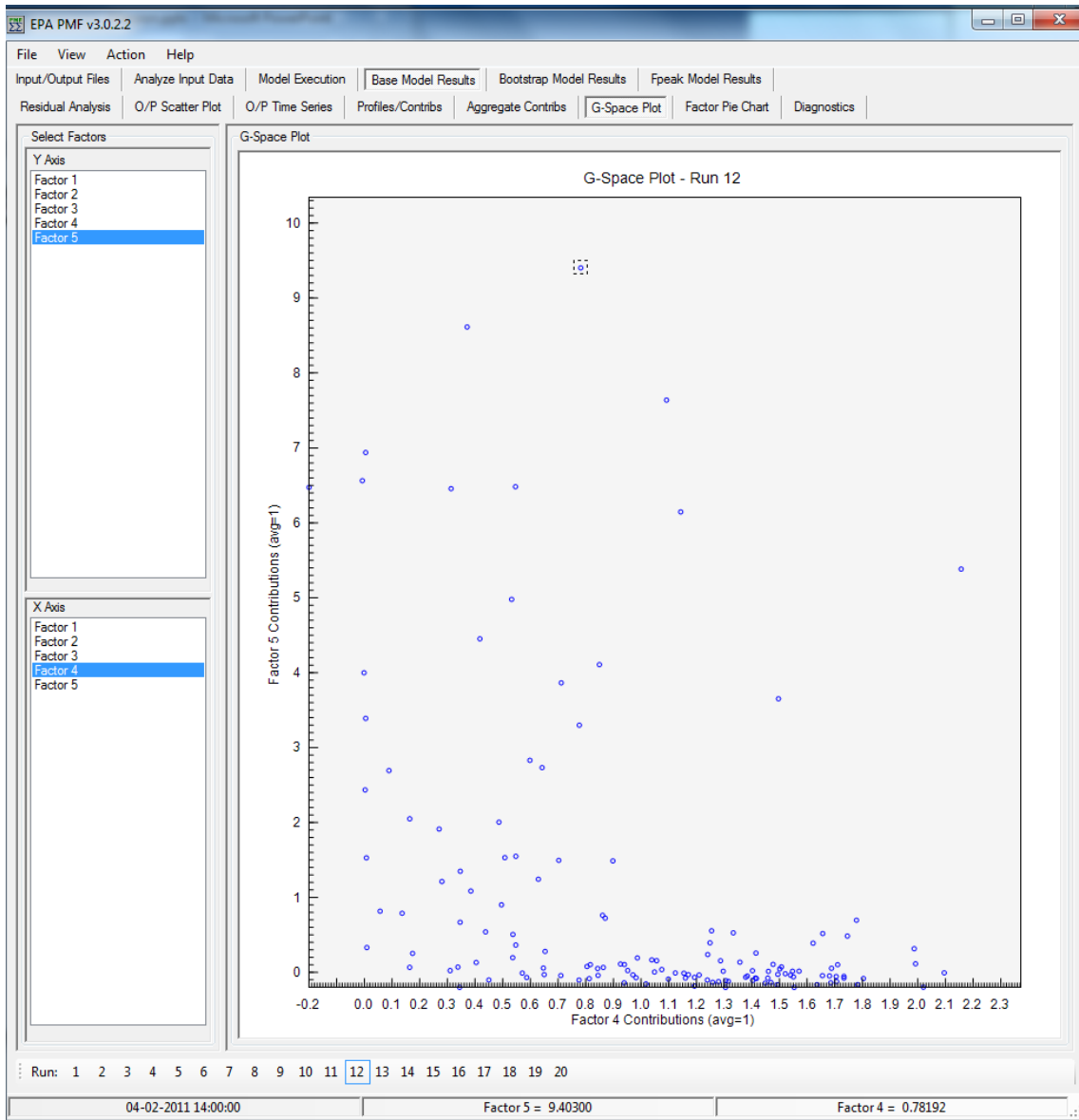


Aggregate Contribs

Objective:

- Display the factors contribution discriminated:
 - by year;
 - season;
 - weekday/weekend

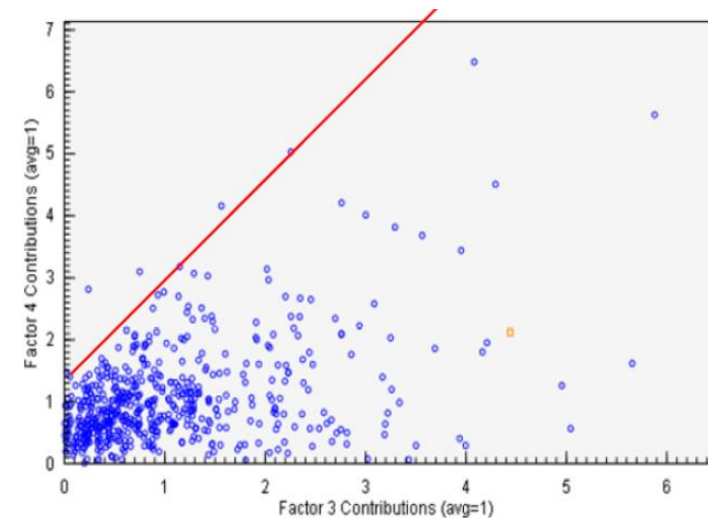
Base model results



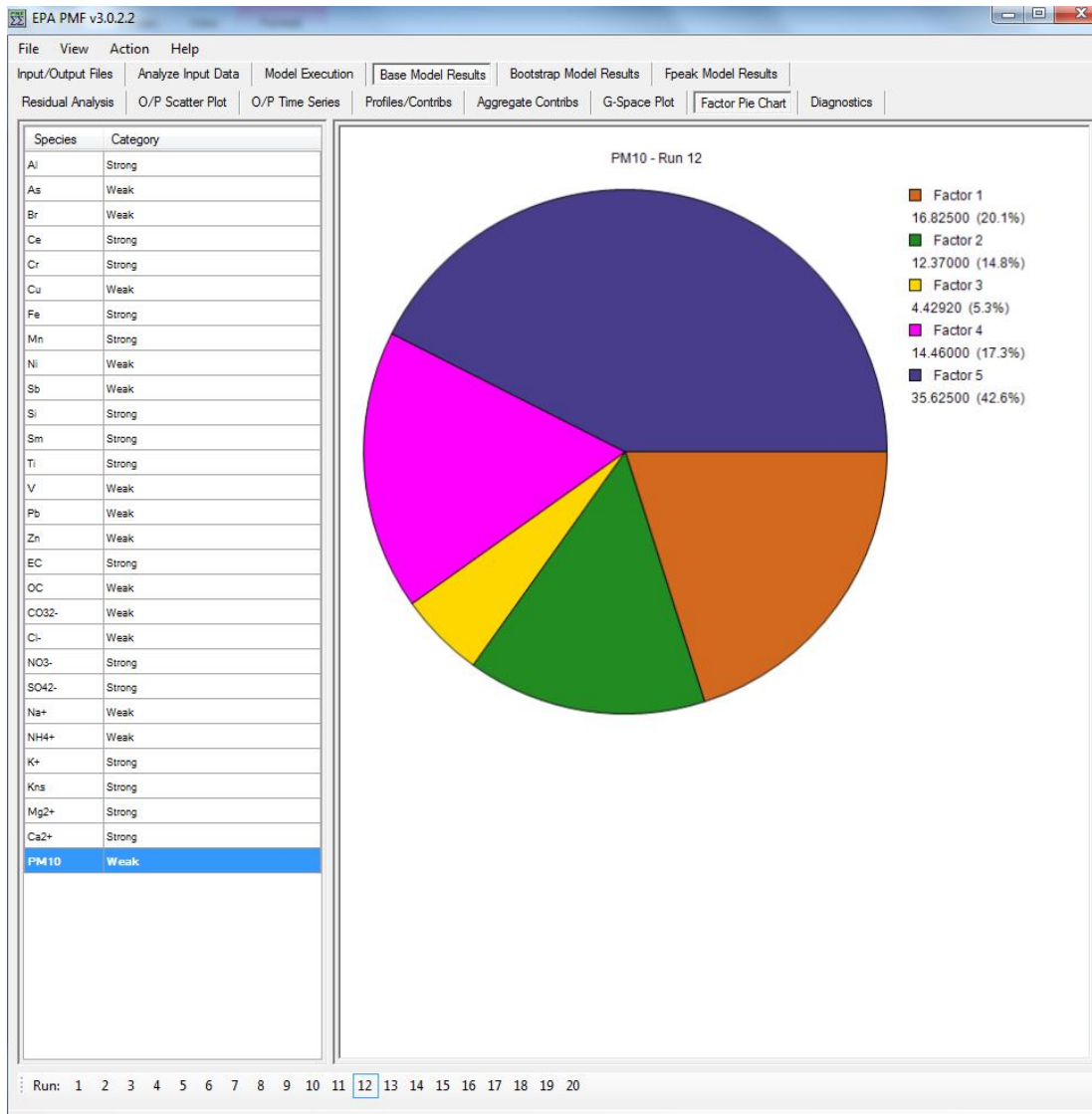
G-Space plot

Objective:

- Display 1 factor contribution versus the other;
- Determine if the solution
 - 1- has filled the solution space – edge of the scatter plot will correspond to the axis
 - 2 - has some rotational ambiguity – appears as an oblique edge on a space plot



Base model results

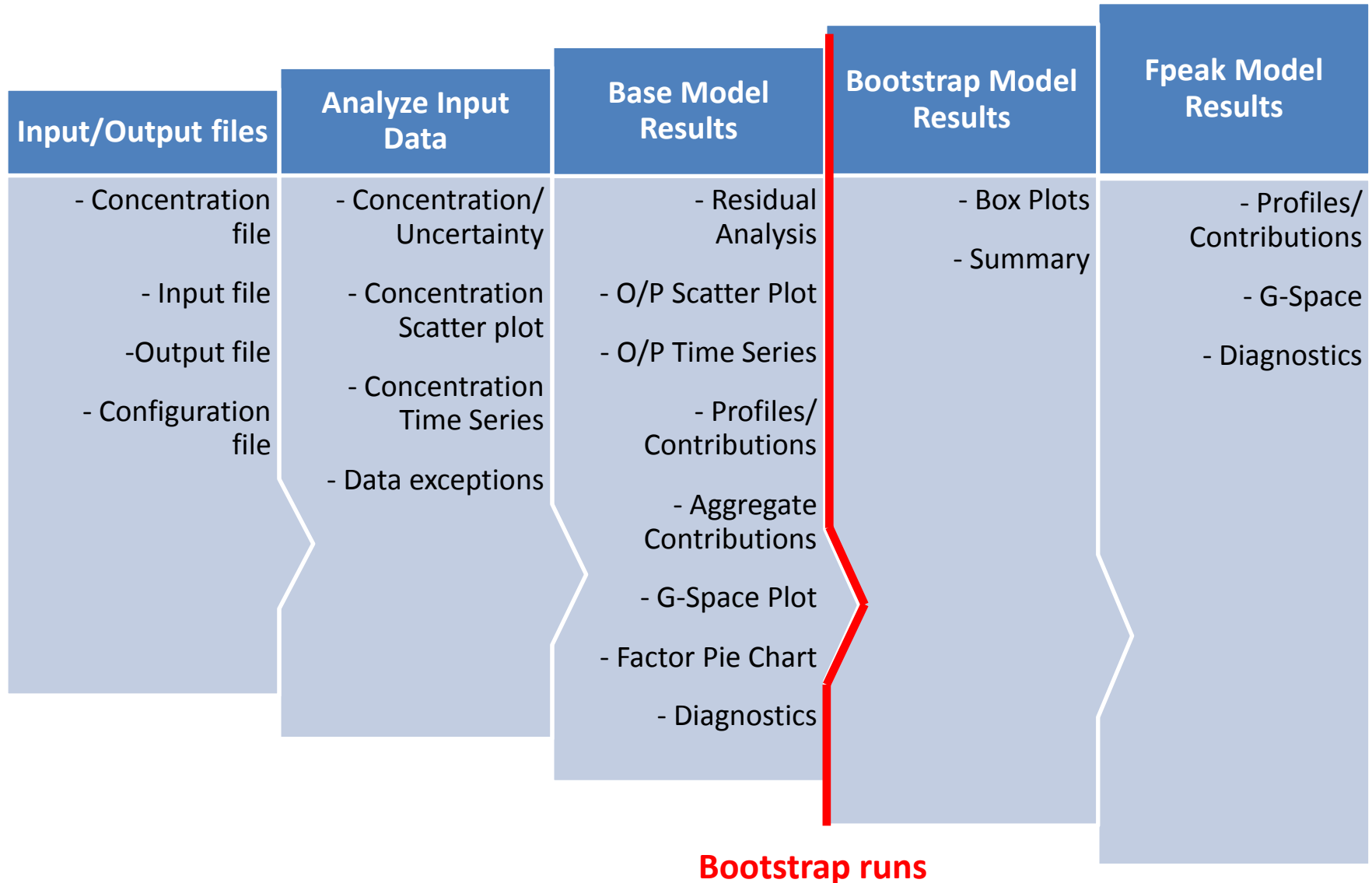


Factor Pie Chart

Objective:

- Display the distribution of each species among the factors resolved by PMF

Order of the operations



Bootstrap runs

Objective: Estimate the stability and uncertainty of the solution

How?

- 1 – Randomly selects non-overlapping blocks of samples and creates a new input data file of the selected samples;
- 2 - PMF is run on the new data set and each bootstrap factor is mapped to a base run factor with which the bootstrap factor has the highest correlation, above a user-specific threshold;
- 3 – If no base factors have a correlation above the threshold for a given bootstrap factor, the factor is considered unmapped;

Bootstrap runs

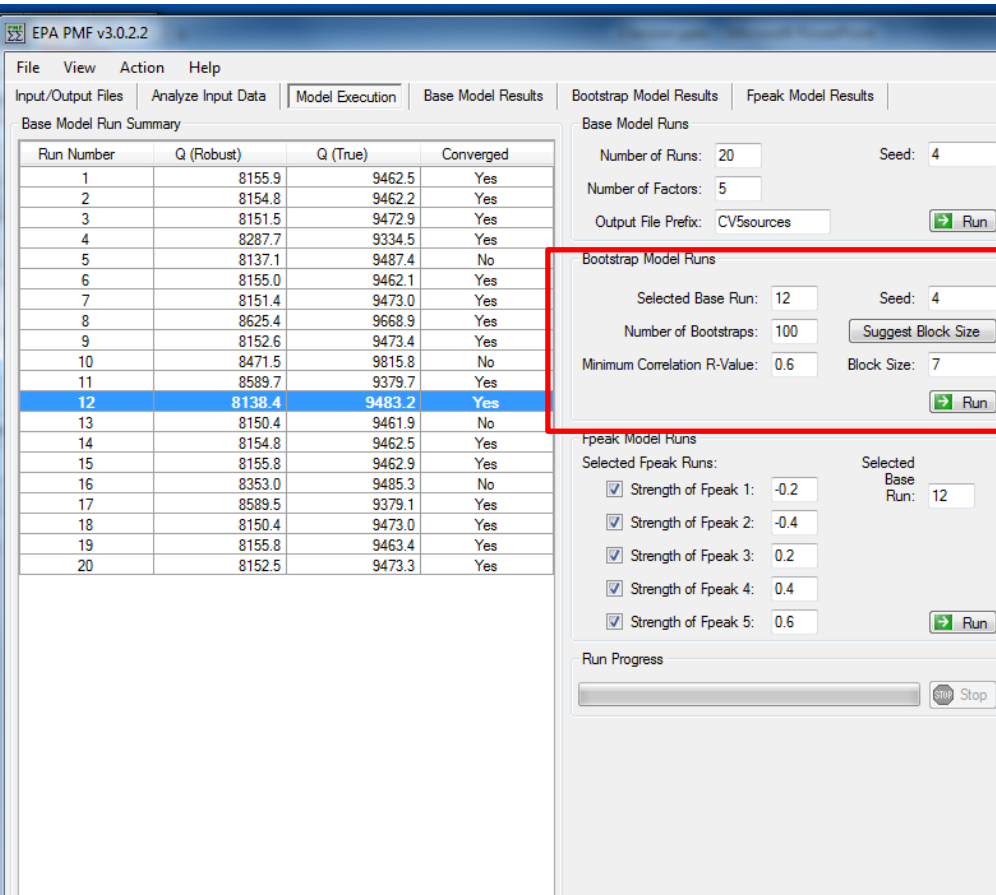
Selected base run – the base run to be used to map each bootstrap run

Number of bootstraps – It is recommended at least 100 bootstrap runs to ensure the robustness of the statistics

Minimum Correlation R-Values – the minimum Pearson correlation coefficient that will be used in the assignment of a bootstrap run factor to a base run factor. Default value 0.6 (can decrease if a large number of factors are unmapped)

Seed – similar to base runs, starting point for iterations

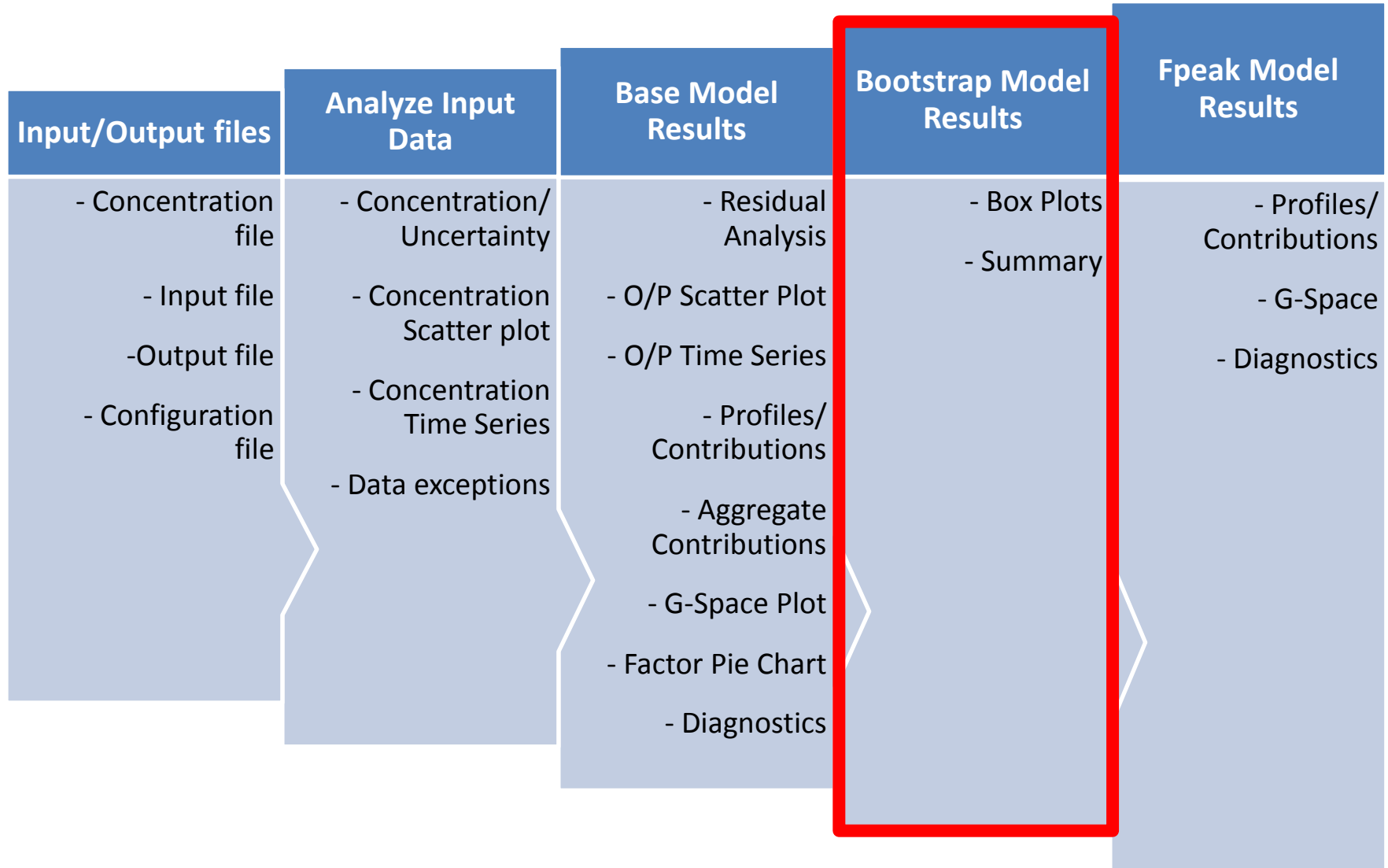
Block size – the number of samples that will be selected in each step for resampling



The screenshot shows the EPA PMF v3.0.2.2 software interface. On the left, the 'Base Model Run Summary' table lists 20 runs. Run 12 is highlighted in blue, indicating it is the selected base run. On the right, the 'Bootstrap Model Runs' configuration panel is shown, which is highlighted with a red box. This panel includes settings for the number of bootstraps (100), the selected base run (12), the minimum correlation R-value (0.6), and the block size (7). The 'Run' button is visible at the bottom of the panel.

Run Number	Q (Robust)	Q (True)	Converged
1	8155.9	9462.5	Yes
2	8154.8	9462.2	Yes
3	8151.5	9472.9	Yes
4	8287.7	9334.5	Yes
5	8137.1	9487.4	No
6	8155.0	9462.1	Yes
7	8151.4	9473.0	Yes
8	8625.4	9668.9	Yes
9	8152.6	9473.4	Yes
10	8471.5	9815.8	No
11	8589.7	9379.7	Yes
12	8138.4	9483.2	Yes
13	8150.4	9461.9	No
14	8154.8	9462.5	Yes
15	8155.8	9462.9	Yes
16	8353.0	9485.3	No
17	8589.5	9379.1	Yes
18	8150.4	9473.0	Yes
19	8155.8	9463.4	Yes
20	8152.5	9473.3	Yes

Order of the operations



Bootstrap Model Results

EPA PMF v3.0.2.2

File View Action Help

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Box Plots Summary

Base model run number: 12
Number of bootstrap runs: 100
Bootstrap random seed: 4
Min. Correlation R-Value: 0.6
Number of factors: 5
Extra modeling uncertainty (%): 5

Mapping of bootstrap factors to base factors:						
	Base Factor 1	Base Factor 2	Base Factor 3	Base Factor 4	Base Factor 5	Unmapped
Boot Factor 1	68	3	1	0	19	9
Boot Factor 2	1	74	1	2	8	14
Boot Factor 3	0	2	98	0	0	0
Boot Factor 4	1	0	1	87	0	11
Boot Factor 5	0	0	0	0	100	0

Q(Robust) Percentile Report:

Min	25th	Median	75th	Max
5907	7236	7571	7951	8596

Variability in factor strengths based on bootstrapping:

Factor	Mean	5th	25th	Median	75th	95th
1	1.1117E+000	5.7463E-001	7.8261E-001	1.0000E+000	1.3257E+000	2.1277E+000
2	1.0659E+000	6.3419E-001	8.5119E-001	1.0000E+000	1.1734E+000	1.8602E+000
3	8.8245E-001	4.0350E-001	6.2090E-001	8.2684E-001	1.0599E+000	1.6719E+000
4	1.1183E+000	8.6227E-001	1.0000E+000	1.0820E+000	1.2304E+000	1.5025E+000
5	1.2804E+000	6.9957E-001	9.4554E-001	1.1886E+000	1.3955E+000	2.0887E+000

Bootstrap run uncertainty statistics:

Factor 1	Base Run	Within	Bootstrap Runs:		5th	25th	Median	75th
	Species Profile	IQR	Mean	Std. Dev.				
	Al 1.1210E+000	Yes	1.1502E+000	3.6885E-001	4.2587E-001	9.5460E-001	1.1411E+000	1.397:
	As 1.2307E-004	Yes	1.2296E-004	2.4260E-005	7.5845E-005	1.0779E-004	1.2200E-004	1.393:
	Br 3.0919E-003	Yes	2.5537E-003	1.0271E-003	7.1530E-004	2.0063E-003	2.5502E-003	3.183:
	Ce 0.0000E+000	Yes	6.6996E-004	1.1220E-003	0.0000E+000	0.0000E+000	2.6660E-005	1.089:
	Cr 2.2490E-004	Yes	3.5007E-004	2.9129E-004	0.0000E+000	1.4106E-004	3.1875E-004	4.773:
	Cu 4.1299E-004	Yes	3.7726E-004	1.7736E-004	0.0000E+000	2.8868E-004	3.8194E-004	4.679:
	Fe 5.6680E-001	Yes	5.7423E-001	1.2714E-001	3.3051E-001	5.0512E-001	5.7938E-001	6.604:

How many bootstrap factors we matched to each base factor

How many bootstrap factors were matched to each base factor

Bootstrap Model Results

EPA PMF v3.0.2.2

FileViewActionHelp

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Box Plots

Summary

Base model run number:12

Number of bootstrap runs:100

Bootstrap random seed:4

Min. Correlation R-Value:0.6

Number of factors:5

Extra modeling uncertainty (%): 5

Mapping of bootstrap factors to base factors:

	Base Factor 1	Base Factor 2	Base Factor 3	Base Factor 4	Base Factor 5	Unmapped
Boot Factor 1	68	3	1	0	19	9
Boot Factor 2	1	74	1	2	8	14
Boot Factor 3	0	2	98	0	0	0
Boot Factor 4	1	0	1	87	0	11
Boot Factor 5	0	0	0	0	100	0

Q(Robust) Percentile Report:

Min	25th	Median	75th	Max
5907	7236	7571	7951	8596

Variability in factor strengths based on bootstrapping:

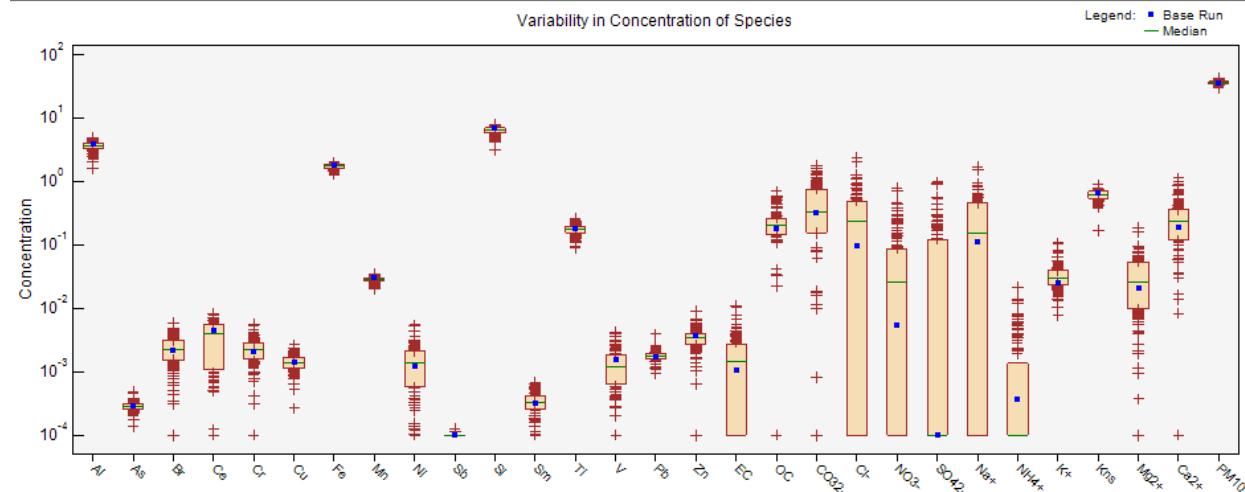
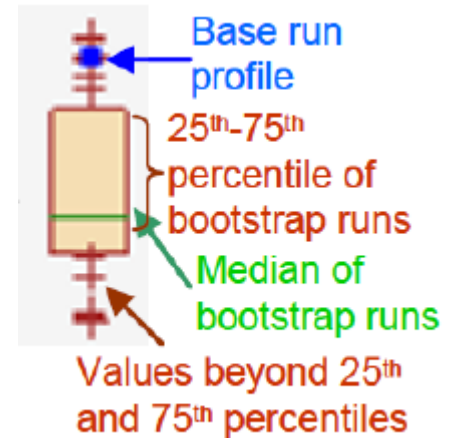
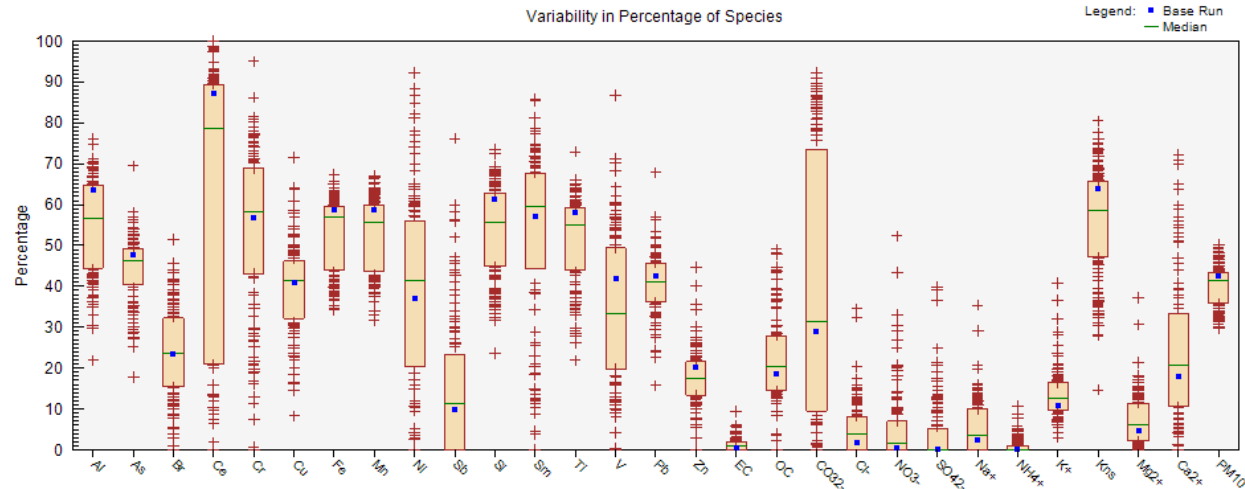
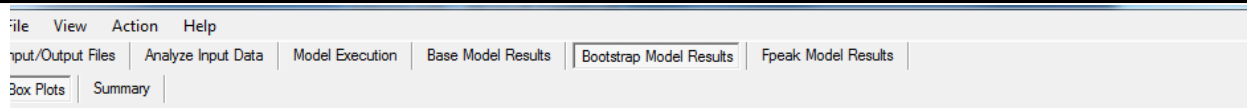
Factor	Mean	5th	25th	Median	75th	95th
1	1.1117E+000	5.7463E-001	7.8261E-001	1.0000E+000	1.3257E+000	2.1277E+000
2	1.0659E+000	6.3419E-001	8.5119E-001	1.0000E+000	1.1734E+000	1.8602E+000
3	8.8245E-001	4.0350E-001	6.2090E-001	8.2684E-001	1.0599E+000	1.6719E+000
4	1.1183E+000	8.6227E-001	1.0000E+000	1.0820E+000	1.2304E+000	1.5025E+000
5	1.2804E+000	6.9957E-001	9.4554E-001	1.1886E+000	1.3955E+000	2.0887E+000

Bootstrap run uncertainty statistics:

Factor 1	Base Run	Within	Bootstrap Runs:						
Species	Profile	IQR	Mean	Std. Dev.	5th	25th	Median	75th	
Al	1.1210E+000	Yes	1.1502E+000	3.6885E-001	4.2587E-001	9.5460E-001	1.1411E+000	1.397:	
As	1.2307E-004	Yes	1.2296E-004	2.4260E-005	7.5845E-005	1.0779E-004	1.2200E-004	1.393:	
Br	3.0919E-003	Yes	2.5537E-003	1.0271E-003	7.1530E-004	2.0063E-003	2.5502E-003	3.183:	
Ce	0.0000E+000	Yes	6.6996E-004	1.1220E-003	0.0000E+000	0.0000E+000	2.6660E-005	1.089:	
Cr	2.2490E-004	Yes	3.5007E-004	2.9129E-004	0.0000E+000	1.4106E-004	3.1875E-004	4.773:	
Cu	4.1299E-004	Yes	3.7726E-004	1.7736E-004	0.0000E+000	2.8868E-004	3.8194E-004	4.679:	
Fe	5.6680E-001	Yes	5.7423E-001	1.2714E-001	3.3051E-001	5.0512E-001	5.7938E-001	6.604:	

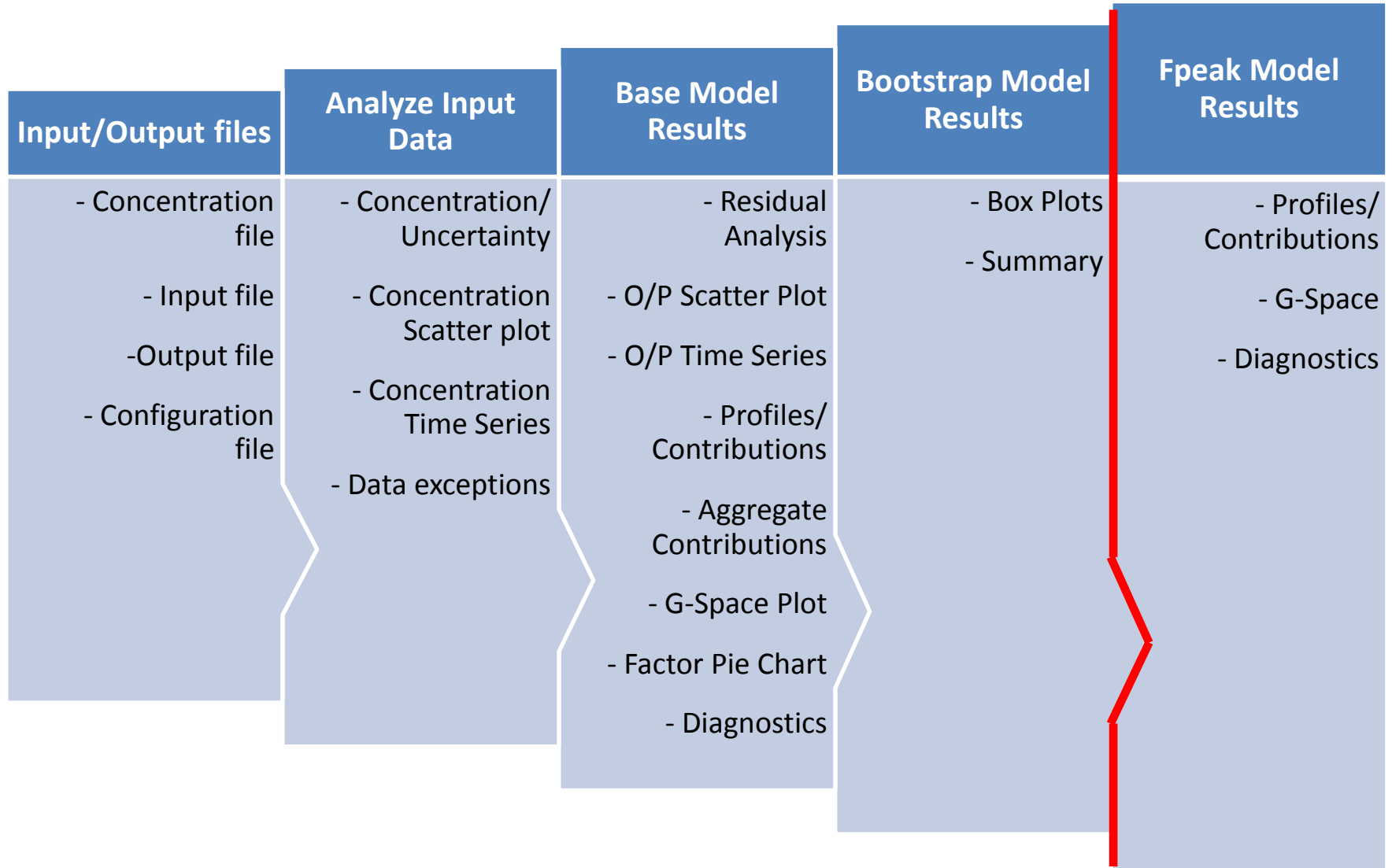
How many bootstrap factors were matched to each base factor

Bootstrap Model Results



	A	B	C	D	E	F	G	H	I	J	K
430	Bootstrap run uncertainty statistics										
431											
432	Variability in concentration of species:										
433											
434	Factor 1										
435		Base Run	Within	Bootstrap Runs:							Uncertainty
436	Species	Profile	IQR	Mean	Std. Dev.	5th	25th	Median	75th	95th	(75th-25th)/2
437	Al	1.12E+00	Yes	1.15E+00	3.69E-01	4.26E-01	9.55E-01	1.14E+00	1.40E+00	1.78E+00	2.21E-01
438	As	1.23E-04	Yes	1.23E-04	2.43E-05	7.58E-05	1.08E-04	1.22E-04	1.39E-04	1.60E-04	1.58E-05
439	Br	3.09E-03	Yes	2.55E-03	1.03E-03	7.15E-04	2.01E-03	2.55E-03	3.18E-03	4.14E-03	5.89E-04
440	Ce	0.00E+00	Yes	6.70E-04	1.12E-03	0.00E+00	0.00E+00	2.67E-05	1.09E-03	3.32E-03	5.45E-04
441	Cr	2.25E-04	Yes	3.50E-04	2.91E-04	0.00E+00	1.41E-04	3.19E-04	4.77E-04	1.01E-03	1.68E-04
442	Cu	4.13E-04	Yes	3.77E-04	1.77E-04	0.00E+00	2.89E-04	3.82E-04	4.68E-04	7.22E-04	8.96E-05
443	Fe	5.67E-01	Yes	5.74E-01	1.27E-01	3.31E-01	5.05E-01	5.79E-01	6.60E-01	7.67E-01	7.77E-02
444	Mn	9.22E-03	Yes	9.46E-03	2.26E-03	5.03E-03	8.06E-03	9.71E-03	1.08E-02	1.34E-02	1.36E-03
445	Ni	0.00E+00	Yes	8.07E-05	2.19E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.62E-04	0.00E+00
446	Sb	0.00E+00	Yes	8.63E-06	1.52E-05	0.00E+00	0.00E+00	0.00E+00	1.26E-05	4.54E-05	6.31E-06
447	Si	2.31E+00	Yes	2.29E+00	6.26E-01	8.78E-01	2.01E+00	2.27E+00	2.72E+00	3.38E+00	3.56E-01
448	Sm	7.67E-05	Yes	9.22E-05	4.70E-05	1.43E-05	7.25E-05	9.00E-05	1.11E-04	1.98E-04	1.90E-05
449	Ti	4.25E-02	Yes	4.67E-02	1.35E-02	2.36E-02	3.78E-02	4.75E-02	5.34E-02	7.44E-02	7.78E-03
450	V	0.00E+00	Yes	2.63E-04	3.64E-04	0.00E+00	0.00E+00	6.59E-05	4.89E-04	1.16E-03	2.45E-04
451	Pb	6.59E-04	Yes	6.76E-04	1.79E-04	3.11E-04	5.87E-04	6.81E-04	7.82E-04	9.71E-04	9.72E-05
452	Zn	1.55E-03	Yes	1.96E-03	1.56E-03	0.00E+00	1.12E-03	1.80E-03	2.42E-03	4.08E-03	6.51E-04
453	EC	2.01E-03	No	1.40E-03	2.68E-03	0.00E+00	0.00E+00	4.46E-04	1.65E-03	6.74E-03	8.26E-04
454	OC	1.72E-01	Yes	1.70E-01	6.42E-02	6.05E-02	1.32E-01	1.69E-01	2.02E-01	2.83E-01	3.51E-02
455	CO32-	7.58E-01	Yes	5.76E-01	2.57E-01	1.13E-01	4.40E-01	6.06E-01	7.63E-01	9.84E-01	1.62E-01
456	Cl-	1.25E+00	Yes	1.26E+00	6.14E-01	3.20E-01	8.65E-01	1.24E+00	1.53E+00	2.44E+00	3.32E-01
457	NO3-	1.54E-01	Yes	1.97E-01	1.45E-01	0.00E+00	7.29E-02	1.86E-01	2.87E-01	5.08E-01	1.07E-01
458	SO42-	1.83E-01	Yes	3.38E-01	2.27E-01	0.00E+00	1.81E-01	3.16E-01	4.59E-01	8.31E-01	1.39E-01
459	Na+	1.09E+00	Yes	1.00E+00	4.85E-01	2.85E-01	7.06E-01	1.01E+00	1.22E+00	1.93E+00	2.59E-01
460	NH4+	0.00E+00	Yes	8.92E-04	2.83E-03	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.00E-03	0.00E+00
461	K+	5.85E-02	Yes	5.72E-02	2.02E-02	2.04E-02	4.63E-02	5.82E-02	6.75E-02	8.74E-02	1.06E-02
462	Kns	2.52E-01	Yes	2.34E-01	7.30E-02	6.78E-02	2.00E-01	2.35E-01	2.86E-01	3.42E-01	4.27E-02
463	Mg2+	1.00E-01	Yes	9.78E-02	4.20E-02	3.42E-02	7.13E-02	9.54E-02	1.18E-01	1.72E-01	2.31E-02
464	Ca2+	4.77E-01	Yes	4.25E-01	1.42E-01	1.39E-01	3.50E-01	4.37E-01	5.24E-01	6.36E-01	8.72E-02
465	PM10	1.68E+01	Yes	1.69E+01	6.40E-01	1.60E+01	1.66E+01	1.69E+01	1.73E+01	1.83E+01	3.47E-01
466											
467	Factor 2										

Order of the operations

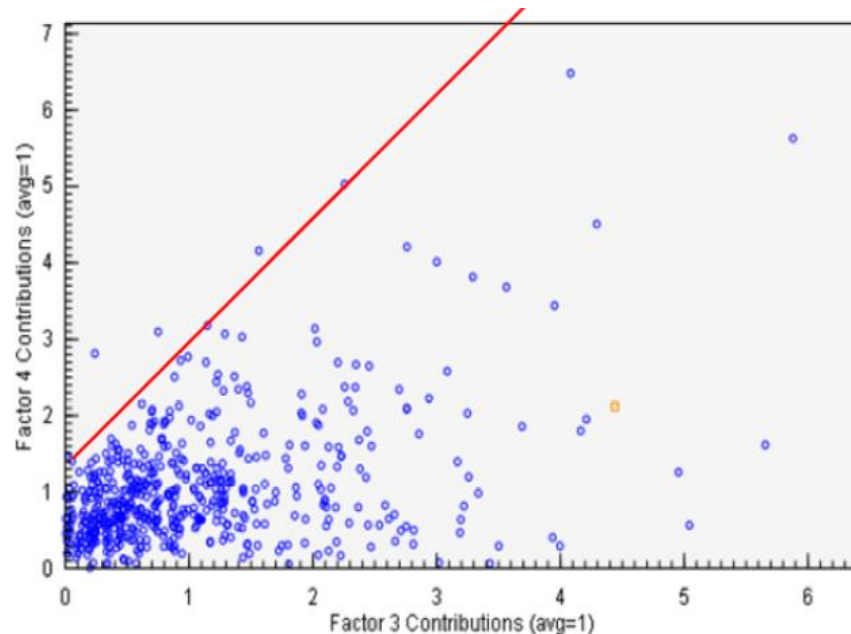


Fpeak runs

Fpeak runs

Rotation ambiguity

- The user should inspect the G-space plots for each pair of factors in the original solution to determine if an incorrect rotation has occurred .
- In this case the solution must to be rotated to the real solution using **Fpeak**



Fpeak runs

FileViewActionHelp

Input/Output Files

Analyze Input Data

Model Execution

Base Model Results

Base Model Run Summary

Run Number	Q (Robust)	Q (True)	Converged
1	8155.9	9462.5	Yes
2	8154.8	9462.2	Yes
3	8151.5	9472.9	Yes
4	8287.7	9334.5	Yes
5	8137.1	9487.4	No
6	8155.0	9462.1	Yes
7	8151.4	9473.0	Yes
8	8625.4	9668.9	Yes
9	8152.6	9473.4	Yes
10	8471.5	9815.8	No
11	8589.7	9379.7	Yes
12	8138.4	9483.2	Yes
13	8150.4	9461.9	No
14	8154.8	9462.5	Yes
15	8155.8	9462.9	Yes
16	8353.0	9485.3	No
17	8589.5	9379.1	Yes
18	8150.4	9473.0	Yes
19	8155.8	9463.4	Yes
20	8152.5	9473.3	Yes

Bootstrap Model Results

Fpeak Model Results

Base Model Runs

Number of Runs: 20

Seed: 4

Number of Factors: 5

Output File Prefix: CV5sources

Run

Bootstrap Model Runs

Selected Base Run: 12

Seed: 4

Number of Bootstraps: 100

Suggest Block Size

Minimum Correlation R-Value: 0.6

Block Size: 7

Run

Fpeak Model Runs

Selected Fpeak Runs:

Strength of Fpeak 1: -0.2

Strength of Fpeak 2: -0.4

Strength of Fpeak 3: 0.2

Strength of Fpeak 4: 0.4

Strength of Fpeak 5: 0.6

Selected Base Run: 12

Run

Run Progress

Stop

Fpeak Model Run Summary

Strength	dQ(Robust)	Q (Robust)	Q (True)	Converged
-0.2	28.7	8167.1	9464.8	Yes
-0.4	67.2	8205.6	9468.0	Yes
0.2	23.7	8162.2	9462.0	Yes
0.4	60.1	8198.5	9469.2	Yes
0.6	129.1	8267.5	9469.0	Yes

HAVE Concentration Data

HAVE Uncertainty Data

HAVE Base Results

HAVE Bootstrap Results

Values should be between -5 and 5
(Fpeak \neq 0)

Fpeak runs

FileViewActionHelp

Input/Output Files

Analyze Input Data

Model Execution

Base Model Results

Base Model Run Summary

Run Number	Q (Robust)	Q (True)	Converged
1	8155.9	9462.5	Yes
2	8154.8	9462.2	Yes
3	8151.5	9472.9	Yes
4	8287.7	9334.5	Yes
5	8137.1	9487.4	No
6	8155.0	9462.1	Yes
7	8151.4	9473.0	Yes
8	8625.4	9668.9	Yes
9	8152.6	9473.4	Yes
10	8471.5	9815.8	No
11	8589.7	9379.7	Yes
12	8138.4	9483.2	Yes
13	8150.4	9461.9	No
14	8154.8	9462.5	Yes
15	8155.8	9462.9	Yes
16	8353.0	9485.3	No
17	8589.5	9379.1	Yes
18	8150.4	9473.0	Yes
19	8155.8	9463.4	Yes
20	8152.5	9473.3	Yes

Bootstrap Model Results

Fpeak Model Results

Base Model Runs

Number of Runs: 20

Seed: 4

Number of Factors: 5

Output File Prefix: CV5sources

Run

Bootstrap Model Runs

Selected Base Run: 12

Seed: 4

Number of Bootstraps: 100

Suggest Block Size

Minimum Correlation R-Value: 0.6

Block Size: 7

Run

Fpeak Model Runs

Selected Fpeak Runs:

Strength of Fpeak 1: -0.2

Strength of Fpeak 2: -0.4

Strength of Fpeak 3: 0.2

Strength of Fpeak 4: 0.4

Strength of Fpeak 5: 0.6

Selected Base Run: 12

Run

Run Progress

Stop

Fpeak Model Run Summary

Strength	dQ(Robust)	Q (Robust)	Q (True)	Converged
-0.2	28.7	8167.1	9464.8	Yes
-0.4	67.2	8205.6	9468.0	Yes
0.2	23.7	8162.2	9462.0	Yes
0.4	60.1	8198.5	9469.2	Yes
0.6	129.1	8267.5	9469.0	Yes

HAVE Concentration Data

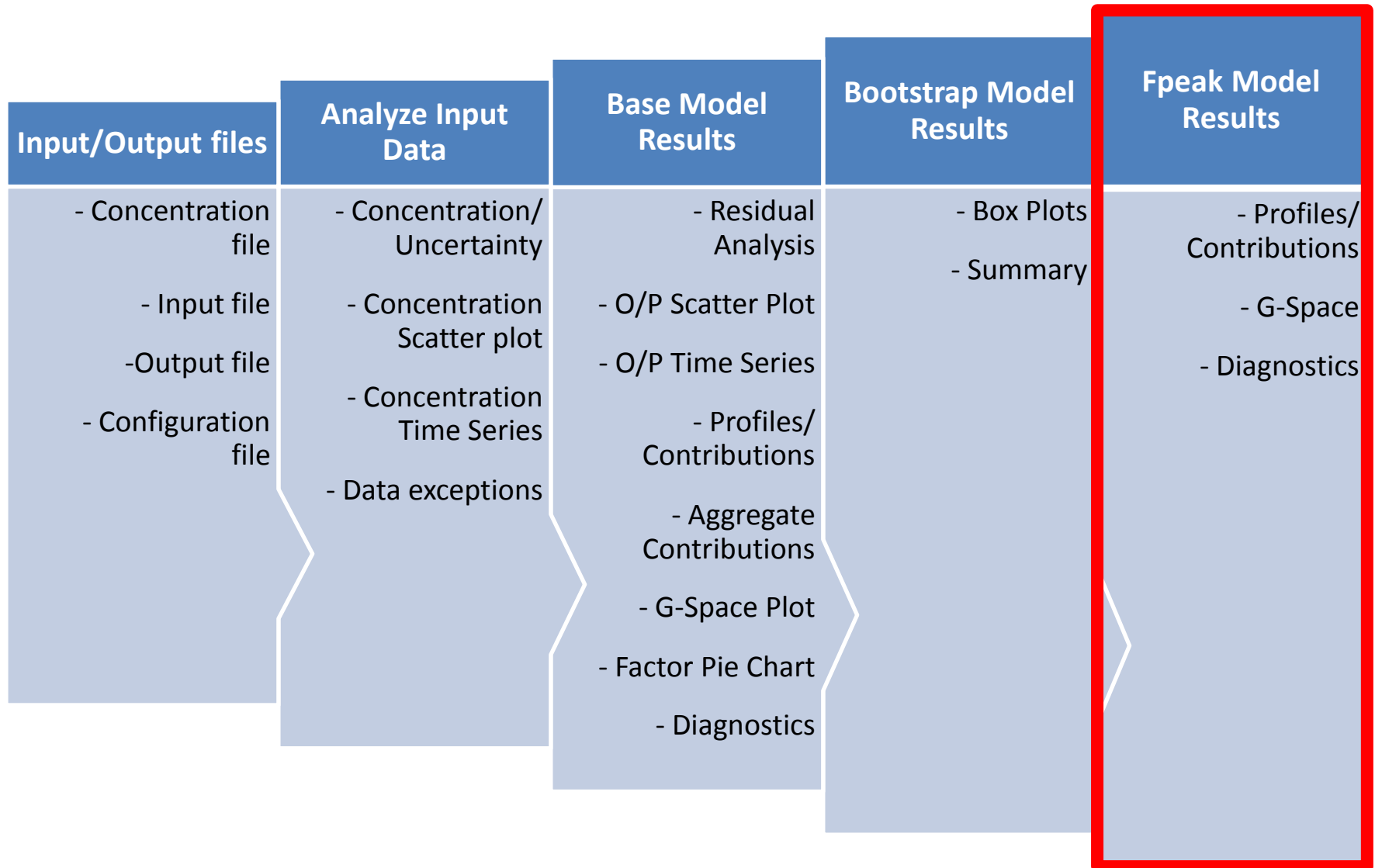
HAVE Uncertainty Data

HAVE Base Results

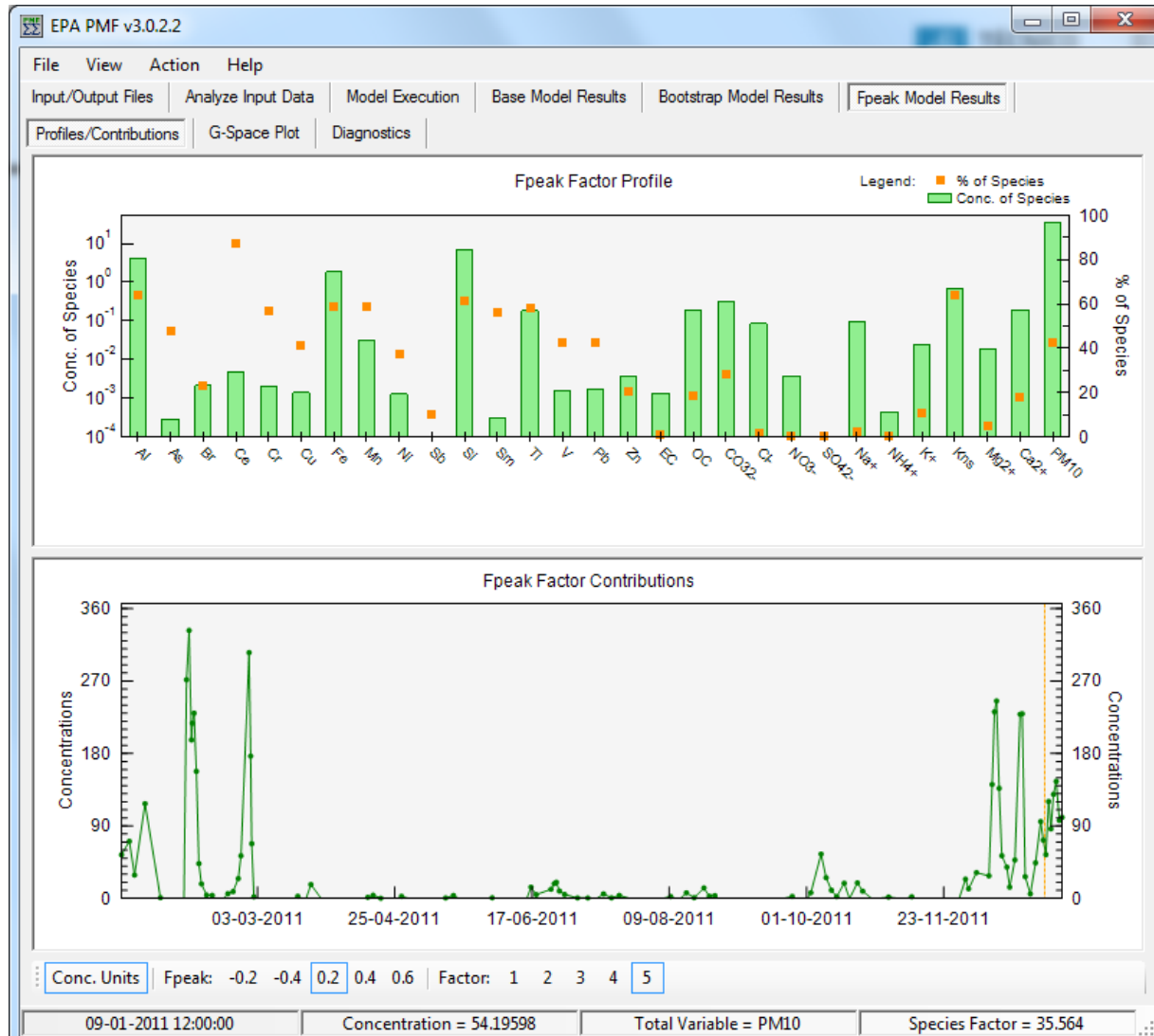
HAVE Bootstrap Results

Values should be between -5 and 5
(Fpeak \neq 0)

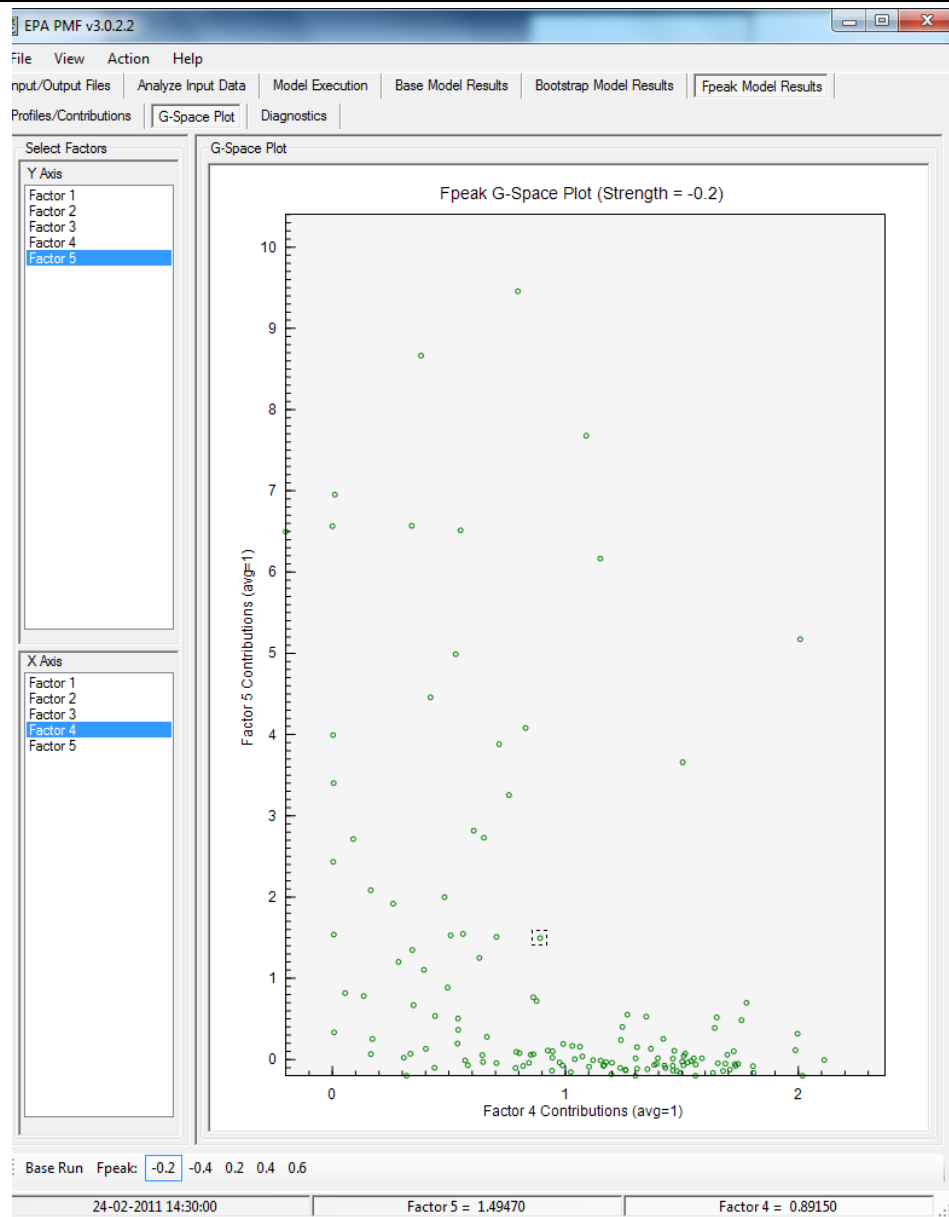
Order of the operations



Fpeak model results



Fpeak model results



Thank you for your attention