

APPENDIX H:
ANNOTATED SAS CODE FOR DOING SOURCE
APPORTIONMENT

Appendix H: Annotated SAS Code for Doing Source Apportionment

This code is set-up for a four-source SA solution using the input data set, bigsas. The output needs to be rescaled to force the relative contributions have a mean of 1. The input data set has the following variables.

val = concentration values

un = the uncertainty value

is-- = these are all class variables, i.e., 0/1 indicators of what the species is that has the concentration value. You can use proc GLMMOD to create these for you, but I find that I need to rename all of the variables. Hence, I create them myself in a data step.

n = is the index for the day. (1 = first set of measurements, 2 = second set of measurements, ...) If this is recoded with a random statement making the contributions random, then SAS will take care of this indexing.

z = 0 for all observations. (This is part of a coding trick to help scale things to make it converge.)

The data set Parmis is “just” a set of starting values for the parameters. The SAS default is to start everything at 1 without this data set. You MUST supply values for the F matrix here. If not, the optimization routines will move all of the source parameters “in sync” and you end up with N identical sources.

The model parameters are:

sigma2 = An over dispersion parameter.

g[n,k] = The elements of the G matrix, the source strengths.

f--1 to f--4 = The profile matrix elements that correspond to particular species.

```
proc nlmixed data=bigsas tech=quanew qpoints=5 diahes maxit=500 ABSXCONV=0.001
ABSFCNV=0.001;
array q[113,4] g1-g452;
parms /data=Parmis;
```

```
mean=(
ismf*(q[n,1]*fml1+q[n,2]*fml2+q[n,3]*fml3+q[n,4]*fml4)+
isbso4*(q[n,1]*fbso1+q[n,2]*fbso2+q[n,3]*fbso3+q[n,4]*fbso4)+
isec*(q[n,1]*fec1+q[n,2]*fec2+q[n,3]*fec3+q[n,4]*fec4)+
isoc*(q[n,1]*foc1+q[n,2]*foc2+q[n,3]*foc3+q[n,4]*foc4)+
isca*(q[n,1]*fca1+q[n,2]*fca2+q[n,3]*fca3+q[n,4]*fca4)+
```

```

iscu*(q[n,1]*fcu1+q[n,2]*fcu2+q[n,3]*fcu3+q[n,4]*fcu4)+
isfe*(q[n,1]*ffe1+q[n,2]*ffe2+q[n,3]*ffe3+q[n,4]*ffe4)+
ismq*(q[n,1]*fmq1+q[n,2]*fmq2+q[n,3]*fmq3+q[n,4]*fmq4)+
ispb*(q[n,1]*fpb1+q[n,2]*fpb2+q[n,3]*fpb3+q[n,4]*fpb4)+
isse*(q[n,1]*fse1+q[n,2]*fse2+q[n,3]*fse3+q[n,4]*fse4)+
issi*(q[n,1]*fsi1+q[n,2]*fsi2+q[n,3]*fsi3+q[n,4]*fsi4)+
0-val)/un;

```

```

model z ~ normal(mean,sigma2);

```

```

bounds 0<=g1-g452<=50, 0 <=fmf1-fmf4, 0 <=fbso1-fbso4, 0 <=fec1-fec4, 0 <=foc1-foc4,
0 <=fca1-fca4, 0 <=fcr1-fcr4, 0 <=fcu1-fcu4, 0 <=ffe1-ffe4, 0 <=fmg1-fmg4,
0 <=fpb1-fpb4, 0 <=fse1-fse4, 0 <=fsi1-fsi4;

```

```

run;

```