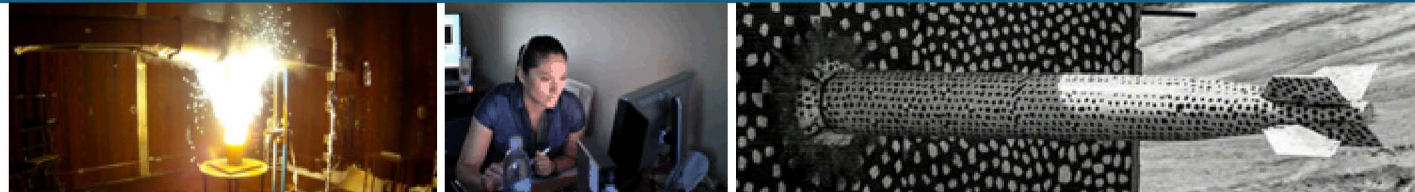


SAND2020-0792PE

CCDFGF Ad-Hoc Analysis

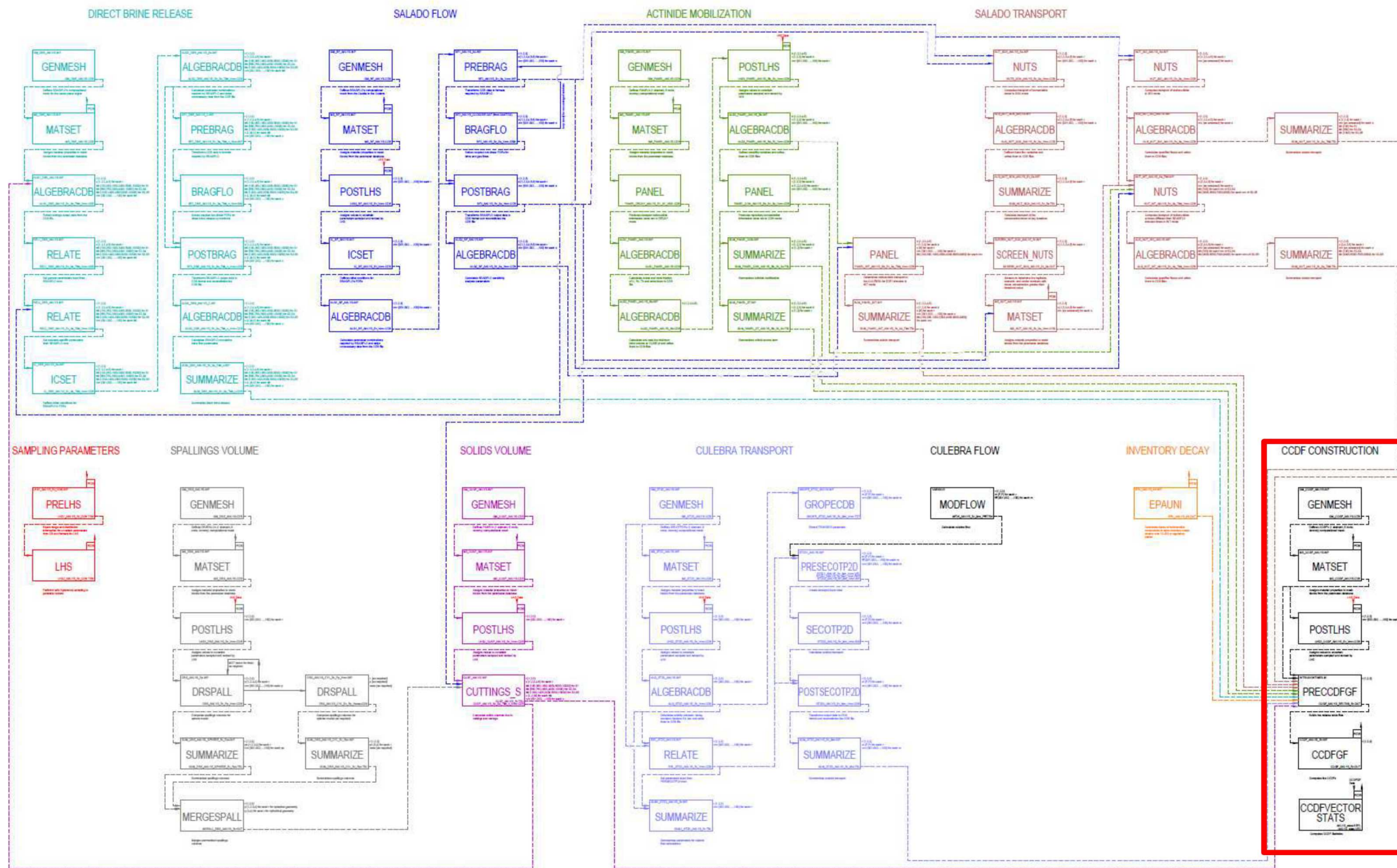


Sarah Brunell

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PRECCDFGF – Pre-Processor for CCDFGF

Collates output from other WIPP PA codes into a single RELTAB file

Release Data

- Direct brine release table volumes from BRAGFLO_DBR
- Direct solids release table volumes from CUTTINGS_S
- Salado transport release tables from NUTS and PANEL
- Culebra transport release tables from SECOTP2D
- Radionuclide concentrations from PANEL

Inventory Data

- CH and RH waste stream data from EPAUNI
- Mobilized radionuclide files from PANEL
- Colloidal mobilization fractions from PANEL

Parameter Data

- Sampled parameter values from LHS
- Constant parameter values from the PA Parameter Database (PAPDB)

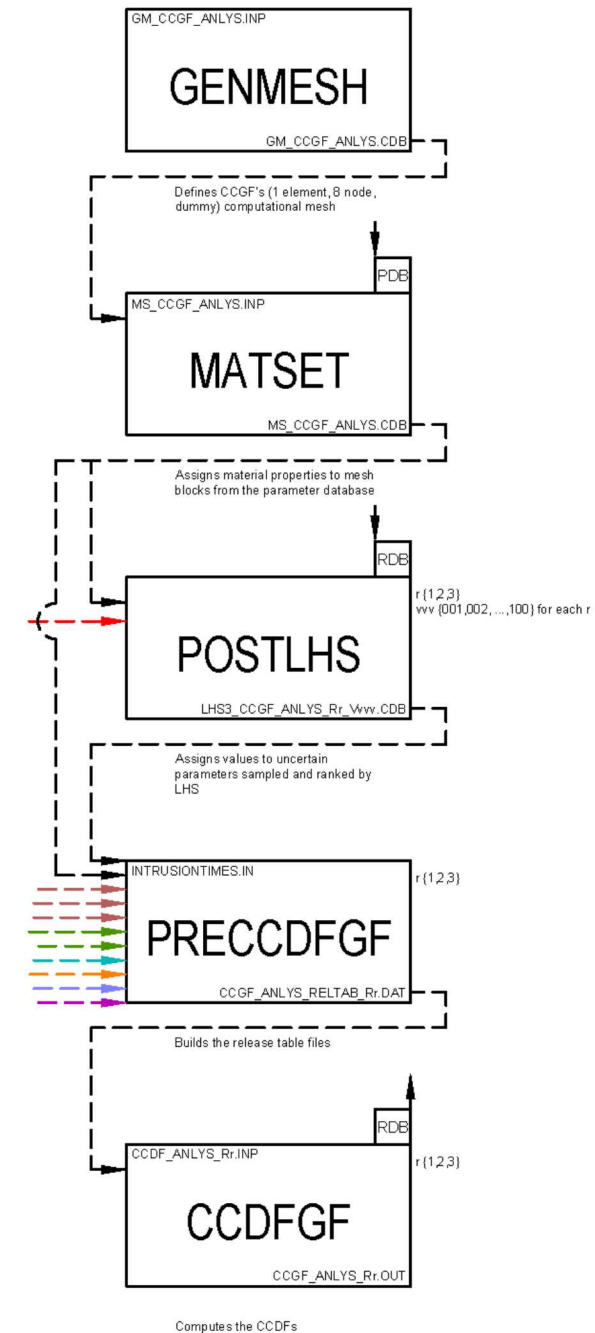
CCDFGF inputs:

One RELTAB file for each replicate

- Created by PRECCDFGF

One control file for each replicate

- User-defined



Release Mechanisms

Cuttings and Cavings Releases

- CUTTINGS_S

Spallings Releases

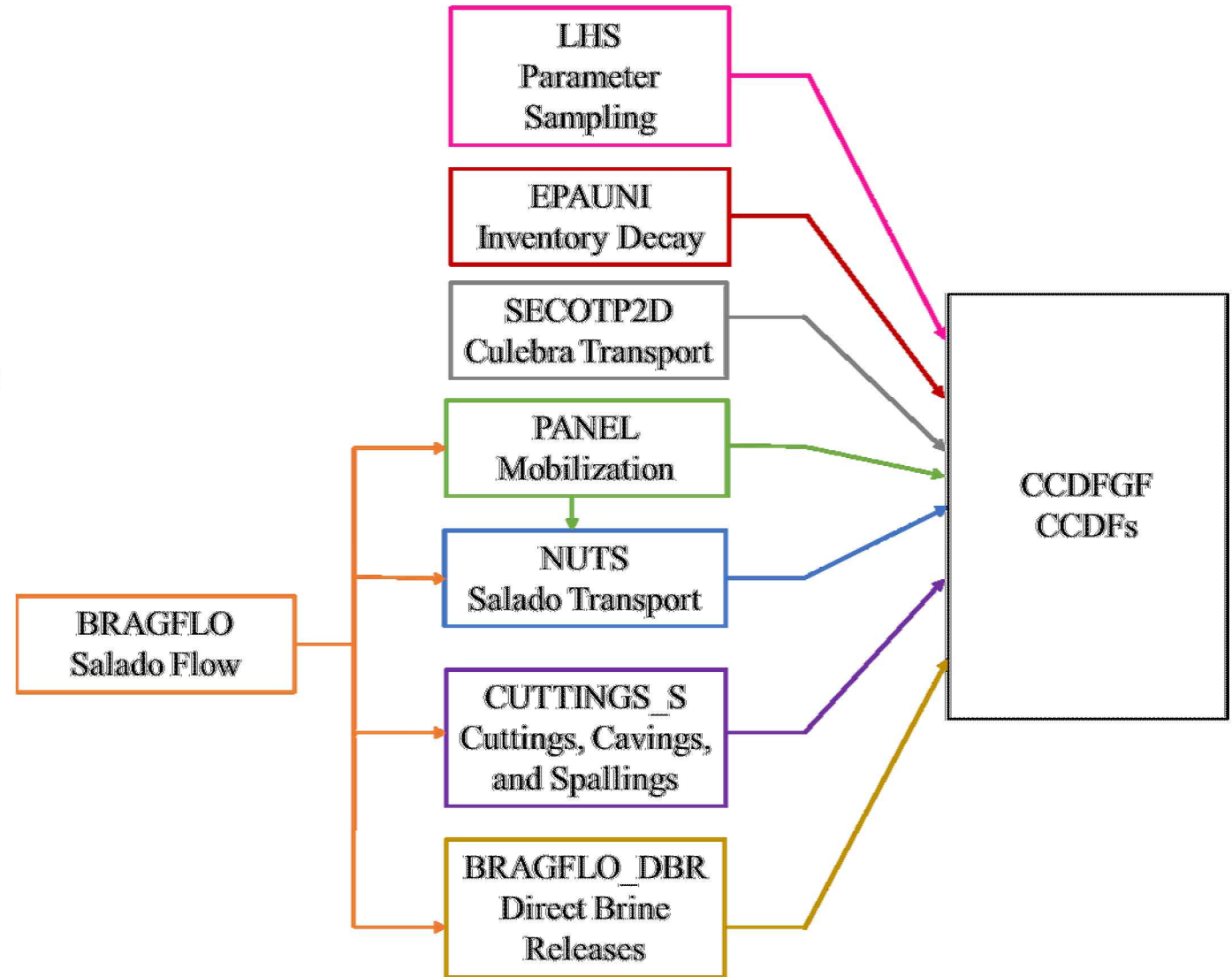
- CUTTINGS_S (volumes)
- EPAUNI/PRECCDFGF (concentrations)

Direct Brine Releases

- BRAGFLO_DBR (volumes)
- PANEL (concentrations)

Releases to/from the Culebra

- Through boreholes to the Culebra
 - NUTS and PANEL
- Through the Culebra to the Land Withdrawal Boundary
 - SECOTP2D



CCDFGF – Code Overview

Assembles results from other WIPP PA codes

- BRAGFLO_DBR, PANEL, NUTS, SECOTP2D, CUTTINGS_S, EPAUNI

Simulates drilling of boreholes at the surface of the repository

- Drilling location, depth (whether the brine pocket is penetrated), plugging pattern vary

Produces one complementary cumulative distribution function (CCDF) for each set of sampled values (parameters)

- One set of parameters = one vector

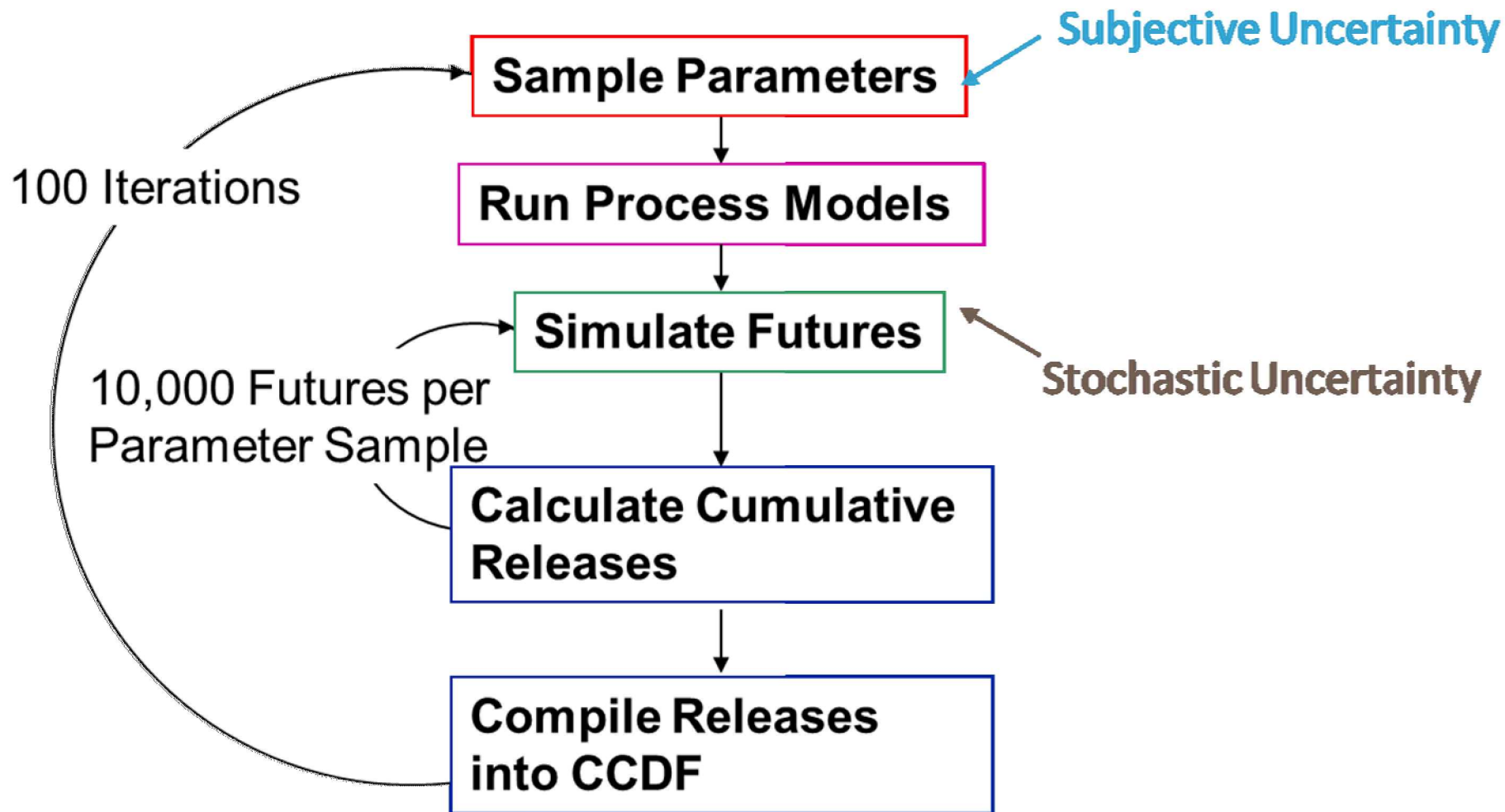
A CCDF defines the probability that cumulative normalized releases will exceed a given level

An individual CCDF represents 10,000 randomly chosen futures for each vector

- 10,000 points per CCDF
- Each future is equally probable
- 100 vectors per replicate, 3 replicates

WIPP compliance is based on the mean CCDF over 3 replicates

- An individual CCDF is NOT relevant for compliance



CCDFGF Outputs

Writes results to the PA_Results database

- Table CCDF_Data
 - Raw binned results
 - Used for creating “horsetail” plots

CCDFVECTORSTATS

- Reads results from CCDF_Data
- Calculates statistics
 - Mean, median, 10th and 90th percentiles*, standard deviation, and standard error
- Writes results to the database PA_Results
 - Vector statistics are written to the table StatsAcrossVectors
 - Replicate statistics are written to the table StatsAcrossReplicates

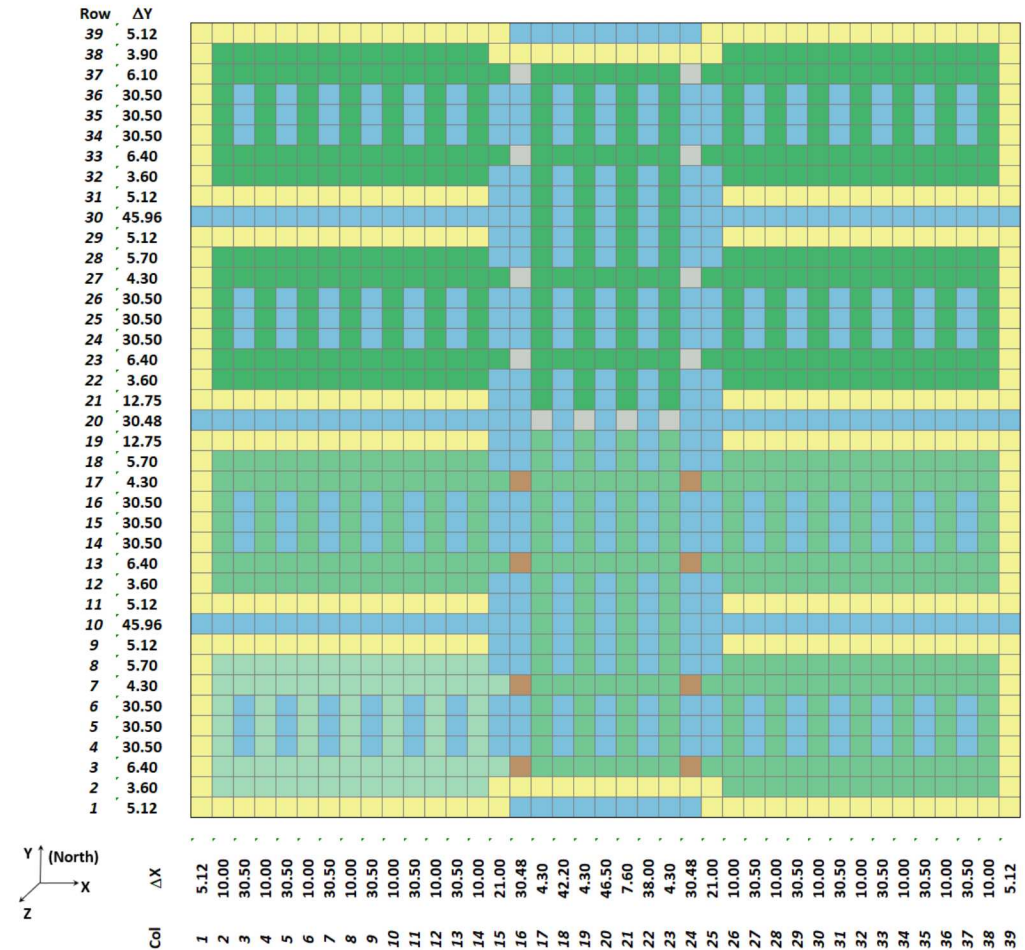
*Percentiles based on order statistics

Node locations

- 144 node locations replaced with panel probabilities

Panel Adjacency

- Defined by number of panel closures
- One or fewer = neighbor



9 CCDFGF Example Runs

Two example runs, making changes at different points:

1. Input (control) file – modify panel neighbor designations
2. Database parameter change – modify drilling rate

General steps are the same for each example:

1. Set up the new analysis in your user parameters database (ParamDB_sbr)
2. Set up the new analysis in your home directory
3. Run the analysis
4. View your results

CCDFGF Example Run A – Control File Change

1. Set up the new analysis in your user parameters database (ParamDB_sbr)*

Export needed tables from ParamDB to Excel using CRA19 as a starting point:

- Analyses
 - This table defines the analysis in your database
- AnalysisToVersion
 - Connects the parameter version you want to use with your analysis

Change the necessary values

Re-import the tables into your user database

*Example software – Toad for MySQL (2017 v. 8.0.0.296)

Export Tables

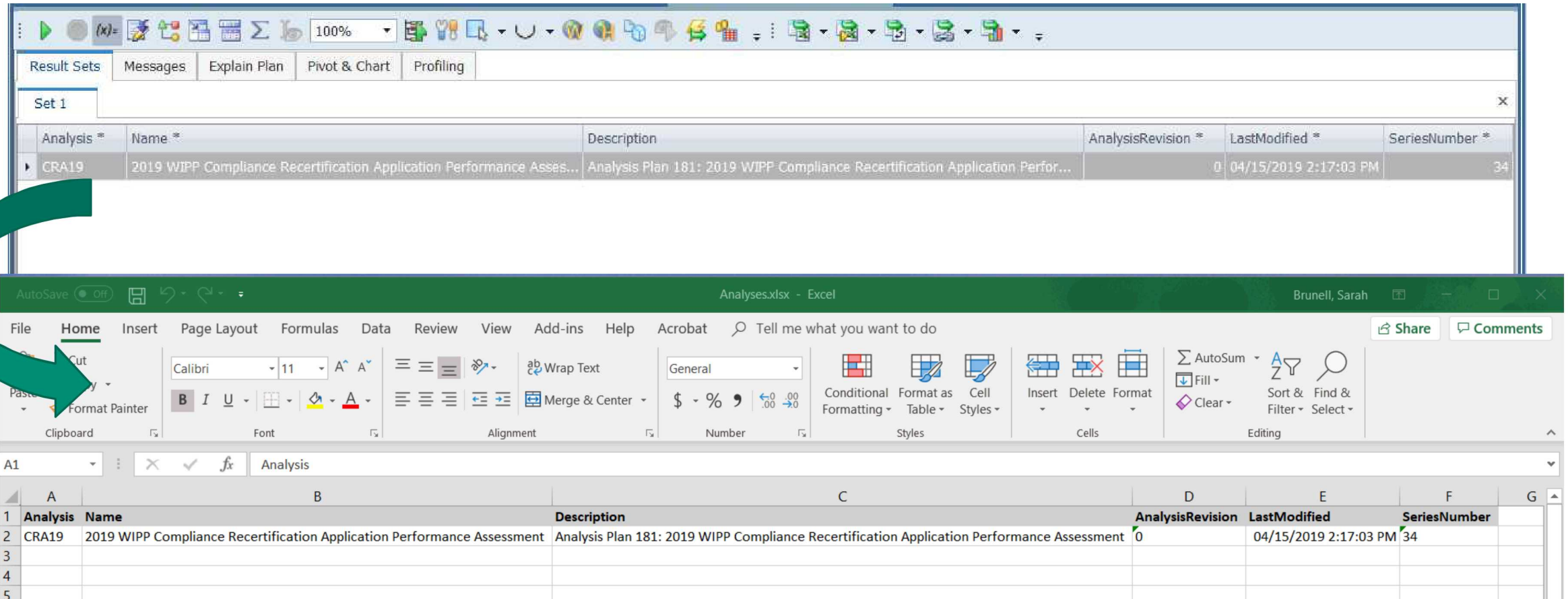
Query the table to retrieve all of the data used for the CRA19 analysis.

Query for table Analyses:

```
SELECT Analyses.Analysis,  
       Analyses.Name,  
       Analyses.Description,  
       Analyses.AnalysisRevision,  
       Analyses.LastModified,  
       Analyses.SeriesNumber  
FROM ParamDB.Analyses Analyses  
WHERE (Analyses.Analysis = 'CRA19')
```

Export Table – Analyses

Verify that the query produces the results you were expecting, then export the results to an Excel file.



The screenshot displays the SQL Server Enterprise Manager interface. The top pane shows the 'Result Sets' tab for 'Set 1', displaying a table with the following data:

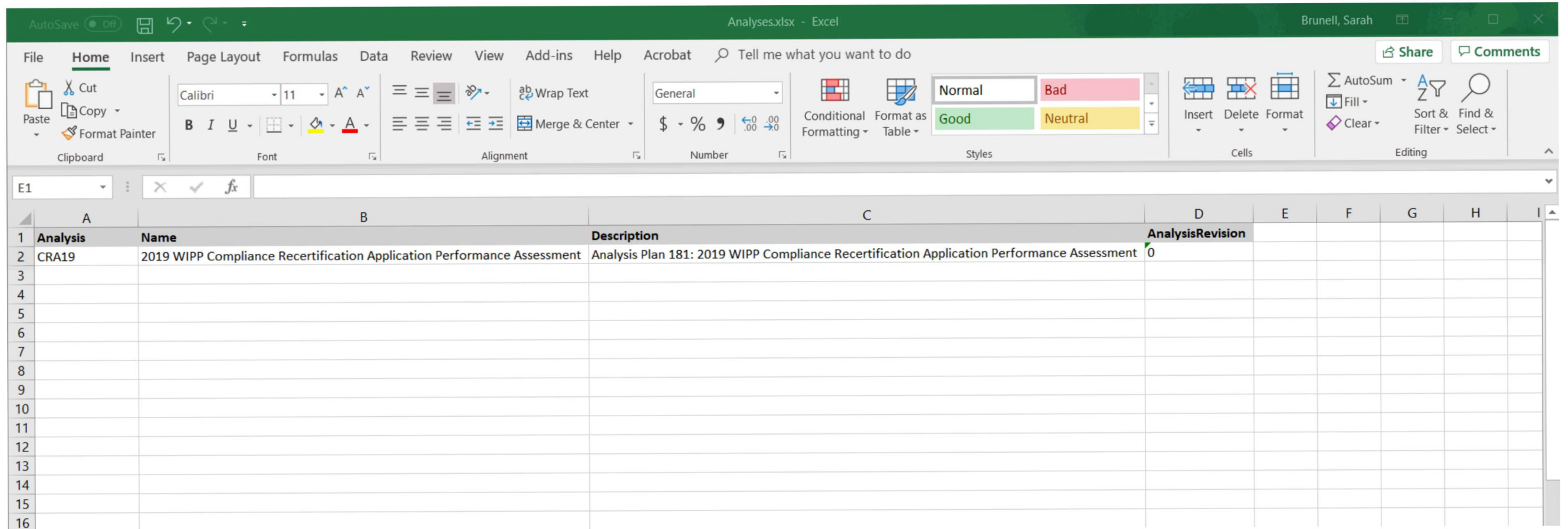
Analysis *	Name *	Description	AnalysisRevision *	LastModified *	SeriesNumber *
CRA19	2019 WIPP Compliance Recertification Application Performance Asses...	Analysis Plan 181: 2019 WIPP Compliance Recertification Application Perfor...	0	04/15/2019 2:17:03 PM	34

The bottom pane shows an Excel spreadsheet named 'Analyses.xlsx' with the same data. The Excel ribbon is visible, showing the 'Home' tab. The data is organized as follows:

Analysis	Name	Description	AnalysisRevision	LastModified	SeriesNumber
CRA19	2019 WIPP Compliance Recertification Application Performance Assessment	Analysis Plan 181: 2019 WIPP Compliance Recertification Application Performance Assessment	0	04/15/2019 2:17:03 PM	34

Table - Analyses

Select and delete the fields that will be auto-populated by the SQL database



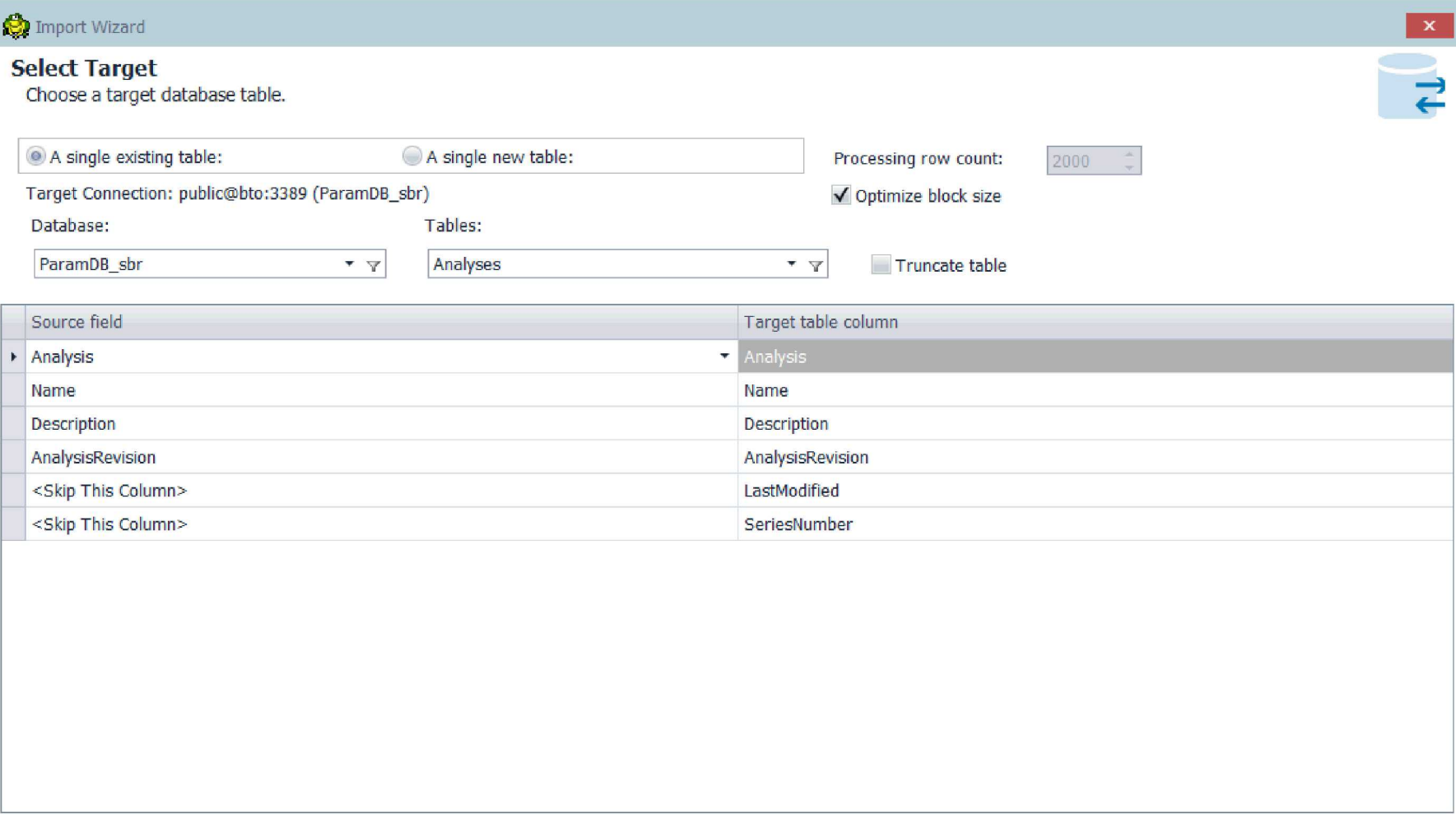
The screenshot shows the Microsoft Excel interface with the 'Analyses.xlsx' file open. The ribbon is set to 'Home'. The table 'Analyses' is displayed with the following data:

Analysis	Name	Description	AnalysisRevision
CRA19	2019 WIPP Compliance Recertification Application Performance Assessment	Analysis Plan 181: 2019 WIPP Compliance Recertification Application Performance Assessment	0

Import Table – Analyses

Import the new data into the existing table “Analyses”

Check that the source name matches the target name.



Import Wizard

Select Target
Choose a target database table.

☒ A single existing table: ☐ A single new table:

Processing row count: 2000

Target Connection: public@bto:3389 (ParamDB_sbr) ☒ Optimize block size

Database: ParamDB_sbr Tables: Analyses ☐ Truncate table

Source field	Target table column
Analysis	Analysis
Name	Name
Description	Description
AnalysisRevision	AnalysisRevision
<Skip This Column>	LastModified
<Skip This Column>	SeriesNumber

Map:

< Back Next > Cancel

Check results

Analysis Query:

```
SELECT Analyses.Analysis,
       Analyses.Name,
       Analyses.Description,
       Analyses.AnalysisRevision,
       Analyses.LastModified,
       Analyses.SeriesNumber
FROM ParamDB_sbr.Analyses Analyses
WHERE (Analyses.Analysis =
'CCDF_DemoA')
```

Query Result:

Result Sets						
Messages						
Explain Plan						
Pivot & Chart						
Profiling						
Set 1						
Set 2						
Analysis *	Name *	Description	AnalysisRevision *	LastModified *	SeriesNumber *	
▶ CCDF_DemoA	CCDFGF EPA Demo A	CCDFGF EPA Demo A - Modified panel neighbor designations	0	11/26/2019 10:19:50 AM	0	

Import Table – Analyses

Option 2 –

Add the analysis directly to the database.

Export Table – AnalysisToVersion

Query the table to retrieve all of the data used for the CRA19 analysis.

Query for table AnalysisToVersion:

```
SELECT AnalysisToVersion.Analysis,  
       AnalysisToVersion.Material,  
       AnalysisToVersion.Property,  
       AnalysisToVersion.Version,  
       AnalysisToVersion.auto_num,  
       AnalysisToVersion.Code,  
       AnalysisToVersion.VersionNumber,  
       AnalysisToVersion.AnalysisRevision,  
       AnalysisToVersion.LastModified  
FROM ParamDB.AnalysisToVersion AnalysisToVersion  
WHERE (AnalysisToVersion.Analysis = 'CRA19')
```

Table - AnalysisToVersion

Verify that the query produces the correct result, then export to an Excel file

Set 1

Analysis *	Material *	Property *	Version *	auto_num *	Code	VersionNumber *	AnalysisRevision *	LastModified *
CRA19	AM	CAPHUM	CCA	320585	BRAGFLO	1	0	04/11/2019 5:10:32 PM
CRA19	AM	CAPMIC	CRA19	320586	BRAGFLO	3	0	04/11/2019 5:10:32 PM
CRA19	AM	CONCINT	CRA19	320587	BRAGFLO	3	0	04/11/2019 5:10:32 PM
CRA19	AM	CONCMIN	CCA	320588	BRAGFLO	1	0	04/11/2019 5:10:32 PM

AutoSave ☐ Off

AnalysisToVersion.xlsx - Excel

File Home Insert Page Layout Formulas Data Review View Add-ins Help Acrobat Tell me what you want to do

Paste Cut Copy Format Painter

Clipboard

Calibri 11 A⁺ A⁻

B I U

Font

Wrap Text

Alignment

Merge & Center

General

Number

Conditional Formatting

Format as Table

A1

Analysis

	A	B	C	D	E	F	G	H	I	J
1	Analysis	Material	Property	Version	auto_num	Code	VersionNumber	AnalysisRevision	LastModified	
2	CRA19	AM	CAPHUM	CCA	320585	BRAGFLO	1	0	04/11/2019 5:10:32 PM	
3	CRA19	AM	CAPMIC	CRA19	320586	BRAGFLO	3	0	04/11/2019 5:10:32 PM	
4	CRA19	AM	CONCINT	CRA19	320587	BRAGFLO	3	0	04/11/2019 5:10:32 PM	
5	CRA19	AM	CONCMIN	CCA	320588	BRAGFLO	1	0	04/11/2019 5:10:32 PM	
6	CRA19	AM	PROPMIC	CRA19	320589	BRAGFLO	3	0	04/11/2019 5:10:32 PM	
7	CRA19	AM241	ATWEIGHT	CCA	320590	BRAGFLO	1	0	04/11/2019 5:10:32 PM	

Table - AnalysisToVersion

Delete the fields that will be auto-populated by the SQL database

	A	B	C	D	E	F	G	H	I	J	K
1	Analysis	Material	Property	Version	Code	VersionNumber	AnalysisRevision				
2	CRA19	AM	CAPHUM	CCA	BRAGFLO	1	0				
3	CRA19	AM	CAPMIC	CRA19	BRAGFLO	3	0				
4	CRA19	AM	CONCINT	CRA19	BRAGFLO	3	0				
5	CRA19	AM	CONCMIN	CCA	BRAGFLO	1	0				
6	CRA19	AM	PROPMIC	CRA19	BRAGFLO	3	0				
7	CRA19	AM241	ATWEIGHT	CCA	BRAGFLO	1	0				
8	CRA19	AM241	DECAYNRG	CRA19	BRAGFLO	1	0				
9	CRA19	AM241	HALFLIFE	CCA	BRAGFLO	1	0				
10	CRA19	AM241	INVCHD	CRA19	BRAGFLO	7	0				
11	CRA19	AM241	INVRHD	CRA19	BRAGFLO	8	0				
12	CRA19	BH_CREEP	CAP_MOD	CCA	BRAGFLO	1	0				
13	CRA19	BH_CREEP	COMP_RCK	CCA	BRAGFLO	1	0				
14	CRA19	BH_CREEP	KPT	CCA	BRAGFLO	1	0				
15	CRA19	BH_CREEP	PC_MAX	CCA	BRAGFLO	1	0				
16	CRA19	BH_CREEP	PCT_A	CCA	BRAGFLO	1	0				

Table - AnalysisToVersion

Change the Analysis name from CRA19 to your analysis name.

This must be the same name as you used in the Analyses table. The entire column must be changed.

G1320											
	A	B	C	D	E	F	G	H	I	J	K
1	Analysis	Material	Property	Version	Code	VersionNumber	AnalysisRevision				
2	CCDF_DemoA	AM	CAPHUM	CCA	BRAGFLO	1	0				
3	CCDF_DemoA	AM	CAPMIC	CRA19	BRAGFLO	3	0				
4	CCDF_DemoA	AM	CONCINT	CRA19	BRAGFLO	3	0				
5	CCDF_DemoA	AM	CONCMIN	CCA	BRAGFLO	1	0				
6	CCDF_DemoA	AM	PROPMIC	CRA19	BRAGFLO	3	0				
7	CCDF_DemoA	AM241	ATWEIGHT	CCA	BRAGFLO	1	0				
8	CCDF_DemoA	AM241	DECAYNRG	CRA19	BRAGFLO	1	0				
9	CCDF_DemoA	AM241	HALFLIFE	CCA	BRAGFLO	1	0				
10	CCDF_DemoA	AM241	INVCHD	CRA19	BRAGFLO	7	0				
11	CCDF_DemoA	AM241	INVRHD	CRA19	BRAGFLO	8	0				
12	CCDF_DemoA	BH_CREEP	CAP_MOD	CCA	BRAGFLO	1	0				
13	CCDF_DemoA	BH_CREEP	COMP_RCK	CCA	BRAGFLO	1	0				
14	CCDF_DemoA	BH_CREEP	KPT	CCA	BRAGFLO	1	0				
15	CCDF_DemoA	BH_CREEP	PC_MAX	CCA	BRAGFLO	1	0				
16	CCDF_DemoA	BH_CREEP	PCT_A	CCA	BRAGFLO	1	0				

Import Table – AnalysisToVersion

Import the new data into the existing table “AnalysisToVersion”

Check that the source name matches the target name.

The screenshot shows the 'Import Wizard' dialog box, specifically the 'Select Target' step. The title bar says 'Import Wizard' with a close button. Below the title, it says 'Select Target' and 'Choose a target database table.' There is a blue cylinder icon with two arrows on the right. The main area has two radio buttons: 'A single existing table:' (selected) and 'A single new table:'. To the right is a 'Processing row count:' field set to '2000'. Below these is 'Target Connection: public@bto:3389 (ParamDB_sbr)' and a checked 'Optimize block size' checkbox. There are two dropdown menus: 'Database:' set to 'ParamDB_sbr' and 'Tables:' set to 'AnalysisToVersion'. A 'Truncate table' checkbox is also present. Below this is a table mapping source fields to target table columns.

Source field	Target table column
Analysis	Analysis
Material	Material
Property	Property
Version	Version
<Skip This Column>	auto_num
Code	Code
VersionNumber	VersionNumber
AnalysisRevision	AnalysisRevision
<Skip This Column>	LastModified

At the bottom, there is a 'Map:' section with two buttons: 'By Position' and 'By Name' (which is selected and highlighted with a blue border). To the right of these are three buttons: '< Back', 'Next >', and 'Cancel'.

Check results

AnalysisToVersion Query:

```
SELECT AnalysisToVersion.Analysis,
       AnalysisToVersion.Material,
       AnalysisToVersion.Property,
       AnalysisToVersion.Version,
       AnalysisToVersion.auto_num,
       AnalysisToVersion.Code,
       AnalysisToVersion.VersionNumber,
       AnalysisToVersion.AnalysisRevision,
       AnalysisToVersion.LastModified
FROM ParamDB_sbr.AnalysisToVersion
AnalysisToVersion
WHERE (AnalysisToVersion.Analysis = 'CCDF_DemoA')
```

Query Result:

Analysis *	Material *	Property *	Version *	auto_num *	Code	VersionNumber *	AnalysisRevision *	LastModified *	
CCDF_DemoA	AM	CAPHUM	CCA	336533	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM	CAPMIC	CRA19	336534	BRAGFLO	3	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM	CONCINT	CRA19	336535	BRAGFLO	3	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM	CONCMIN	CCA	336536	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM	PROPMIC	CRA19	336537	BRAGFLO	3	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM241	ATWEIGHT	CCA	336538	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM241	DECAYNRG	CRA19	336539	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM241	HALFLIFE	CCA	336540	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM241	INVCHD	CRA19	336541	BRAGFLO	7	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	AM241	INVRHD	CRA19	336542	BRAGFLO	8	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	CAP_MOD	CCA	336543	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	COMP_RCK	CCA	336544	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	KPT	CCA	336545	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PC_MAX	CCA	336546	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PCT_A	CCA	336547	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PCT_EXP	CCA	336548	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PO_MIN	CCA	336549	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PORE_DIS	CCA	336550	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	POROSITY	CCA	336551	BRAGFLO	1	0	11/26/2019 12:40:17 PM	
CCDF_DemoA	BH_CREEP	PRMX_LOG	CCA	336552	BRAGFLO	1	0	11/26/2019 12:40:17 PM	

CCDFGF Example Run A – Control File Change

2. Set up the new analysis in your home directory*

Create the directory structure

Copy an existing analysis (CRA19) as a starting point.

Edit any necessary input files

*Example software: MobaXterm v. 12.2

Create the directory structure

Starting directory: /home/sbrunel/Analyses/

```
-bash-4.4$ mkdir CCDF_DemoA
-bash-4.4$ cd CCDF_DemoA/
-bash-4.4$ cp -r /home/sbrunel/run_scripts/* .
-bash-4.4$ mv setup_CRA19.sh setup_CCDF_DemoA.sh
-bash-4.4$ mv run_CRA19.sh run_CCDF_DemoA.sh
```

This is what the directory looks like:

```
-bash-4.4$ pwd
/home/sbrunel/Analyses/CCDF_DemoA
-bash-4.4$ ls
INP                run_CCDF_DemoA.sh  Scripts            setup_CCDF_DemoA.sh
-bash-4.4$ █
```

Edit the Input File(s)

The directory INP contains input files for all of the codes.

We are going to focus on just the input files needed to run CCDFGF.

Move into the input directory and look at its contents:

```
-bash-4.4$ cd INP/  
-bash-4.4$ ls
```

Edit the Input File(s)



```
-bash-4.4$ ls
alg_nut_iso_CRA19.inp      alg3_panel_CRA19_b4.inp  bf1_dbr_CRA19_s1_100_L.inp  ic_dbr_CRA19_s4.inp      nut_iso_CRA19_s2.inp
alg_nut_scn_CRA19.inp    alg3_panel_CRA19_b5.inp  bf1_dbr_CRA19_s1_100_M.inp  ic_dbr_CRA19_s5.inp      nut_iso_CRA19_s3.inp
alg1_bf_CRA19.inp        bf1_CRA19_s1_mod1.inp    bf1_dbr_CRA19_s1_100_U.inp  lhs1_CRA19_r1_con.inp    nut_iso_CRA19_s4.inp
alg1_dbr_CRA19.inp       bf1_CRA19_s1_mod2.inp    bf1_dbr_CRA19_U.inp        lhs1_CRA19_r2_con.inp    nut_iso_CRA19_s5.inp
alg1_panel_CRA19.inp     bf1_CRA19_s1.inp        bf2_CRA19_closure.dat      lhs1_CRA19_r3_con.inp    nut_scn_CRA19_s1.inp
alg2_bf_CRA19.inp        bf1_CRA19_s2_mod1.inp    ccgf_CRA19_control_r1.inp  ms_bf_CRA19.inp          nut_scn_CRA19_s2.inp
alg2_dbr_CRA19_s1.inp    bf1_CRA19_s2_mod2.inp    ccgf_CRA19_control_r2.inp  ms_ccgf_CRA19.inp        nut_scn_CRA19_s3.inp
alg2_dbr_CRA19_s2.inp    bf1_CRA19_s2.inp        ccgf_CRA19_control_r3.inp  ms_cusp_CRA19.inp        nut_scn_CRA19_s4.inp
alg2_dbr_CRA19_s3.inp    bf1_CRA19_s3_mod1.inp    cusp_CRA19.inp            ms_dbr_CRA19.inp        nut_scn_CRA19_s5.inp
alg2_dbr_CRA19_s4.inp    bf1_CRA19_s3_mod2.inp    epu_CRA19_ch_misc.inp     ms_nut_CRA19.inp        rel1_dbr_CRA19.inp
alg2_dbr_CRA19_s5.inp    bf1_CRA19_s3.inp        epu_CRA19_ch.inp          ms_panel_CRA19.inp      rel2_dbr_CRA19_s1.inp
alg2_panel_CRA19_b1.inp  bf1_CRA19_s4_mod1.inp    epu_CRA19_rh_misc.inp     nut_int_CRA19_s2_t00100.inp  rel2_dbr_CRA19_s2.inp
alg2_panel_CRA19_b2.inp  bf1_CRA19_s4_mod2.inp    epu_CRA19_rh.inp          nut_int_CRA19_s3_t03000.inp  rel2_dbr_CRA19_s3.inp
alg2_panel_CRA19_b3.inp  bf1_CRA19_s4.inp        gm_bf_CRA19.inp           nut_int_CRA19_s3_t05000.inp  rel2_dbr_CRA19_s4.inp
alg2_panel_CRA19_b4.inp  bf1_CRA19_s5_mod1.inp    gm_ccgf_CRA19.inp         nut_int_CRA19_s3_t07000.inp  rel2_dbr_CRA19_s5.inp
alg2_panel_CRA19_b5.inp  bf1_CRA19_s5_mod2.inp    gm_cusp_CRA19.inp         nut_int_CRA19_s3_t09000.inp  sum_dbr.inp
alg3_dbr_CRA19_L.inp     bf1_CRA19_s5.inp        gm_dbr_CRA19.inp          nut_int_CRA19_s4_t00100.inp  sum_panel_con.inp
alg3_dbr_CRA19_M.inp     bf1_CRA19_s6_mod1.inp    gm_panel_CRA19.inp        nut_int_CRA19_s5_t03000.inp  sum_panel_int.inp
alg3_dbr_CRA19_U.inp     bf1_CRA19_s6_mod2.inp    ic_bf_CRA19.inp           nut_int_CRA19_s5_t05000.inp  sum_panel_st.inp
alg3_panel_CRA19_b1.inp  bf1_CRA19_s6.inp        ic_dbr_CRA19_s1.inp       nut_int_CRA19_s5_t07000.inp
alg3_panel_CRA19_b2.inp  bf1_dbr_CRA19_L.inp     ic_dbr_CRA19_s2.inp       nut_int_CRA19_s5_t09000.inp
alg3_panel_CRA19_b3.inp  bf1_dbr_CRA19_M.inp     ic_dbr_CRA19_s3.inp       nut_iso_CRA19_s1.inp
-bash-4.4$
```

Edit the Input File(s)



```
-bash-4.4$ ls
alg_nut_iso_CRA19.inp      alg3_panel_CRA19_b4.inp  bf1_dbr_CRA19_s1_100_L.inp  ic_dbr_CRA19_s4.inp      nut_iso_CRA19_s2.inp
alg_nut_scn_CRA19.inp      alg3_panel_CRA19_b5.inp  bf1_dbr_CRA19_s1_100_M.inp  ic_dbr_CRA19_s5.inp      nut_iso_CRA19_s3.inp
alg1_bf_CRA19.inp          bf1_CRA19_s1_mod1.inp    bf1_dbr_CRA19_s1_100_U.inp  lhs1_CRA19_r1_con.inp    nut_iso_CRA19_s4.inp
alg1_dbr_CRA19.inp          bf1_CRA19_s1_mod2.inp    bf1_dbr_CRA19_U.inp         lhs1_CRA19_r2_con.inp    nut_iso_CRA19_s5.inp
alg1_panel_CRA19.inp        bf1_CRA19_s1.inp         bf2_CRA19_closure.dat       lhs1_CRA19_r3_con.inp    nut_scn_CRA19_s1.inp
alg2_bf_CRA19.inp          bf1_CRA19_s2_mod1.inp    ccgf_CRA19_control_r1.inp    ms_bf_CRA19.inp          nut_scn_CRA19_s2.inp
alg2_dbr_CRA19_s1.inp       bf1_CRA19_s2_mod2.inp    ccgf_CRA19_control_r2.inp    ms_ccgf_CRA19.inp        nut_scn_CRA19_s3.inp
alg2_dbr_CRA19_s2.inp       bf1_CRA19_s2.inp         ccgf_CRA19_control_r3.inp    ms_cusp_CRA19.inp        nut_scn_CRA19_s4.inp
alg2_dbr_CRA19_s3.inp       bf1_CRA19_s3_mod1.inp    cusp_CRA19.inp              ms_dbr_CRA19.inp         nut_scn_CRA19_s5.inp
alg2_dbr_CRA19_s4.inp       bf1_CRA19_s3_mod2.inp    epu_CRA19_ch_misc.inp       ms_nut_CRA19.inp         rel1_dbr_CRA19.inp
alg2_dbr_CRA19_s5.inp       bf1_CRA19_s3.inp         epu_CRA19_ch.inp            ms_panel_CRA19.inp       rel2_dbr_CRA19_s1.inp
alg2_panel_CRA19_b1.inp     bf1_CRA19_s4_mod1.inp    epu_CRA19_rh_misc.inp       nut_int_CRA19_s2_t00100.inp  rel2_dbr_CRA19_s2.inp
alg2_panel_CRA19_b2.inp     bf1_CRA19_s4_mod2.inp    epu_CRA19_rh.inp            nut_int_CRA19_s3_t03000.inp  rel2_dbr_CRA19_s3.inp
alg2_panel_CRA19_b3.inp     bf1_CRA19_s4.inp         gm_bf_CRA19.inp             nut_int_CRA19_s3_t05000.inp  rel2_dbr_CRA19_s4.inp
alg2_panel_CRA19_b4.inp     bf1_CRA19_s5_mod1.inp    gm_ccgf_CRA19.inp           nut_int_CRA19_s3_t07000.inp  rel2_dbr_CRA19_s5.inp
alg2_panel_CRA19_b5.inp     bf1_CRA19_s5_mod2.inp    gm_cusp_CRA19.inp           nut_int_CRA19_s3_t09000.inp  sum_dbr.inp
alg3_dbr_CRA19_L.inp        bf1_CRA19_s5.inp         gm_dbr_CRA19.inp            nut_int_CRA19_s4_t00100.inp  sum_panel_con.inp
alg3_dbr_CRA19_M.inp        bf1_CRA19_s6_mod1.inp    gm_panel_CRA19.inp          nut_int_CRA19_s5_t03000.inp  sum_panel_int.inp
alg3_dbr_CRA19_U.inp        bf1_CRA19_s6_mod2.inp    ic_bf_CRA19.inp             nut_int_CRA19_s5_t05000.inp  sum_panel_st.inp
alg3_panel_CRA19_b1.inp     bf1_CRA19_s6.inp         ic_dbr_CRA19_s1.inp         nut_int_CRA19_s5_t07000.inp
alg3_panel_CRA19_b2.inp     bf1_dbr_CRA19_L.inp      ic_dbr_CRA19_s2.inp         nut_int_CRA19_s5_t09000.inp
alg3_panel_CRA19_b3.inp     bf1_dbr_CRA19_M.inp      ic_dbr_CRA19_s3.inp         nut_iso_CRA19_s1.inp
-bash-4.4$
```

Edit the Input File(s)

Rename the input file(s) you are going to use (only replicate 1 for this example):

```
-bash-4.4$ mv ccgf_CRA19_control_r1.inp ccgf_CCDF_DemoA_control_r1.inp
```

Edit that file.

Edit the Input File(s)

```

GNU nano 2.0.9                               File: ccgf CCDF DemoA control rl.inp
CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2        OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2        FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F          1000 SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F          1000 BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUNDOFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09
!
=====
! PURPOSE:      CCDFGF Control Input file for replicate 1
! ANALYSIS:     CRA19
! ANALYSIS PLAN: AP-181
! ANALYST:      Sarah B. Brunell
! DATE:         03/07/19
!
^G Get Help      ^O WriteOut      ^R Read File      ^Y Prev Page      ^K Cut Text      ^C Cur Pos
^X Exit          ^J Justify       ^W Where Is       ^V Next Page     ^U UnCut Text    ^T To Spell

```

Change analysis name

Edit neighbor relationships

Edit the Input File(s)

```

GNU nano 2.0.9                               File: ccqf CCDF DemoA control r1.inp
CCDFGF Control Input file for CCDF_DemoA, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2        OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2        FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F          1000 SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F          1000 BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUNDOFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 10
4 M 0.10439087 10
5 L 0.10439087 10
6 M 0.10439087 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09
!
=====
! PURPOSE:      CCDFGF Control Input file for replicate 1
! ANALYSIS:     CRA19
! ANALYSIS PLAN: AP-181
! ANALYST:      Sarah B. Brunell
! DATE:         03/07/19

[ Read 60 lines ]

^G Get Help      ^O WriteOut      ^R Read File      ^Y Prev Page      ^K Cut Text      ^C Cur Pos
^X Exit          ^J Justify       ^W Where Is      ^V Next Page     ^U UnCut Text    ^T To Spell

```

Change analysis name

Edit neighbor relationships

Setup the new analysis

Move back into the CCDF_DemoA directory:

```
-bash-4.4$ cd ..
```

Edit the header information in the file `setup_CCDF_DemoA.sh`

```
-bash-4.4$ nano setup_CCDF_DemoA.sh
```

Setup the new analysis

Change header information
to match the new analysis.

```

GNU nano 2.0.9                               File: setup_CCDF_DemoA.sh

#!/bin/sh
# syntax ./setup_Analysis &

# CRA19 Rev. 0 - Compliance Recertification Application 2019

# Define analysis names and tags
New_Analysis="CRA19"
New_Tag="CRA19 Rev. 0"
Old_Analysis="APCS"

# Get old analysis files
./Scripts/getAnalysisFiles.sh ${Old_Analysis}

# Rename old analysis file names to new
./Scripts/renameAnalysisFiles.sh ${Old_Analysis} ${New_Analysis}

# Overwrite/update analysis files
cp ./INP/alg*.inp ./${Old_Analysis}/ALGEBRACDB/Input/
cp ./INP/bf1*.inp ./${Old_Analysis}/PREBRAG/Input/
cp ./INP/gm*.inp ./${Old_Analysis}/GENMESH/Input/
cp ./INP/ic*.inp ./${Old_Analysis}/ICSET/Input/
cp ./INP/ms*.inp ./${Old_Analysis}/MATSET/Input/
cp ./INP/lhs1*.inp ./${Old_Analysis}/PRELHS/Input/
cp ./INP/nut*.inp ./${Old_Analysis}/NUTS/Input/
cp ./INP/cusp*.inp ./${Old_Analysis}/CUTTINGS_S/Input/
cp ./INP/rel*.inp ./${Old_Analysis}/RELATE/Input/
cp ./INP/ccgf*.inp ./${Old_Analysis}/CCDFGF/Input/
cp ./INP/epu*.inp ./${Old_Analysis}/EPAUNI/Input/
cp ./INP/sum*.inp ./${Old_Analysis}/SUMMARIZE/Input/

# Move analysis files
./Scripts/moveAnalysisFiles.sh ${Old_Analysis} ${New_Analysis}

# Get run scripts
./Scripts/getRunScripts.sh ${New_Analysis}

# Install analysis files (inputs and run scripts)
./Scripts/installAnalysisFiles.sh ${New_Analysis} ${New_Tag}

# Run the analysis
#nohup ./run_${New_Analysis}.sh ${Old_Analysis} ${New_Analysis} &

[ Read 41 lines ]

^G Get Help      ^O WriteOut      ^R Read File     ^Y Prev Page     ^K Cut Text      ^C Cur Pos
^X Exit          ^J Justify       ^W Where Is     ^V Next Page     ^U UnCut Text    ^T To Spell

```

Setup the new analysis

Change header information
to match the new analysis.

```

GNU nano 2.0.9                                File: setup CCDF DemoA.sh

#!/bin/sh
# syntax ./setup_Analysis &

# CCDF_DemoA - CCDFGF EPA Demo A - Redefine Neighbor Relationships

# Define analysis names and tags
New_Analysis="CCDF_DemoA"
New_Tag="CCDF_DemoA Rev. 0"
Old_Analysis="CRA19"

# Get old analysis files
./Scripts/getAnalysisFiles.sh ${Old_Analysis}

# Rename old analysis file names to new
./Scripts/renameAnalysisFiles.sh ${Old_Analysis} ${New_Analysis}

# Overwrite/update analysis files
cp ./INP/alg*.inp ./${Old_Analysis}/ALGEBRACDB/Input/
cp ./INP/bf1*.inp ./${Old_Analysis}/PREBRAG/Input/
cp ./INP/gm*.inp ./${Old_Analysis}/GENMESH/Input/
cp ./INP/ic*.inp ./${Old_Analysis}/ICSET/Input/
cp ./INP/ms*.inp ./${Old_Analysis}/MATSET/Input/
cp ./INP/lhs1*.inp ./${Old_Analysis}/PRELHS/Input/
cp ./INP/nut*.inp ./${Old_Analysis}/NUTS/Input/
cp ./INP/cusp*.inp ./${Old_Analysis}/CUTTINGS_S/Input/
cp ./INP/rel*.inp ./${Old_Analysis}/RELATE/Input/
cp ./INP/ccgf*.inp ./${Old_Analysis}/CCDFGF/Input/
cp ./INP/epu*.inp ./${Old_Analysis}/EPAUNI/Input/
cp ./INP/sum*.inp ./${Old_Analysis}/SUMMARIZE/Input/

# Move analysis files
./Scripts/moveAnalysisFiles.sh ${Old_Analysis} ${New_Analysis}

# Get run scripts
./Scripts/getRunScripts.sh ${New_Analysis}

# Install analysis files (inputs and run scripts)
./Scripts/installAnalysisFiles.sh ${New_Analysis} ${New_Tag}

# Run the analysis
#nohup ./run_${New_Analysis}.sh ${Old_Analysis} ${New_Analysis} &

^G Get Help      ^O WriteOut      ^R Read File     ^Y Prev Page     ^K Cut Text      ^C Cur Pos
^X Exit          ^J Justify       ^W Where Is      ^V Next Page     ^U UnCut Text    ^T To Spell
original editor: https://www.chiark.greenend.org.uk/~sgthorpe/nano/

```

CCDFGF Example Run A – Control File Change

Run the script to setup the analysis:

```
-bash-4.4$ ./setup_CCDF_DemoA.sh
```

After running the setup script, this is what the directory looks like:

```
-bash-4.4$ ls
Analyses          MyLoadedFiles    MySandboxes      Scripts
INP               MyRepositories   run_CCDF_DemoA.sh setup_CCDF_DemoA.sh
-bash-4.4$
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1-3 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKTO=/home/run_mast/GD/Analyses/$1 \
  EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKTO=/home/run_mast/GD/Analyses/$1 \
  LHS CCDFGF
# EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKTO=/home/run_mast/GD/Analyses/$1 \
  LHS CCDFGF
# EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKTO=/home/run_mast/GD/Analyses/$1 \
LHS CCDFGF
# EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKTO=/home/run_mast/GD/Analyses/$1 \
  LHS CCDFGF
# EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

Edit the run script.

Double check:

Number of replicates

Results database

CVSROOT directory

Parameter database

Which codes to run

```
GNU nano 2.0.9 File: run_CCDF_DemoA.sh
#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  LINKTO=/home/run_mast/GD/Analyses/$1 \
  LHS CCDFGF
# EPAUNI LHS BRAGFLO PANEL NUTS CUTTINGS_S BRAGFLO_DBR CCDFGF
```

CCDFGF Example Run A – Control File Change

3. Run the analysis

```
-bash-4.4$ ./run_CCDF_DemoA.sh CRA19 CCDF_DemoA
```

4. Check that it completed normally

Analysis Details

CCDF_DemoA executed by sbrunel

Code	Log	Input	Start Date	ElapsedTime	Progress	Status
CCDFGF	Log	Inp	2019-11-26 13:58:31	0:0:29	100%	Completed
LHS	Log	Inp	2019-11-26 13:58:10	0:0:0	100%	Completed
Code	Log	Input	Start Date	ElapsedTime	Progress	Status

CCDFGF Example Run B – Database Parameter Change

General steps are the same for each example:

1. Set up the new analysis in your user parameters database (ParamDB_sbr)
2. Set up the new analysis in your home directory
3. Run the analysis
4. View your results

CCDFGF Example Run B – Database Parameter Change

Set up the new analysis in your user parameters database (ParamDB_sbr)*

Export needed tables from ParamDB using CRA19 as a starting point:

- Analyses
 - This table defines the analysis in your database
- ParamAttributes
 - Adds the new parameter information to the database
- AnalysisToVersion
 - Connects the parameter version you want to use with your analysis

Change the necessary values

Re-import the tables into your user database

*Example software – Toad for MySQL (2017 v. 8.0.0.296)

Export Table - Analyses

This will happen exactly the same as the previous example.

1. Query the CRA19 analysis
2. Export the table as an Excel file
3. Add the new analysis in
4. Remove the CRA19 analysis
5. Import the table back into your user database

OR

1. Enter the analysis name directly into the database

Export Table - ParamAttributes

This export process is slightly different.

We only want to export the specific MATERIAL:PARAMETER entries for CRA19 that we want to change.

- We are using CRA19 for our query here because it is the most recent analysis
- Any parameter version should work.

For this example, that is GLOBAL:LAMBDAD (drilling rate, we're going to double it here)

****Note:**

You could add new parameters directly to the database, however parameters need specific information that may span multiple database entries (e.g. distribution information).

Copying and editing the existing parameter value ensures

- None of this information is missed.
- You can verify the parameter you are editing has a form that you expect it to (constant vs. distribution).

Export Table - ParamAttributes

ParamAttributes Query:

```
SELECT ParamAttributes.Material,
ParamAttributes.Property,
ParamAttributes.Version,
ParamAttributes.Attribute,
ParamAttributes.value,
ParamAttributes.EffectiveDate,
ParamAttributes.VersionNumber,
ParamAttributes.LastModified,
ParamAttributes.vString
FROM ParamDB.ParamAttributes ParamAttributes
WHERE      (ParamAttributes.Material = 'GLOBAL')
AND (ParamAttributes.Property = 'LAMBDAD')
AND (ParamAttributes.Version = 'CRA19')
```

Query Results:

Set 1									
	Material *	Property *	Version *	Attribute *	value *	EffectiveDate *	VersionNumber *	LastModified *	vString *
▶	GLOBAL	LAMBDAD	CRA19	Distribution	0	04/15/2019 12:00:00 AM	6	04/15/2019 4:07:08 PM	Constant
	GLOBAL	LAMBDAD	CRA19	Value	0.0099	04/15/2019 12:00:00 AM	6	04/15/2019 4:07:11 PM	

Update the Version, value, and VersionNumber fields to match your new analysis.

[illegible]

Export Table – ParamAttributes

Remove auto-populated fields.
Update the Version, value, and VersionNumber fields to match your new analysis.

G1

✕

✓

fx

VersionNumber

	A	B	C	D	E	F	G	H	I	J	K
1	Material	Property	Version	Attribute	value	EffectiveDate	VersionNumber	vString			
2	GLOBAL	LAMBDAD	CCDF_DemoB	Distribution	0	04/15/2019 12:00:00 AM	7	Constant			
3	GLOBAL	LAMBDAD	CCDF_DemoB	Value	0.0198	04/15/2019 12:00:00 AM	7				
4											
5											
6											
7											
8											
9											

Import the table back into your user copy of the ParamAttributes table.

Export Table – AnalysisToVersion

Query the table to retrieve all of the data used for the CRA19 analysis, as before.

Query for table AnalysisToVersion:

```
SELECT AnalysisToVersion.Analysis,  
       AnalysisToVersion.Material,  
       AnalysisToVersion.Property,  
       AnalysisToVersion.Version,  
       AnalysisToVersion.auto_num,  
       AnalysisToVersion.Code,  
       AnalysisToVersion.VersionNumber,  
       AnalysisToVersion.AnalysisRevision,  
       AnalysisToVersion.LastModified  
FROM ParamDB.AnalysisToVersion AnalysisToVersion  
WHERE (AnalysisToVersion.Analysis = 'CRA19')
```

Table - AnalysisToVersion

Remove auto-populate fields.

Change the Analysis name from CRA19 to your analysis name.

	A	B	C	D	E	F	G	H	I	J
1	Analysis	Material	Property	Version	Code	VersionNumber	AnalysisRevision			
2	CCDF_DemoB	AM	CAPHUM	CCA	BRAGFLO	1	0			
3	CCDF_DemoB	AM	CAPMIC	CRA19	BRAGFLO	3	0			
4	CCDF_DemoB	AM	CONCINT	CRA19	BRAGFLO	3	0			
5	CCDF_DemoB	AM	CONCMIN	CCA	BRAGFLO	1	0			
6	CCDF_DemoB	AM	PROPMIC	CRA19	BRAGFLO	3	0			
7	CCDF_DemoB	AM241	ATWEIGHT	CCA	BRAGFLO	1	0			
8	CCDF_DemoB	AM241	DECAYNRG	CRA19	BRAGFLO	1	0			
9	CCDF_DemoB	AM241	HALFLIFE	CCA	BRAGFLO	1	0			
10	CCDF_DemoB	AM241	INVCHD	CRA19	BRAGFLO	7	0			
11	CCDF_DemoB	AM241	INVRHD	CRA19	BRAGFLO	8	0			
12	CCDF_DemoB	BH_CREEP	CAP_MOD	CCA	BRAGFLO	1	0			
13	CCDF_DemoB	BH_CREEP	COMP_RCK	CCA	BRAGFLO	1	0			
14	CCDF_DemoB	BH_CREEP	KPT	CCA	BRAGFLO	1	0			
15	CCDF_DemoB	BH_CREEP	PC_MAX	CCA	BRAGFLO	1	0			
16	CCDF_DemoB	BH_CREEP	PCT_A	CCA	BRAGFLO	1	0			

Table - AnalysisToVersion

Search for the MATERIAL:PROPERTY that you are changing for this analysis.

1229	CCDF_DemoB	AM241	EPAREL	CCA	PRECCDFGF	1	0			
1230	CCDF_DemoB	AM241	HALFLIFE	CCA	PRECCDFGF	1	0			
1231	CCDF_DemoB	BLOWOUT	HREPO	CCA	PRECCDFGF	1	0			
1232	CCDF_DemoB	BOREHOLE	WUF	CRA19	PRECCDFGF	8	0			
1233	CCDF_DemoB	GLOBAL	FPICD	TBM	PRECCDFGF	2	0			
1234	CCDF_DemoB	GLOBAL	FPICM	TBM	PRECCDFGF	2	0			
1235	CCDF_DemoB	GLOBAL	LAMBDAD	CRA19	PRECCDFGF	6	0			
1236	CCDF_DemoB	GLOBAL	MINERT	CCA	PRECCDFGF	1	0			
1237	CCDF_DemoB	GLOBAL	ONEPLG	CRA19	PRECCDFGF	4	0			
1238	CCDF_DemoB	GLOBAL	PBRINE	CRA14_SEN4	PRECCDFGF	4	0			
1239	CCDF_DemoB	GLOBAL	PLGPAT	CCA	PRECCDFGF	1	0			
1240	CCDF_DemoB	GLOBAL	TA	CCA	PRECCDFGF	1	0			
1241	CCDF_DemoB	GLOBAL	THREEPLG	CRA19	PRECCDFGF	4	0			
1242	CCDF_DemoB	GLOBAL	TPICD	CCA	PRECCDFGF	1	0			
1243	CCDF_DemoB	GLOBAL	TPICM	CCA	PRECCDFGF	1	0			
1244	CCDF_DemoB	GLOBAL	TWOPLG	CRA19	PRECCDFGF	4	0			
1245	CCDF_DemoB	PU239	ATWEIGHT	CCA	PRECCDFGF	1	0			
1246	CCDF_DemoB	PU239	EPAREL	CCA	PRECCDFGF	1	0			

Table - AnalysisToVersion

Edit both version and VersionNumber fields to match the ParamAttributes entry.

Import this back into the AnalysisToVersion table.

1229	CCDF_DemoB	AM241	EPAREL	CCA	PRECCDFGF	1	0			
1230	CCDF_DemoB	AM241	HALFLIFE	CCA	PRECCDFGF	1	0			
1231	CCDF_DemoB	BLOWOUT	HREPO	CCA	PRECCDFGF	1	0			
1232	CCDF_DemoB	BOREHOLE	WUF	CRA19	PRECCDFGF	8	0			
1233	CCDF_DemoB	GLOBAL	FPICD	TBM	PRECCDFGF	2	0			
1234	CCDF_DemoB	GLOBAL	FPICM	TBM	PRECCDFGF	2	0			
1235	CCDF_DemoB	GLOBAL	LAMBDAD	CCDF_DemoB	PRECCDFGF	7	0			
1236	CCDF_DemoB	GLOBAL	MINERT	CCA	PRECCDFGF	1	0			
1237	CCDF_DemoB	GLOBAL	ONEPLG	CRA19	PRECCDFGF	4	0			
1238	CCDF_DemoB	GLOBAL	PBRINE	CRA14_SEN4	PRECCDFGF	4	0			
1239	CCDF_DemoB	GLOBAL	PLGPAT	CCA	PRECCDFGF	1	0			
1240	CCDF_DemoB	GLOBAL	TA	CCA	PRECCDFGF	1	0			
1241	CCDF_DemoB	GLOBAL	THREEPLG	CRA19	PRECCDFGF	4	0			
1242	CCDF_DemoB	GLOBAL	TPICD	CCA	PRECCDFGF	1	0			
1243	CCDF_DemoB	GLOBAL	TPICM	CCA	PRECCDFGF	1	0			
1244	CCDF_DemoB	GLOBAL	TWOPLG	CRA19	PRECCDFGF	4	0			
1245	CCDF_DemoB	PU239	ATWEIGHT	CCA	PRECCDFGF	1	0			
1246	CCDF_DemoB	PU239	EPAREL	CCA	PRECCDFGF	1	0			

Create the directory structure

Starting directory: /home/sbrunel/Analyses/

```
-bash-4.4$ mkdir CCDF_DemoB
-bash-4.4$ cd CCDF_DemoB/
-bash-4.4$ cp -r /home/sbrunel/run_scripts/* .
-bash-4.4$ mv setup_CRA19.sh setup_CCDF_DemoB.sh
-bash-4.4$ mv run_CRA19.sh run_CCDF_DemoB.sh
```

This is what the directory looks like:

```
-bash-4.4$ pwd
/home/sbrunel/Analyses/CCDF_DemoB
-bash-4.4$ ls
INP                run_CCDF_DemoB.sh  Scripts            setup_CCDF_DemoB.sh
-bash-4.4$ █
```

Edit the Input File(s)

Since we are using the same input files as CRA19, there is nothing to do in this step.

Setup the new analysis

Edit the header information in the file `setup_CCDF_DemoB.sh` and run the script.

```
GNU nano 2.0.9                                File: setup_CCDF_DemoB.sh

#!/bin/sh
# syntax ./setup_Analysis &

# CCDF_DemoB Rev. 0 - CCDFGF EPA Demo B - Database Parameter Change

# Define analysis names and tags
New_Analysis="CCDF_DemoB"
New_Tag="CCDF_DemoB Rev. 0"
Old_Analysis="CRA19"

# Get old analysis files
./Scripts/getAnalysisFiles.sh ${Old_Analysis}

# Rename old analysis file names to new
./Scripts/renameAnalysisFiles.sh ${Old_Analysis} ${New_Analysis}
```

Run the new analysis

Edit and execute the run script (run all 3 replicates this time):

```
GNU nano 2.0.9 File: run_CCDF_DemoB.sh

#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1-3 -b=1-5 -rdb=PA_Results_sbr \
    -Descrip="$2 R0" \
    -LegTitle="$2" \
    -R=0 \
    -AnalRev=0 \
    -CVSROOT=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
    -db=ParamDB_sbr \
    -LHSanalysis=$2 \
    -LHSRev=0 \
    -RDBkey=$2 \
    -VER=LOG_PULLS \
    -Ranalysis=$2 \
    -Revision=0 \
    -LINKTO=/home/run_mast/GD/Analyses/$1 \
LHS CCDFGF
```

CCDFGF Post-Processing Results

Look at Example Run B – Database parameter change (GLOBAL:LAMBDAD)

The results of this run are stored in the database specified in the run script:

```
GNU nano 2.0.9                                File: run_CCDF_DemoB.sh

#!/bin/sh
# syntax nohup ./run_Analysis Old_Analysis New_Analysis &
# Run the analysis
id
$CVSLIB/bin/Run.py True $2 -r=1-3 -b=1-5 -rdb=PA_Results_sbr \
  -Descrip="$2 R0" \
  -LegTitle="$2" \
  -R=0 \
  -AnalRev=0 \
  -CVSR00T=/home/sbrunel/Analyses/$2/MyRepositories/$2 \
  -db=ParamDB_sbr \
  -LHSanalysis=$2 \
  -LHSRev=0 \
  -RDBkey=$2 \
  -VER=LOG_PULLS \
  -Ranalysis=$2 \
  -Revision=0 \
  -LINKT0=/home/run_mast/GD/Analyses/$1 \
  LHS CCDFGF
```

CCDFGF Post-Processing Results

Raw results are stored in the table “CCDF_Data”

- Used for horsetail plots

Replicate statistics are stored in the table “StatsAcrossReplicates”

Vector statistics are stored in the table “StatsAcrossVectors”

Use a python script (or other plotting device of your choice) to access the database and produce final plots.

CCDFGF Post-Processing Results

Need to be able to visualize data in various ways

- Horesetails
- Vector means
- Replicate means

By contribution

- By release mechanism
- By radionuclide
- Release volumes vs. total contribution

Current Script:

- Written in python 2.7
- Type of plot is a command-line input
- Variable to be plotted is an input file

CCDFGF Post-Processing Results

C:\Users\sbrunel\Documents\EPA-PA-Training\Ad Hoc Calc Slides\DemoB-Plots\ccdfplotfromdb.py - Notepad++

File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?



ccdfplotfromdb.py x runit.bat x

```

1  """ CCDFPlotFromDB.py - post-processing statistics and plotting script for ccdf database data
2      Coded by: Brad Day, SANDIA
3      Date: 5/8/2018
4      Description:
5
6      Command Line: python ccdfpostdb.py -d databases -u usernames -p passwords
7      -i inputfile -o outputfile -r "1 2 3" -a 0,1,...,8 -l 0,1,...,10 -f filename
8
9  """
10 # avgflag = (0 = none (horsetails), 1 = over vectors, 2 = over replicates,
11 # 3 = 0,1, 4 = 0,2, 5 = 1,2, 6 = 0,1,2, 7 = 2 with confidence limits,
12 # 8 = 7 with table), 10 = all mean release components for each analysis
13
14
15 import MySQLdb as mdb
16 import numpy as np
17 import matplotlib.pyplot as plt
18 import matplotlib.ticker as ticker
19 import matplotlib as mpl
20 from matplotlib.ticker import FormatStrFormatter
21 import argparse
22 import csv
23
24
25 def main():
26 #
27 # Read command line arguments
28 parser = argparse.ArgumentParser(description='CCDF Plot From DB')
29 parser.add_argument('-d', '--database', help='Database names', required=True)
30 parser.add_argument('-u', '--username', help='User names', required=True)
31 parser.add_argument('-p', '--password', help='Passwords', required=True)
32 parser.add_argument('-i', '--input', help='Analysis names', required=True)
33 parser.add_argument('-v', '--version', help='Analysis versions', required=False)
34 parser.add_argument('-o', '--output', help='Output file name', required=True)
35 parser.add_argument('-l', '--replicate', help='Replicate numbers', required=True)

```

CCDFGF Post-Processing Results

vars-2.txt - Notepad

File Edit Format View Help

```
Cuttings and Cavings,TRUE
Spallings,TRUE
Direct Brine,TRUE
Total From Culebra,TRUE
Total To Culebra,FALSE
Total,TRUE
```

*C:\Users\sbrunel\Documents\EPA-PA-Training\Ad Hoc Calc Slides\DemoB-Plots\runit.bat - Notepad++

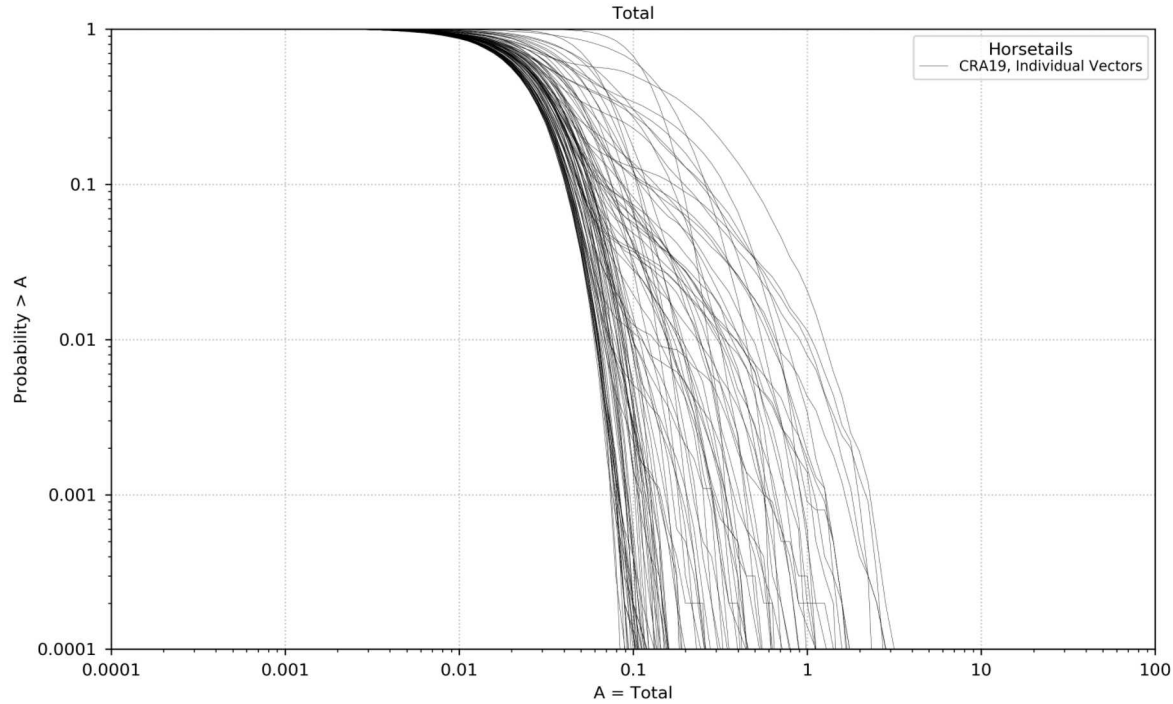
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?



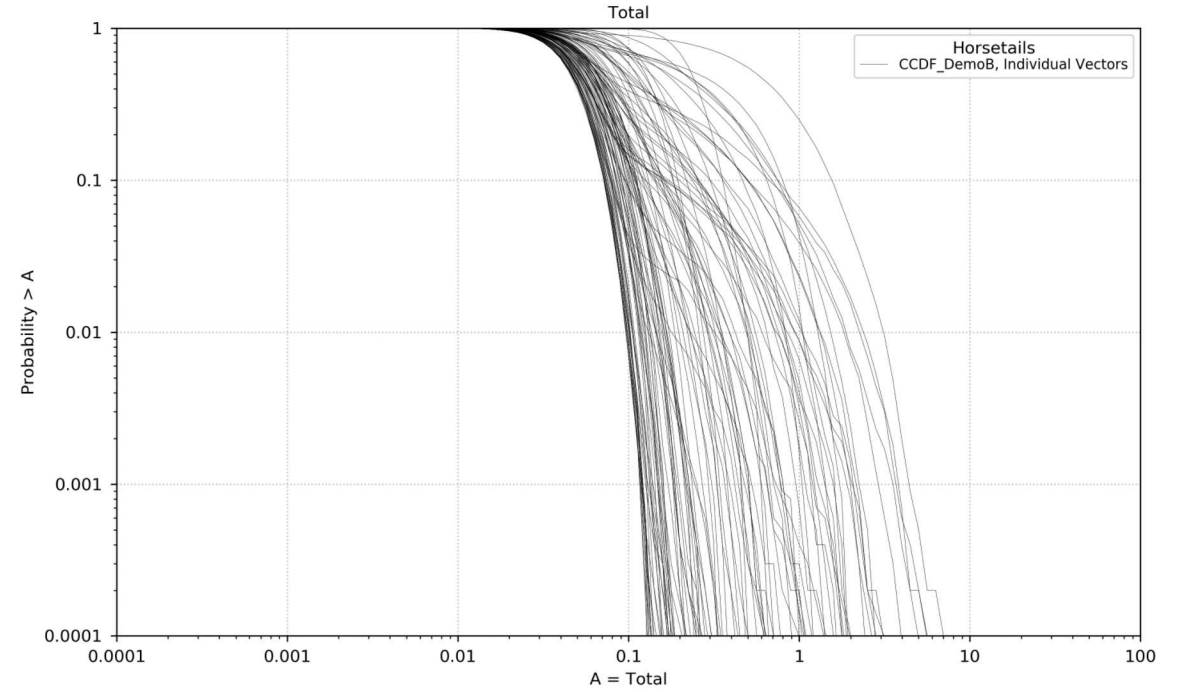
runit.bat

```
1 REM Create horsetail plots
2 python CCDFPlotFromDB.py -d "PA_Results" -u "public public" -p "public public" -i "CRA19" -o "1-CRA19_r1" -r "1" -a "0" -f "vars-1.txt" -l "1"
3 python CCDFPlotFromDB.py -d "PA_Results_sbr" -u "public public" -p "public public" -i "CCDF_DemoB" -o "1-DemoB_r1" -r "1" -a "0" -f "vars-1.txt" -l "1"
4
5 REM Replicate means with confidence limits
6 python CCDFPlotFromDB-fix_color.py -d "PA_Results PA_Results_sbr" -u "public public" -p "public public" -i "CRA19 CCDF_DemoB" -o "4-CRA19_DemoB" -r "1 2 3" -a "7" -f "vars-2.txt" -l "3"
7
8 REM Volumes - long x-axis
9 python CCDFPlotFromDB-volumes.py -d "PA_Results PA_Results_sbr" -u "public public" -p "public public" -i "CRA19 CCDF_DemoB" -o "5-CRA19_DemoB" -r "1 2 3" -a "2" -f "vars-3.txt"
10
11
12
```

CCDFGF Example Run 2 Results

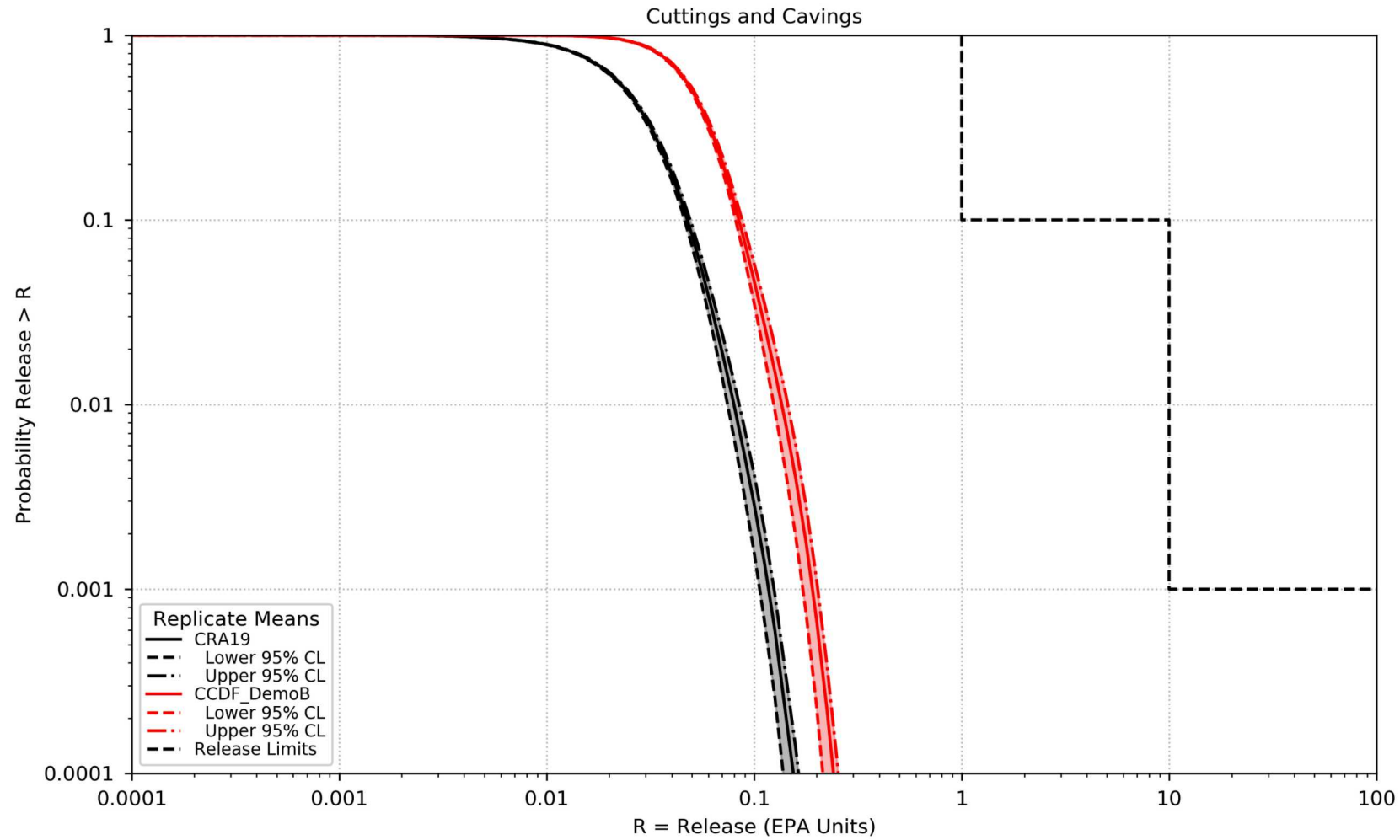


CRA19 Results

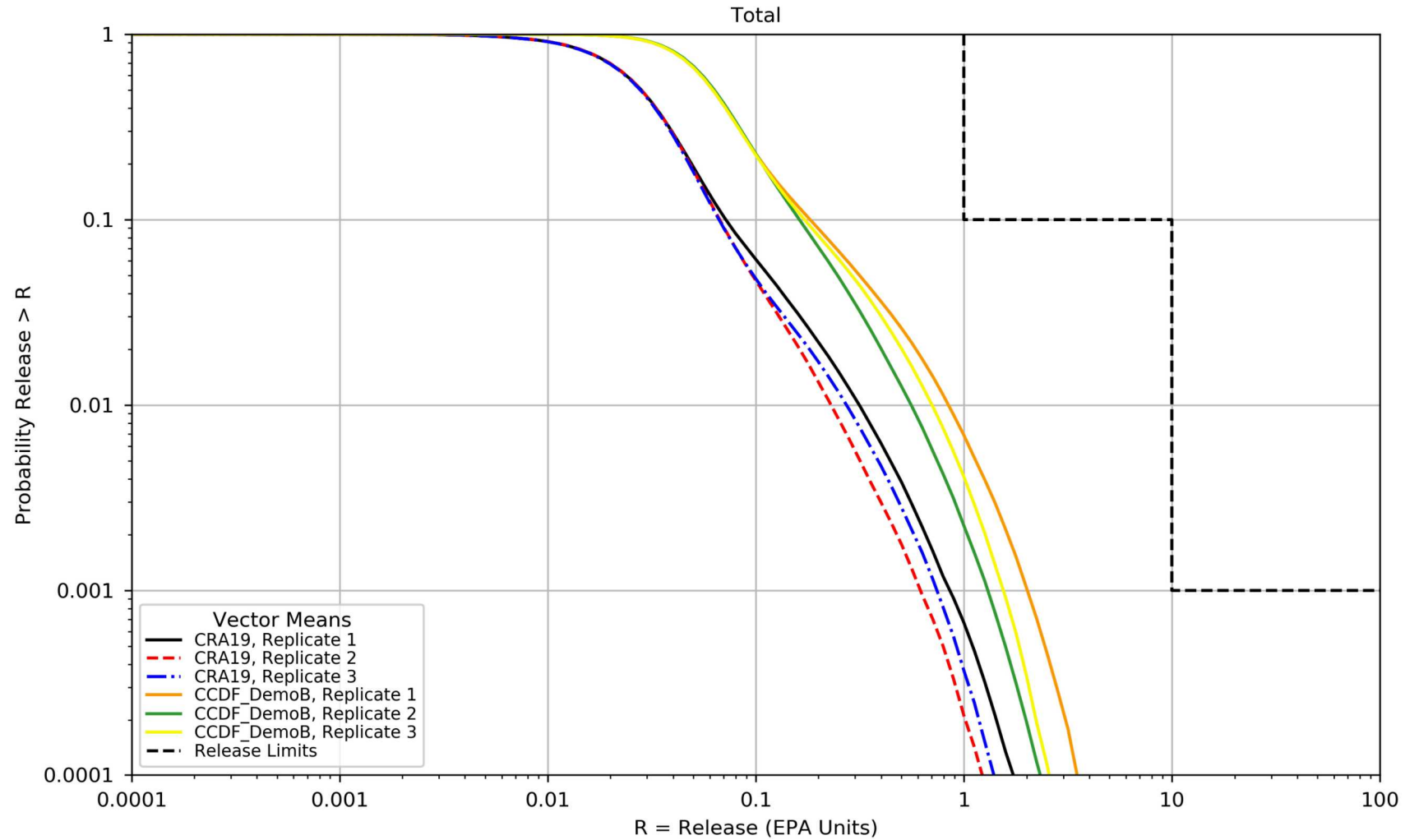


CCDF_DemoB Results

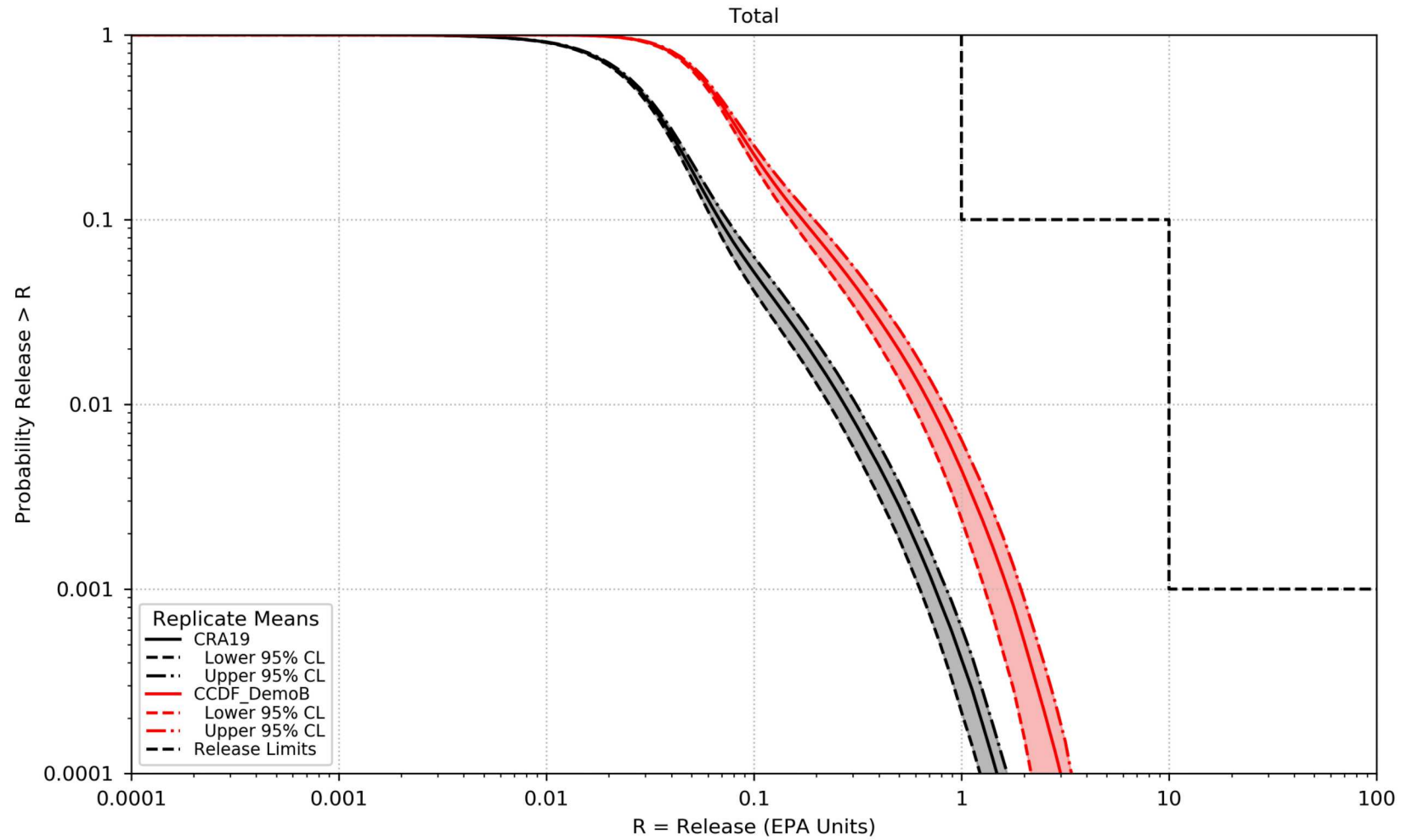
CCDFGF Example Run 2 Results



CCDFGF Example Run 2 Results

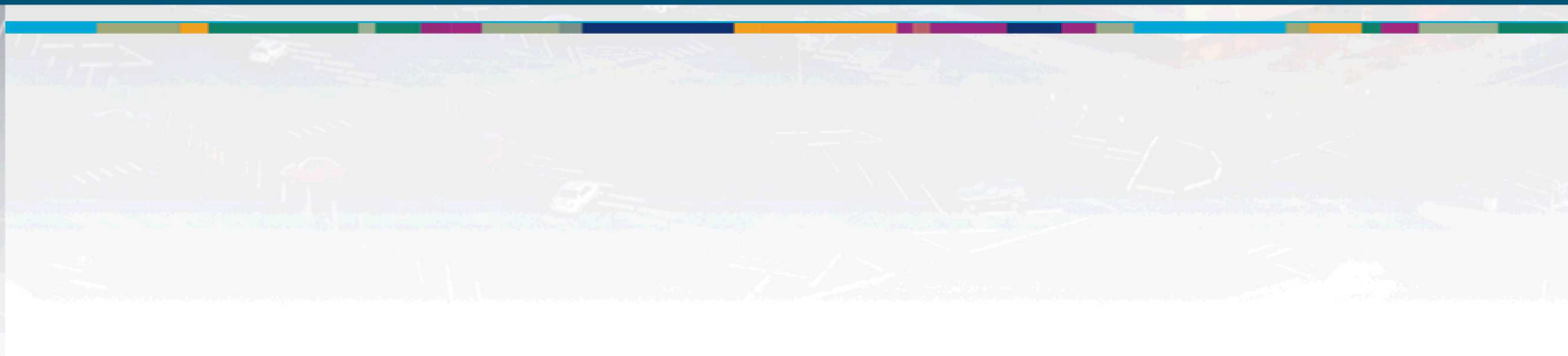
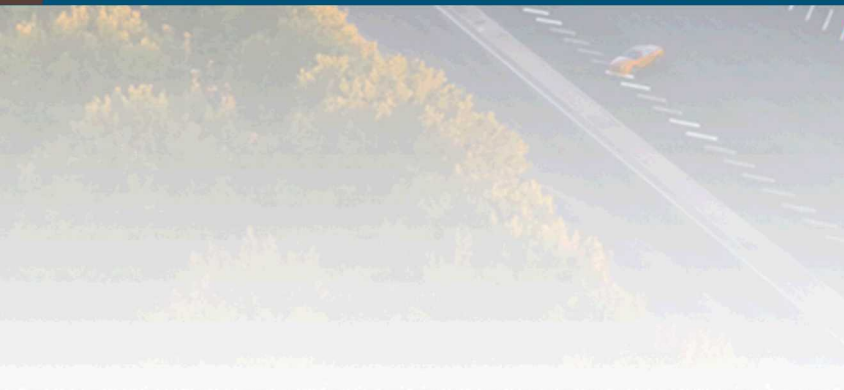


CCDFGF Example Run 2 Results





CCDFGF – Control File



CCDFGF – Control File

User-generated input file

Controls execution of CCDFGF

One file per replicate

- e.g. ccgf_CRA19_control_r1.inp
- Each has a unique random number generator seed

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19 replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Analysis Name

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1       NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000      NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000    SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000    BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832    RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Replicate Number

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F          1000 SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F          1000 BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Number of CH and RH waste streams to average per intrusion

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2        OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2        FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000      NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Number of intrusions to
deplete brine pocket
- Set high
(no depletion occurs)

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Number of panels (max 10)

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Panel Number

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
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340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUND OFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
F          Write summary statistics
F          Export the mean and median across observations within frequency (Y)
0          Number of order statistics to be exported
1 7 8      The order statistics to be exported
0          Number of result-histogram minimum and maximum override values (X-axis)
10         Number of panels followed by Panel number, group, probability and neighbors
1 U 0.10439087 10
2 U 0.10439087 10
3 M 0.10439087 04 05 06 09 10
4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Panel Group (lower, middle, upper)

Low impact on CCDFGF

- Only Spallings, DBR releases
- First intrusion only

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
1000       NUMBER OF INTRUSIONS TO DEplete EACH BRINE POCKET
F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
340832     RANDOM NUMBER GENERATOR SEED
1.0E-6     RELATIVE ROUNDOFF TOLERANCE
0          Generate only(0), read(1) or store(2) random numbers
T          Use repository-scale concentrations for spalling calculations
F          Use volume fraction as probability for release of cuttings
T          Write the binned distribution data to a file
F          Write tables of the sorted results
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4 M 0.10439087 03 05 06 09 10
5 L 0.10439087 03 04 06 09 10
6 M 0.10439087 03 04 05 09 10
7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Probability of Intrusion

Defined by
Panel Volume/Repository Volume

CCDFGF – Control File

```

CCDFGF Control Input file for CRA19, replicate 1
(SECOND TITLE RECORD)
10000      NUMBER OF FUTURES PER OBS
2          NUMBER OF OBSERVATION FOR DETAILED PRINT
1 2       OBSERVATION INDICE
2          NUMBER OF FUTURES FOR DETAILED PRINT
1 2       FUTURES INDICES
10000.     END TIME (YR)
F          Simulate variable borehole diameters
0.3111 0.3111 0.3111 BOREHOLE DIAMETER RANGE AND MODE ABOVE REPOSITORY (M)
3 1        NUMBER OF WASTE STREAMS TO AVG FOR CH WASTES AND RH WASTES
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F 1000     SPALLINGS REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
F 1000     BLOWOUT REFERENCE (T=AFTER E1) AND NUMBER OF INTRUSIONS
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7 U 0.10439087 10
8 U 0.10439087 10
9 M 0.07910030 03 04 05 06 10
10 U 0.08577271 01 02 03 04 05 06 07 08 09

```

Panel Neighbors

CRA19:
One or fewer panel closures
separating them