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subject: Impact analysis for the software problem report SPR 22-001 for PRELHS Version 2.45

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1. Introduction

This memorandum documents the impact of the issues described in SPR 22-001 (Sandia National Laboratories, 2022) for PRELHS Version 2.45 (Feng, 2021) on release estimates reported in CRA-2019.

PRELHS is used in WIPP Performance Assessments (PA) to read probability distributions from the parameter database ParamDB and write them to an output transfer file. The probability distributions describe so-called subjective uncertainty in the parameters input to WIPP PA (Helton, 1998). The PRELHS output transfer file is read by the PA code LHS. LHS uses Latin hypercube sampling to sample the distribution for each parameter. LHS places the samples into vectors, a single vector containing one sample from each input parameter. The LHS sample size, usually 100, forms a group of vectors called a replicate. LHS writes the replicates to the database PA_Results. A typical run of PA comprises 3 replicates and thus a total of 300 vectors.

The issues described in SPR 22-001 concern user-supplied cumulative probability distributions. Statement of facts:

(1) PRELHS expects user-supplied cumulative probability distributions to begin at cumulative probability zero and end at cumulative probability one. Several distributions in CRA-2019 began with a probability greater than zero. As a result, LHS incorrectly sampled these distributions. While in most cases sampling errors were small, a few parameter samples were significantly affected. The parameters concerned are: SOLMOD3:SOLVAR, SOLMOD4:SOLVAR, and GLOBAL:PBRINE.

(2) PRELHS may read user-supplied cumulative distribution entries from the database in an incorrect order if parameter values are repeated. Probability increments between samples read in the wrong order may then be computed as negative. Following a negative probability increment, some LHS samples may be incorrect. In CRA-2019 this occurred only for the parameter STEEL:CORRMCO2 and errors in the LHS samples were negligible.

These issues are addressed in PRELHS Version 2.46. If a user supplied distribution does not start at probability zero, or does not end at probability one, then PRELHS Version 2.46 aborts. To ensure that distributions are obtained in the correct order, PRELHS Version 2.46 retrieves entries from the database by OrderIndex rather than by (parameter) Value as in previous versions. As a final check, PRELHS Version 2.46 aborts if a negative cumulative probability increment is detected.

This memorandum documents the impact on CRA-2019 releases of correcting the distributions for SOLMOD3:SOLVAR, SOLMOD4:SOLVAR, and GLOBAL:PBRINE. By utilizing PRELHS Version 2.46, the impact assessment described here also includes the effects of reading the distribution for STEEL:CORRMCO2 in the correct order. The corrections were implemented in a new analysis named LHS_IMP. The only other difference between LHS_IMP and CRA-2019 is that LHS_IMP was run on WIPP's Linux cluster, while CRA-2019 was run on Solaris. The migration to Linux did not significantly change the results (Long and King, 2022).

The next section provides a brief review of how PRELHS and LHS manipulate user-supplied cumulative distributions. Section 3 then gives the distributions in question as input to CRA-2019 and Section 4 the corrected distributions input to LHS_IMP. Section 5 compares sample values for the two SOLVARs, which are the parameters most affected by the changes mentioned above. Releases are discussed in Section 6 and the report concludes with a brief summary and impact assessment.

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2. User-supplied cumulative distributions in PRELHS and LHS

A user-supplied cumulative probability distribution is described in ParamDB as a list of parameter values and corresponding cumulative probabilities, say (V_i, P_i), where i varies between 1 and the number of points, N, in the distribution. After retrieving the distribution from the database, PRELHS forms probability increments dP_i:

$$dP_i = P_{i+1} - P_i \quad , i = 1, \ldots, N-1 \quad . \tag{1}$$

An N_{th} increment, dP_N, is set to zero. PRELHS then writes (V_i, dP_i), i varying from 1 to N, to the transfer file for input to LHS. Reading the transfer file, LHS first sets the starting probability to zero and then seeks to re-form the remainder of the original distribution by summing the probability increments. Note that this approach will be successful only if the original distribution had $P_1 = 0$. Code LHS assumes this to be the case, as well as $P_N = 1$; both are necessary for successful Latin hypercube sampling. Figure 1 sketches the case where the starting probability in the database distribution is greater than zero. The cumulative distribution reconstructed by LHS in this case is shifted down by an amount P_1 compared to the original distribution.

A separate issue occurs where a cumulative distribution has repeated parameter values and the values are retrieved in the wrong order. If correctly entered, the database version of the distribution has $P_{i+1} \geq P_i$ and $V_{i+1} \geq V_i$. If, for example, $V_{i+1}=V_i$ and the points are retrieved in reverse order, then clearly a negative probability increment can be generated. Where this is the case, the cumulative distribution re-formed by LHS will be shifted down after the negative probability increment. The error is corrected immediately following the repeated parameter values, that is, as soon as the retrieval of points in the correct order is resumed.

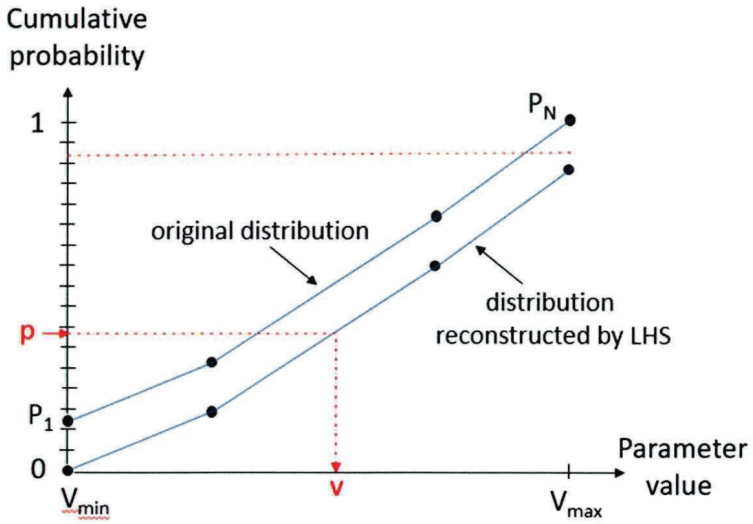

Figure 1. Cumulative probability distribution with nonzero starting probability and LHS reconstruction

To implement Latin hypercube sampling, code LHS divides the cumulative probability range [0,1] into N_V equal-sized intervals, where N_V is the number of vectors in a replicate. Within each interval, LHS generates a uniformly random probability and then interpolates the corresponding parameter value. The interpolated parameter value is placed into one of the N_V parameter vectors. Figure 1 shows the process when the cumulative distribution has a starting probability greater than zero: random cumulative probability p yields interpolated parameter value v, which is larger than would be obtained from the

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original distribution. Note also that the maximum cumulative probability for the LHS reconstructed distribution is equal to $P_N - P_1$. As a consequence, interpolation will fail outright at cumulative probabilities greater than $P_N - P_1$, as sketched in the figure. Interpolations at high cumulative probabilities are associated with the largest parameter values.

3. CRA-2019 Distributions

ParamDB's CRA-2019 distributions for parameters SOLMOD3:SOLVAR, SOLMOD4:SOLVAR, GLOBAL:PBRINE and STEEL:CORRMCO2 are reproduced in Table 1 below. Only points near the start and end of the distributions are shown, as well as a few interior points in the case of STEEL:CORRMCO2. (See Appendix A for the full distributions for SOLMOD3:SOLVAR, SLOMOD4:SOLVAR and GLOBAL:PBRINE.) Note that the first three distributions do not start with cumulative probability zero and that two of the parameter values shown for STEEL:CORRMCO2 are the same. The quantity N in the table is the total number of points in each distribution.

Table 1. Cumulative probability distributions for analysis CRA-2019

SOLMOD3:SOLVAR		SOLMOD4:SOLVAR		GLOBAL:PBRINE		STEEL:CORRMCO2	
N = 82		N = 44		N = 54		N = 125	
Value	Prob	Value	Prob	Value	Prob	Value	Prob
-1.14251	0.0122	-2.0098	0.0227	0.04	0.002	0.000000000000000634	0
-0.932358	0.02439	-1.4885	0.0455	0.05	0.004	0.000000000000000761	0.008065
-0.875954	0.03659	-1.3031	0.0682	0.06	0.006	0.00000000000000184	0.016129
-0.805676	0.04878	-1.0158	0.0909	0.07	0.014		
-1.14251	0.0122	-0.9475	0.1136	0.08	0.023		
						0.00000000000000831	0.314516
…		…		…		0.00000000000000837	0.322581
						0.00000000000000837	0.330645
2.343682	0.9512	0.8897	0.9091	0.53	0.993		
2.372998	0.9634	1.1567	0.9318	0.54	0.997		
2.627935	0.9756	1.2526	0.9545	0.55	0.998	0.0000000000000566	0.983871
2.683488	0.9878	1.2953	0.9773	0.56	0.999	0.0000000000000659	0.991935
2.971474	1	1.4266	1	0.57	1	0.0000000000000792	1

Figure 2 plots the four CRA-2019 database distributions as well as their reconstructions by program LHS. Shifts in the cumulative distributions are clearly visible for the SOLVAR parameters; it should also be noted that the SOLVARs are logarithmic quantities so that even small shifts in value may be significant. For GLOBAL:PBRINE, the starting probability of 0.002 causes a shift that is just noticeable in the figure, while any discrepancies between database and reconstructed versions of the STEEL:CORRMCO2 distribution are not visible at all.

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For SOLMOD3:SOLVAR the largest cumulative probability in the reconstructed distribution is 0.9878[1]; the procedure for interpolating a parameter value will thus fail for cumulative probability interval 0.99-1.0, and may fail for interval 0.98-0.99[2]. Interpolation failures will occur in all replicates. For SOLMOD4:SOLVAR the maximum reconstructed cumulative probability is 0.9773: interpolation will thus fail in two intervals, and possibly three, for SOLMOD4:SOLVAR. For GLOBAL:PBRINE the maximum reconstructed cumulative probability is 0.998: interpolation will thus fail in at most one interval for GLOBAL:PBRINE. The STEEL:CORRMCO2 distribution begins at probability zero and has a reconstructed maximum of 0.99967; the discrepancy here is caused by numerical round-off and is unlikely to bring about an interpolation failure.

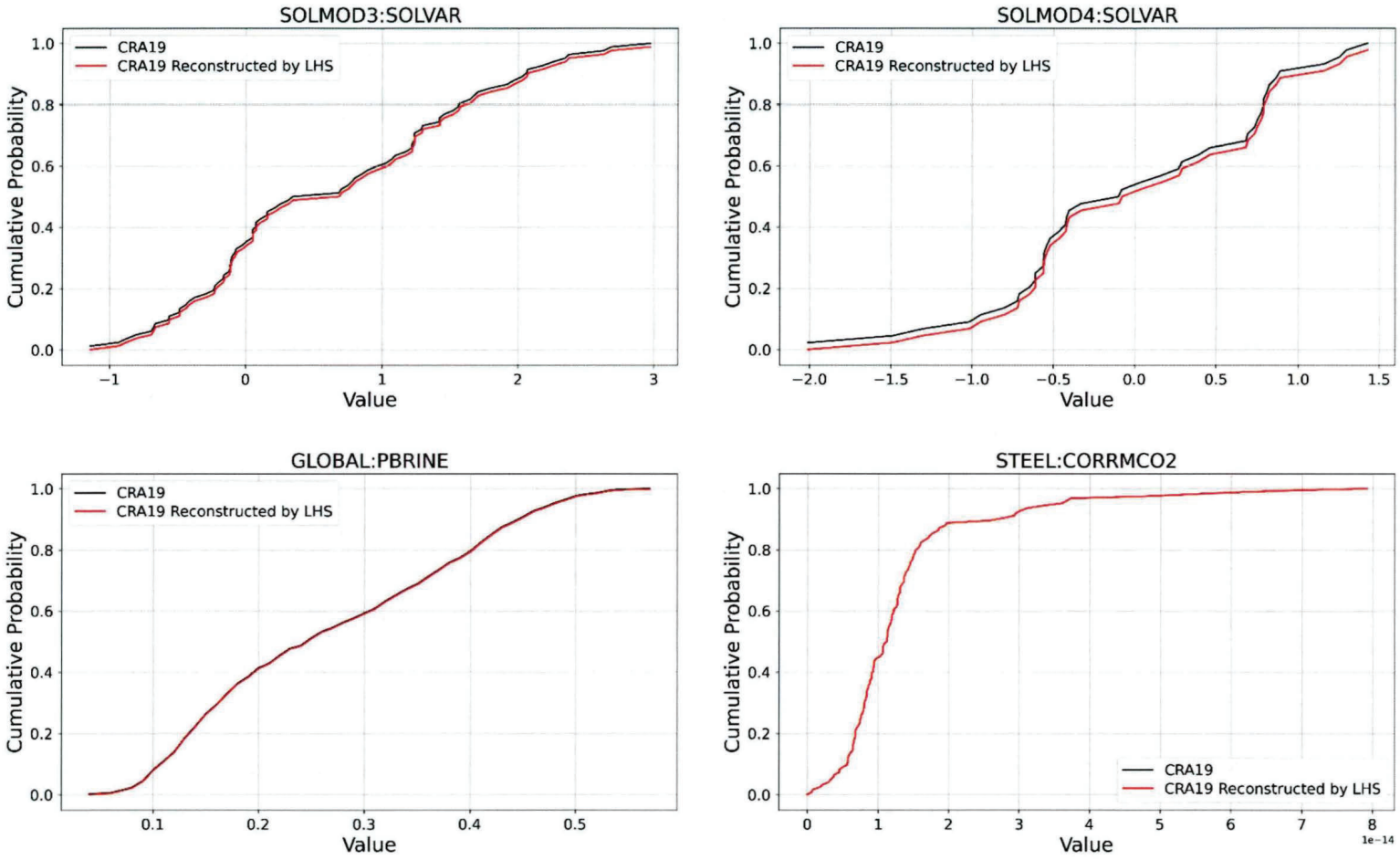

Figure 2. Cumulative distributions input to CRA-2019 (black) and the distributions reconstructed by LHS (red).

4. LHS_IMP Distributions

Subsets of the four distributions as input to Analysis LHS_IMP are shown in Table 2. (See Appendix A for full distributions of both SOLVARs and GLOBAL:PBRINE.) The SOLVAR distributions have the same number of points and the same parameter values as in CRA-2019, but they now start at probability

[1] P_N-P_1

[2] The Latin hypercube sampling interval is 0.01, that is $1/N_V$, where N_V=100.

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zero and have probability increment 1/(N−1). For GLOBAL_PBRINE, a point with cumulative probability zero has been inserted into the beginning of the distribution; otherwise, this distribution is unchanged. The distribution for STEEL:CORRMCO2 is the same for analyses CRA-2019 and LHS_IMP: changes made to PRELHS Version 2.46 mean that it will be read in the correct order for LHS_IMP. All four distributions start at probability zero and end at probability one.

Table 2. Cumulative probability distributions for analysis LHS_IMP

SOLMOD3:SOLVAR		SOLMOD4:SOLVAR		GLOBAL:PBRINE		STEEL:CORRMCO2	
N = 82		N = 44		N = 55		N = 125	
Value	Prob	Value	Prob	Value	Prob	Value	Prob
-1.14251	0	-2.0098	0	0.04	0	0.000000000000000634	0
-0.932358	0.012346	-1.4885	0.023256	0.04	0.002	0.000000000000000761	0.008065
-0.875954	0.024691	-1.3031	0.046512	0.05	0.004	0.00000000000000184	0.016129
-0.805676	0.037037	-1.0158	0.069767	0.06	0.006		
-0.694681	0.049383	-0.9475	0.093023	0.07	0.014		
						0.00000000000000831	0.314516
…		…		…		0.00000000000000837	0.322581
						0.00000000000000837	0.330645
2.343682	0.950617	0.8897	0.906977	0.53	0.993		
2.372998	0.962963	1.1567	0.930233	0.54	0.997		
2.627935	0.975309	1.2526	0.953488	0.55	0.998	0.0000000000000566	0.983871
2.683488	0.987654	1.2953	0.976744	0.56	0.999	0.0000000000000659	0.991935
2.971474	1	1.4266	1	0.57	1	0.0000000000000792	1

Figure 3 below compares the distributions input to CRA-2019 with the distributions input to LHS_IMP. The CRA-2019 distributions in Figure 3 are the same as in Figure 2.

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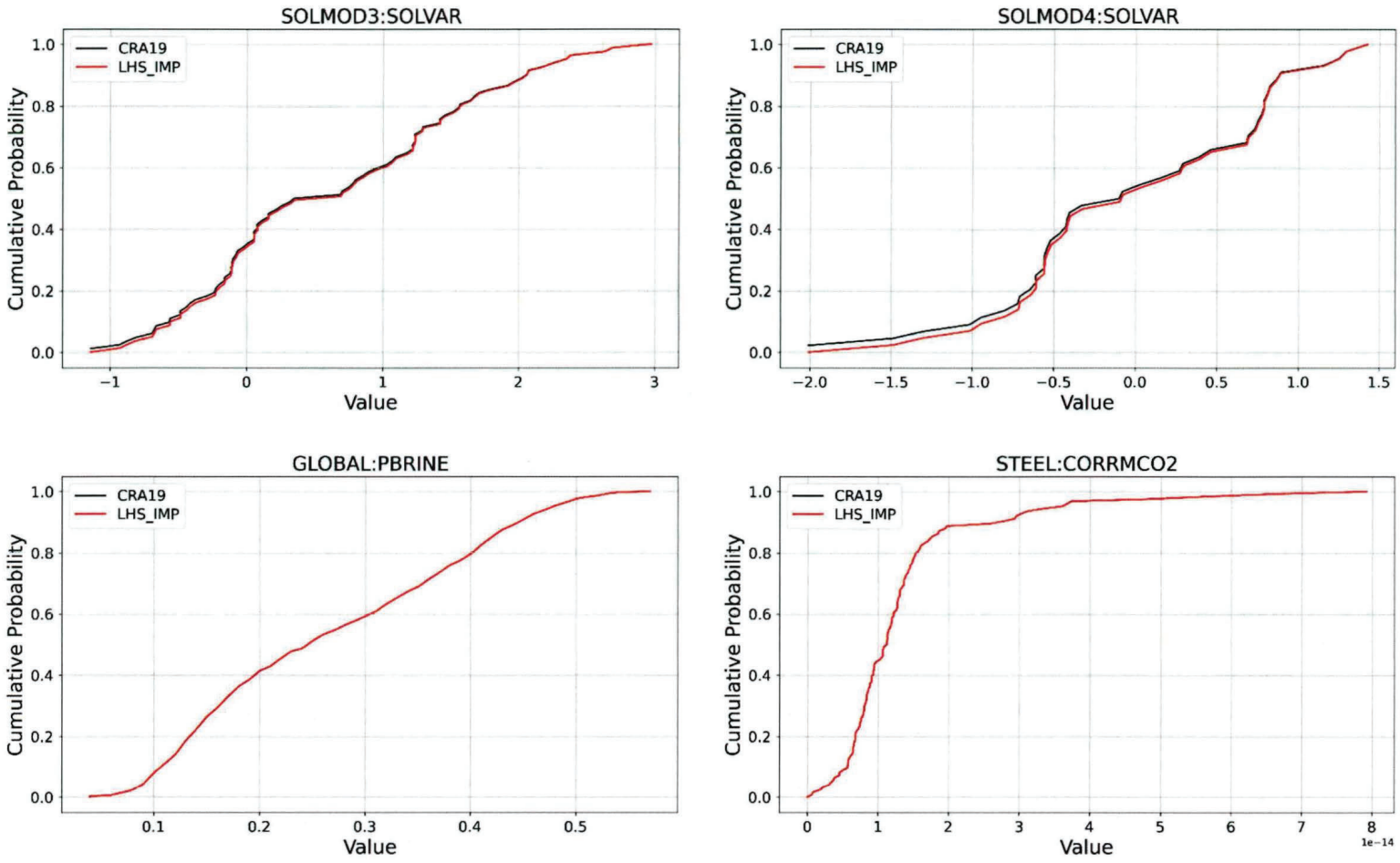

Figure 3. Cumulative distributions input to CRA-2019 (black) and LHS_IMP (red)

5. Latin Hypercube Sampling in CRA-2019 and LHS_IMP

Latin hypercube sampling of the SOLVAR distributions is shown in Figure 4. The samples plotted in black are from the three CRA-2019 replicates. As discussed above, samples are drawn from distributions that have been reconstructed by code LHS. The samples plotted in black in Figure 4 are drawn from the distribution labeled "CRA19 Reconstructed by LHS" in Figure 2.

The SOLVAR samples for analysis LHS_IMP are shown in red Figure 4. Because of the corrections discussed above, as well as changes to code PRELHS, input and LHS-reconstructed distributions are identical in analysis LHS_IMP. Samples shown in red in Figure 4 are thus drawn from the SOLVAR distributions labeled "LHS_IMP" in Figure 3.

Figure 4 indicates that where code LHS successfully interpolated a sample, the SOLVAR samples are mostly just slightly less for LHS_IMP compared to CRA-2019. The few large discrepancies occur where interpolation failed, that is, at high probabilities for both SOLVARs in CRA-2019. Where a failure occurred, code LHS output a parameter value of zero. The zeros can be seen in all three CRA-2019

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replicates in Figure 4. Note from the figure that the zeros replace what should have been high parameter values.[3]

There were no LHS interpolation failures in CRA-2019 for either GLOBAL:PBRINE or STEEL:CORRMCO2. As might be anticipated from Figures 2 and 3, Latin hypercube samples for these parameters are virtually identical in CRA-2019 and LHS_IMP and are not reproduced here.

6. Impact on releases

Curves of mean total releases for analyses CRA-2019 and LHS_IMP are compared in Figure 5. The means for each analysis are the result of averaging over all three replicates. The figure shows small increases in mean total releases at low probabilities for LHS_IMP compared to CRA-2019. Contributing to total releases are direct brine releases, or DBRs, releases to the Culebra, spallings, and cuttings and cavings. Mean curves for DBRs are plotted in Figure 6; the other contributors to total releases are almost identical for CRA-2019 and LHS_IMP and are not shown here. Comparing Figures 5 and 6, increases in total releases in analysis LHS_IMP are attributable to increases in DBRs.

DBRs occur following a borehole intrusion into the repository. DBRs are calculated as the product of two quantities: (i) the volume of brine released from the repository up the borehole; and (ii) the concentration of radionuclides within the brine at the time of the intrusion. Using a stepwise regression analysis, Zeitler (2019) showed that the dominant parameter impacting DBRs in CRA-2019 is SOLMOD3:SOLVAR. Further, the regression coefficient is positive, indicating that increases in SOLMOD3:SOLVAR tend to produce increases in DBRs. SOLMOD3:SOLVAR is used in PA to determine an uncertainty factor that multiples baseline solubilities for actinides having oxidation state +III. In fact, the baseline solubility multiplier is $10^{\text{SOLMOD3:SOLVAR}}$; small changes in SOLMOD3:SOLVAR can thus bring about significant changes in the concentration of radionuclides in repository brine. Zeitler (2019) used stepwise regression to further show that SOLMOD3:SOLVAR does not impact variability in DBR volumes. In summary, total release differences between CRA-2019 and LHS_IMP are driven by differences in DBRs; SOLMOD3:SOLVAR is the dominant parameter controlling DBRs; SOLMOD3:SOLVAR affects DBRs by changing the concentration of radionuclides in the brine released from the repository, not by changing the volume of brine flowing up the borehole.[4]

From the left side of Figure 4, most of the sampled values for SOLMOD3:SOLVAR are either slightly less, or about the same, for LHS_IMP compared to CRA-2019. On the other hand, a small number of zero values brought about by interpolation failures in CRA-2019 are replaced in LHS_IMP by parameter values approaching SOLMOD3:SOLVAR's maximum; for these samples, the solubility multiplier will increase by more than two orders of magnitude in LHS_IMP. This tradeoff between a large number of small decreases to SOLMOD3:SOLVAR, versus a small number of large increases, determines how mean releases for LHS_IMP compare to those in CRA-2019.

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[3] In Figure 4, cumulative probability increments uniformly, first for the points that were successfully interpolated and then for the points where interpolation failed. The starting cumulative probability in the figure is 0.01 and the probability increment is also 0.01. Interpolation failures were detected as parameter values equal to zero; the failures are known to occur at the highest probabilities and to be associated with the largest parameter values.

[4] Zeitler's (2019) stepwise analysis also identifies STEEL:CORRMCO2 and GLOBAL:PBRINE as parameters affecting DBRs; however, their impacts are secondary compared to SOLMOD3:SOLVAR and changes affecting their distributions in analysis LHS_IMP are minor.

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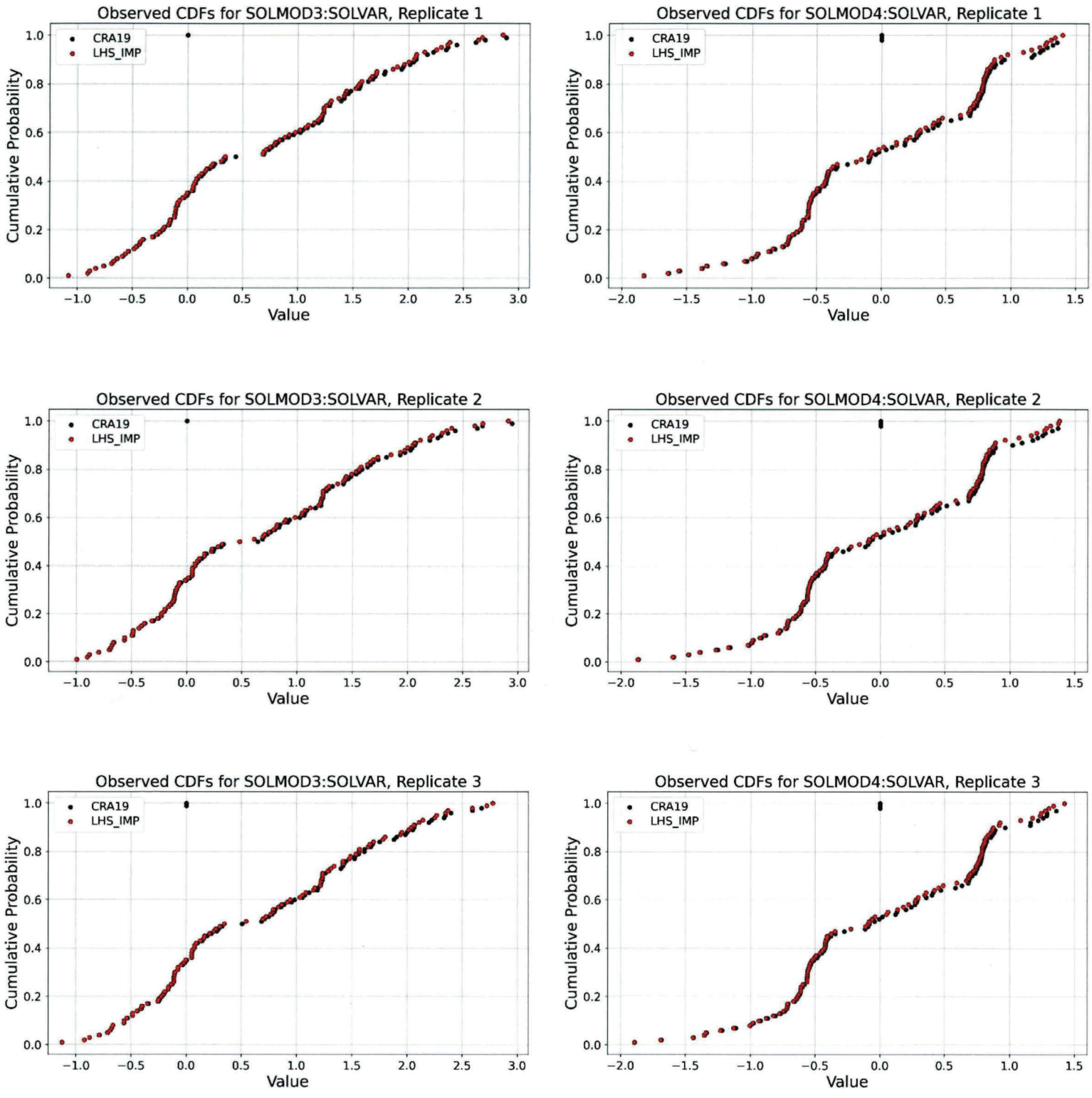

Figure 4. Latin hypercube sampling for SOLMOD3 and SOLMOD4: CRA-2019 (black) and LHS_IMP (red)

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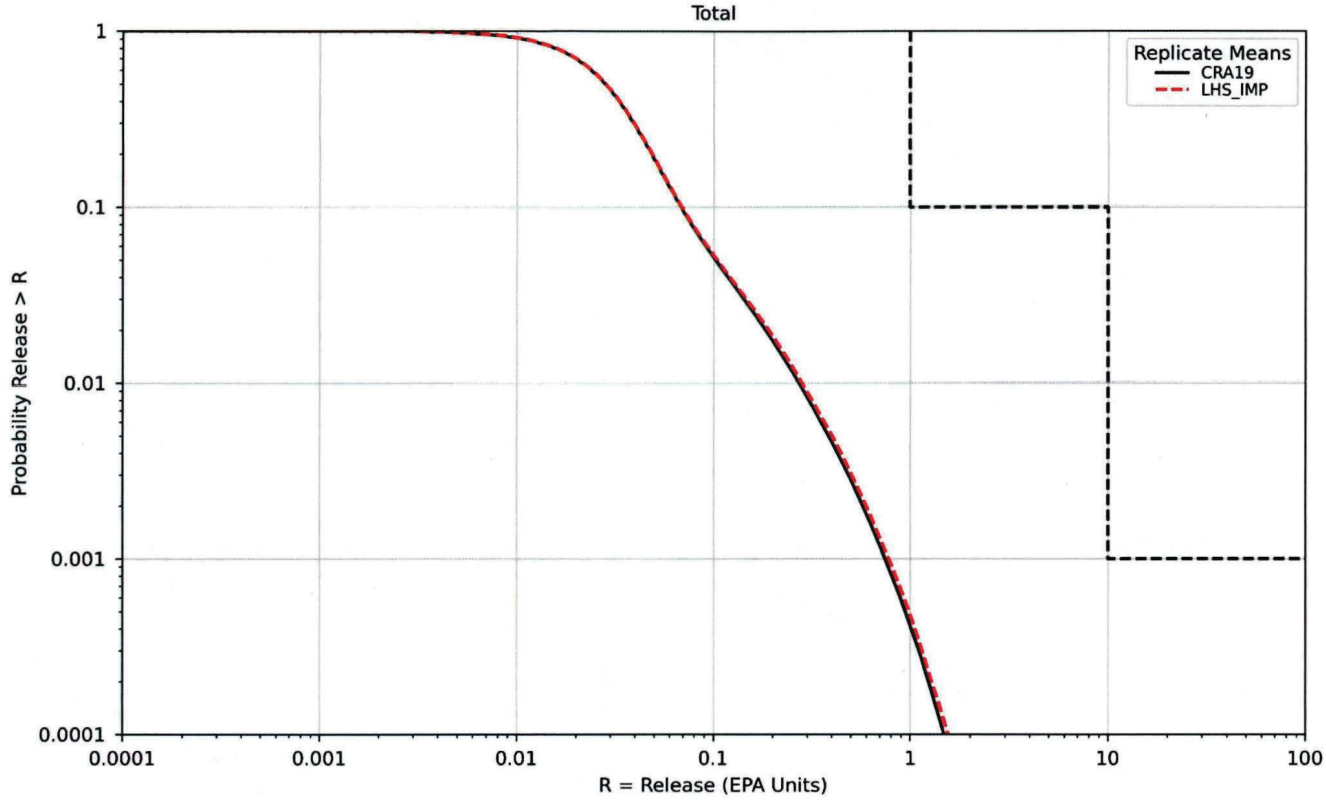

Figure 5. Total releases for CRA-2019 (black) and LHS_IMP (red), averaged over replicates.

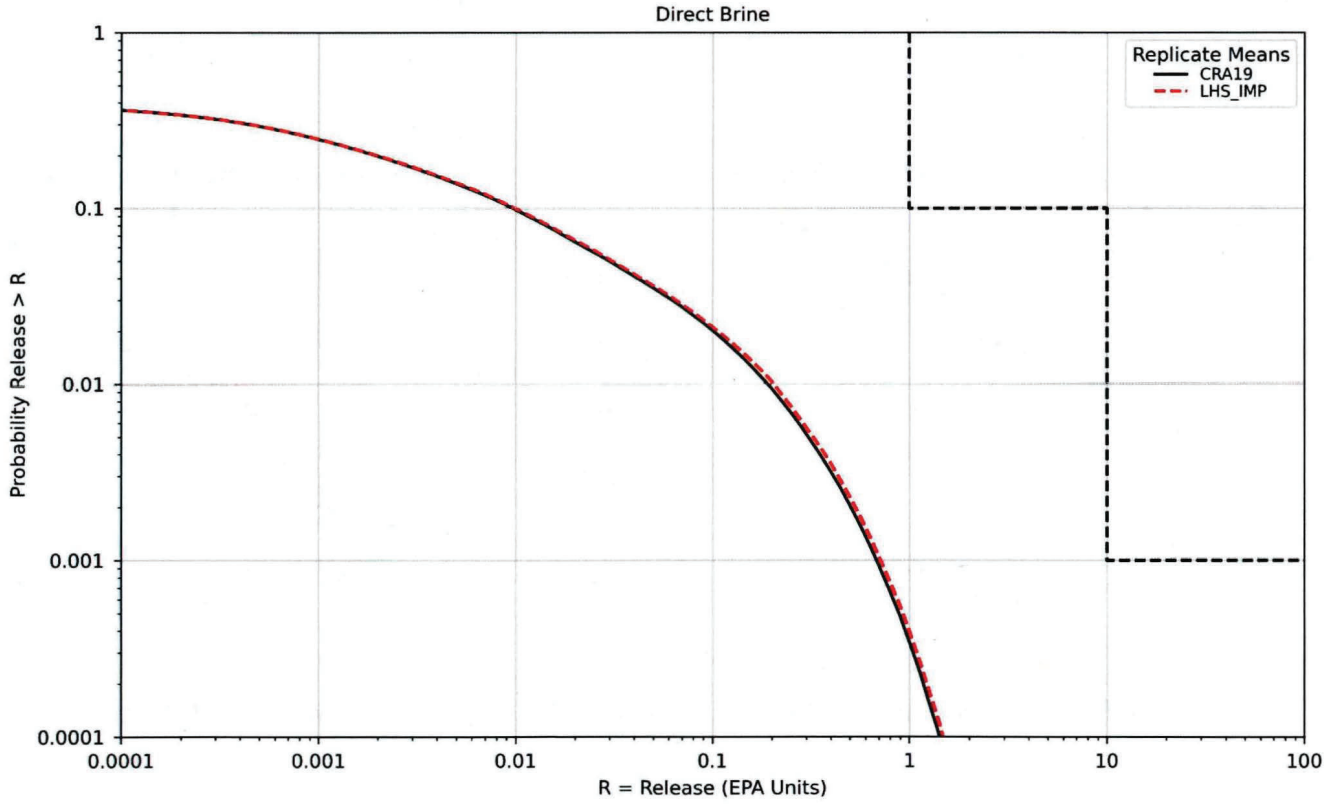

Figure 6. Direct brine releases for CRA-2019 (black) and LHS_IMP (red), averaged over replicates

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Figure 7 shows the cumulative total release curves, or horsetails, for the vectors in each of the three replicates, with CRA-2019 replicates on the left and LHS_IMP replicates on the right. Figure 8 plots the corresponding horsetails for DBRs. As expected, for both total releases and DBRs, most horsetails shift slightly to the left (towards smaller releases), while a few shift significantly to the right (towards larger releases). Mean curves are shown in red in Figures 7 and 8. The means for Replicates 1 and 3 – total releases and DBRs – are very similar in LHS_IMP and CRA-2019, indicating the effectiveness of the tradeoff discussed above. Mean releases for Replicate 2, however, are greater at low probabilities in LHS_IMP than in CRA-2019. In CRA-2019, only one vector in Replicate 2 was assigned a value of zero for SOLMOD3:SOLVAR as a result of an interpolation failure (see Figure 4). The zero was assigned in Replicate 2, Vector 31. In LHS_IMP, the SOLMOD3:SOLVAR value in Replicate 2, Vector 31 is 2.912, which is the maximum value for SOLMOD3:SOLVAR in any vector in all three LHS_IMP replicates. In Figures 7 and 8, LHS_IMP's Replicate 2, Vector 31 horsetail is the one with the highest releases at cumulative probabilities less than about 0.3.

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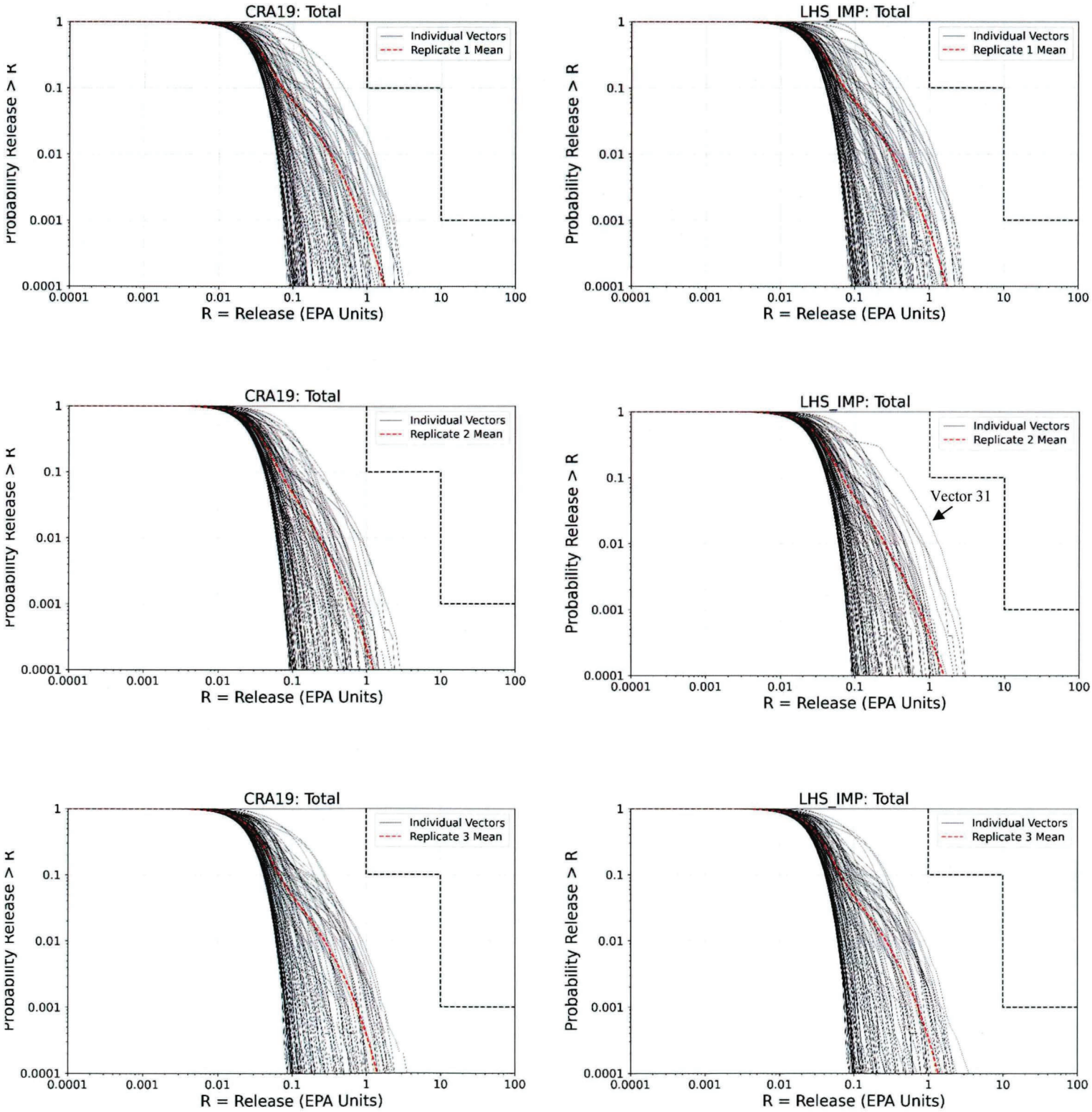

Figure 7. Cumulative total releases for individual vectors in Replicates 1 – 3: CRA-2019 (left); LHS_IMP (right).

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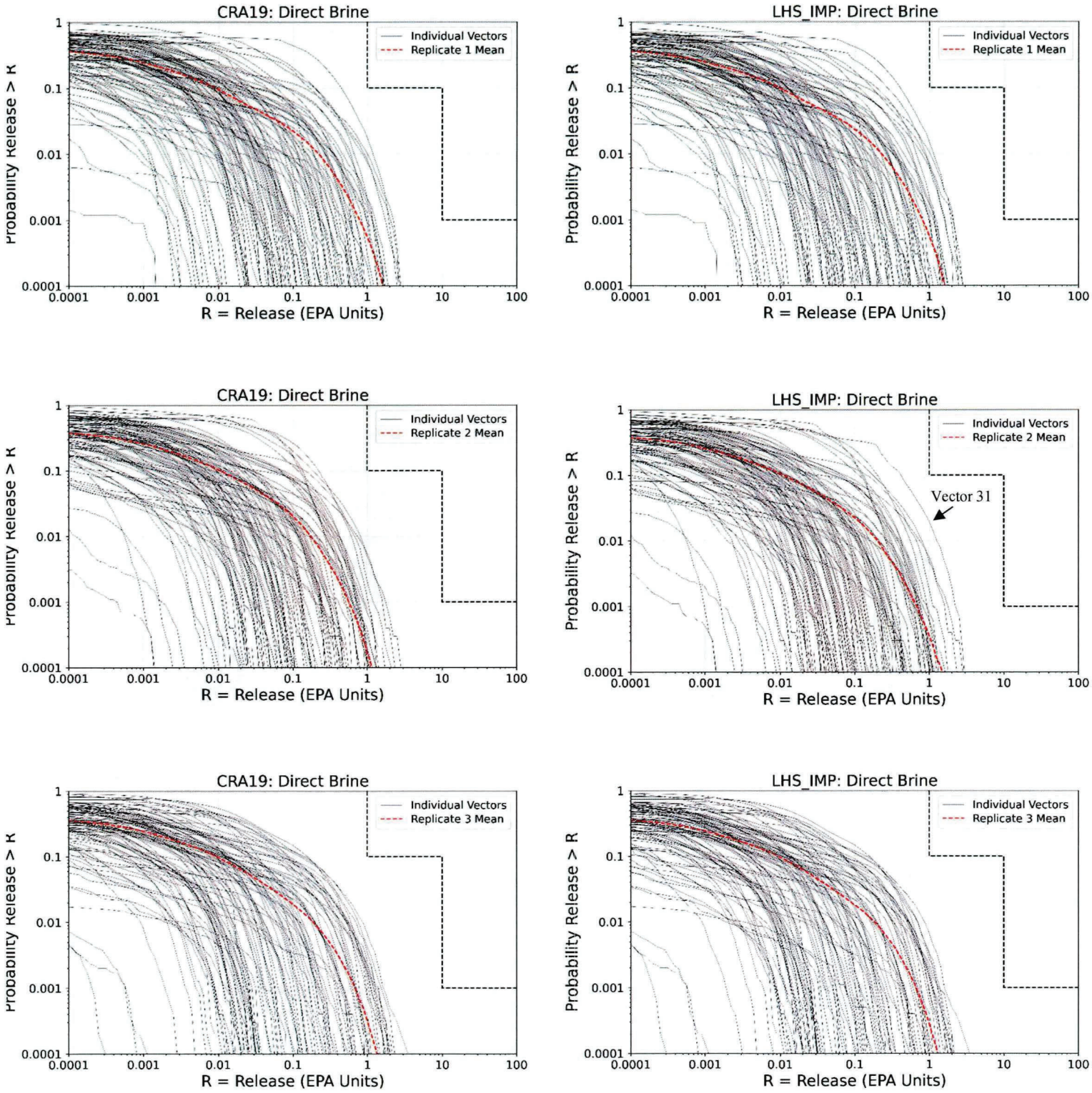

Figure 8. Cumulative DBRs for individual vectors in Replicates 1 – 3: CRA-2019 (left); LHS_IMP (right).

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Finally, Figure 9 illustrates the total mobilization potential in CRA-2019 and LHS_IMP for each of PA's five primary actinides. Each box plot shows the first and third quartiles, the median, whiskers set at the 2nd and 98th percentiles, and outliers as black diamonds; the mean is also plotted as a green triangle. The plots were generated from data output by PA code PANEL, for BRAGFLO Scenario 2, and for the minimum brine dilution factor. Data from all three replicates are used to create the box plots. A detailed description of PANEL can be found in Sarathi (2019). The box plots for CRA-2019 in Figure 9 are identical to those for CRA-2019 in Sarathi's Figure 14. Figure 9 indicates mostly small increases in quartile and mean concentration limits in LHS_IMP compared to CRA-2019.

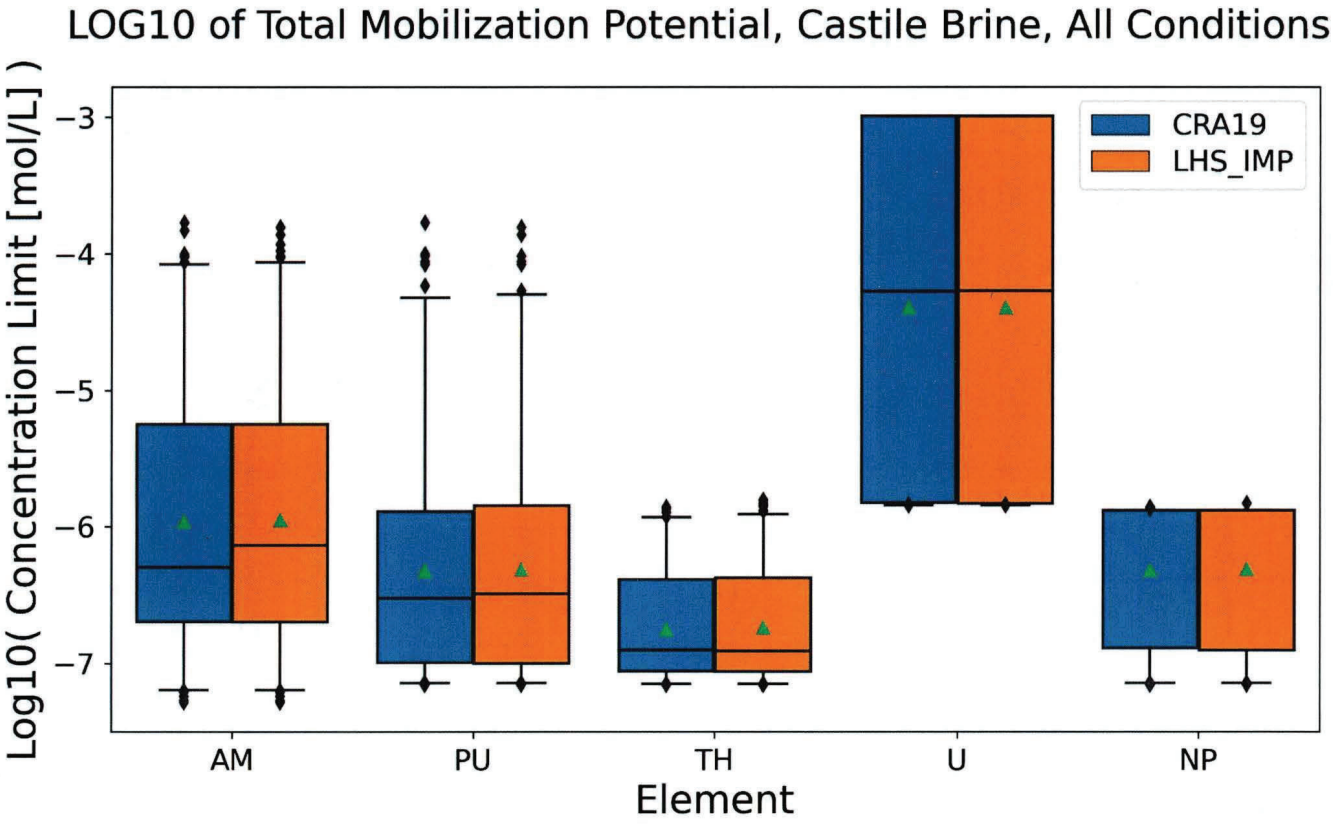

Figure 9. Log10 of total mobilization potential for base elements, all replicates: CRA-2019 (blue); LHS_IMP (orange)

7. Summary

PA code PRELHS expects user-supplied cumulative probability distributions to begin at cumulative probability zero and end at cumulative probability one. In CRA-2019, cumulative distributions for SOLMOD3:SOLVAR, SOLMOD4:SOLVAR and GLOBAL:PBRINE had a starting probability that was greater than zero. A consequence for these PA parameters was that Latin hypercube sampling in CRA-2019 obtained parameter values that were, in most cases, slightly larger than intended. The effect was negligible for GLOBAL:PBRINE, but more significant for the SOLVARs. It was also the case for the SOLVARs that the nonzero starting probability caused Latin hypercube sampling to fail for several

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samples where cumulative probabilities approached one. As a result, zeros were assigned to a few PA vectors that should have been given the largest SOLVAR values.

The user-supplied distribution for STEEL:CORRMCO2 had a number of repeated parameter values which caused some points in the distribution to be extracted from the database in the wrong order in CRA-2019. As a result, some small negative increments in cumulative probability were generated, affecting the cumulative distribution in the neighborhood of the repeated parameter values. The effects of this on the sampling of STEEL:CORRMCO2 were negligible.

A new PA, named LHS_IMP, was run to determine the impact of correcting the distributions for SOLMOD3:SOLVAR, SOLMOD4:SOLVAR and GLOBAL:PBRINE, and the impact of correcting the ordering of STEEL:CORRMCO2. Analysis LHS_IMP used PRELHS Version 2.46, which checks that user-supplied distributions are defined correctly and reads distributions with repeated parameter values in the correct order. Total releases for analysis LHS_IMP were the same as in CRA-2019 at high cumulative probabilities and only slightly greater than in CRA-2019 at low cumulative probabilities. Differences at low probabilities were due to increased DBRs. The parameter that most affects DBRs is SOLMOD3:SOLVAR. A small number of large values for SOLMOD3:SOLVAR that were absent in CRA-2019 vectors were most impactful in increasing DBRs in LHS_IMP. In the future, PRELHS Version 2.46 will prevent users from incorrectly defining cumulative probability distributions.

Analysis LHS_IMP has been archived in CVS. The location of the archive is /data/cvs/CVSLIB/WIPP_EXTERNAL/SPR 22-001.

8. References

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Appendix A

The cumulative probability distributions for SOLMOD3:SOLVAR, SOLMOD4:SOLVAR and GLOBAL:PBRINE were modified for input to analysis LHS_IMP. The tables below give the full distributions for these three parameters for both CRA-2019 and LHS_IMP.

Table 3. SOLMOD3:SOLVAR. Cumulative probability distributions for CRA-2019 and LHS_IMP.

	SOLMOD3:SOLVAR			
	CRA-2019		LHS_IMP	
	N = 82		N = 82	
OrderIndex	Value	Probability	Value	Prob
1	-1.14251	0.0122	-1.14251	0
2	-0.932358	0.02439	-0.932358	0.012346
3	-0.875954	0.03659	-0.875954	0.024691
4	-0.805676	0.04878	-0.805676	0.037037
5	-0.694681	0.06098	-0.694681	0.049383
6	-0.677855	0.07317	-0.677855	0.061728
7	-0.665805	0.08537	-0.665805	0.074074
8	-0.56653	0.09756	-0.56653	0.08642
9	-0.562972	0.1098	-0.562972	0.098765
10	-0.487951	0.122	-0.487951	0.111111
11	-0.486971	0.1341	-0.486971	0.123457
12	-0.442671	0.1463	-0.442671	0.135802
13	-0.417617	0.1585	-0.417617	0.148148
14	-0.376826	0.1707	-0.376826	0.160494
15	-0.291642	0.1829	-0.291642	0.17284
16	-0.23211	0.1951	-0.23211	0.185185
17	-0.228885	0.2073	-0.228885	0.197531
18	-0.202533	0.2195	-0.202533	0.209877
19	-0.166077	0.2317	-0.166077	0.222222
20	-0.160532	0.2439	-0.160532	0.234568
21	-0.122178	0.2561	-0.122178	0.246914
22	-0.114771	0.2683	-0.114771	0.259259
23	-0.112331	0.2805	-0.112331	0.271605
24	-0.108348	0.2927	-0.108348	0.283951
25	-0.100004	0.3049	-0.100004	0.296296
26	-0.079188	0.3171	-0.079188	0.308642

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27	-0.069364	0.3293	-0.069364	0.320988
28	-0.025201	0.3415	-0.025201	0.333333
29	0.00703	0.3537	0.00703	0.345679
30	0.048993	0.3659	0.048993	0.358025
31	0.049039	0.378	0.049039	0.37037
32	0.049806	0.3902	0.049806	0.382716
33	0.074136	0.4024	0.074136	0.395062
34	0.074136	0.4146	0.074136	0.407407
35	0.106091	0.4268	0.106091	0.419753
36	0.155677	0.439	0.155677	0.432099
37	0.160394	0.4512	0.160394	0.444444
38	0.215051	0.4634	0.215051	0.45679
39	0.254326	0.4756	0.254326	0.469136
40	0.313025	0.4878	0.313025	0.481481
41	0.346357	0.5	0.346357	0.493827
42	0.685282	0.5122	0.685282	0.506173
43	0.701582	0.5244	0.701582	0.518519
44	0.74939	0.5366	0.74939	0.530864
45	0.778205	0.5488	0.778205	0.54321
46	0.80209	0.561	0.80209	0.555556
47	0.850272	0.5732	0.850272	0.567901
48	0.889953	0.5854	0.889953	0.580247
49	0.95297	0.5976	0.95297	0.592593
50	1.02872	0.6098	1.02872	0.604938
51	1.068567	0.622	1.068567	0.617284
52	1.095435	0.6341	1.095435	0.62963
53	1.170804	0.6463	1.170804	0.641975
54	1.215464	0.6585	1.215464	0.654321
55	1.217682	0.6707	1.217682	0.666667
56	1.232646	0.6829	1.232646	0.679012
57	1.236077	0.6951	1.236077	0.691358
58	1.23617	0.7073	1.23617	0.703704
59	1.285946	0.7195	1.285946	0.716049
60	1.295231	0.7317	1.295231	0.728395
61	1.41886	0.7439	1.41886	0.740741
62	1.419674	0.7561	1.419674	0.753086

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63	1.451948	0.7683	1.451948	0.765432
64	1.51897	0.7805	1.51897	0.777778
65	1.557256	0.7927	1.557256	0.790123
66	1.570299	0.8049	1.570299	0.802469
67	1.643798	0.8171	1.643798	0.814815
68	1.672233	0.8293	1.672233	0.82716
69	1.703691	0.8415	1.703691	0.839506
70	1.792566	0.8537	1.792566	0.851852
71	1.916789	0.8659	1.916789	0.864198
72	1.963935	0.878	1.963935	0.876543
73	2.023033	0.8902	2.023033	0.888889
74	2.059652	0.9024	2.059652	0.901235
75	2.068615	0.9146	2.068615	0.91358
76	2.175439	0.9268	2.175439	0.925926
77	2.251789	0.939	2.251789	0.938272
78	2.343682	0.9512	2.343682	0.950617
79	2.372998	0.9634	2.372998	0.962963
80	2.627935	0.9756	2.627935	0.975309
81	2.683488	0.9878	2.683488	0.987654
82	2.971474	1	2.971474	1

Table 4. SOLMOD4:SOLVAR. Cumulative probability distributions for CRA-2019 and LHS_IMP.

	SOLMOD4:SOLVAR			
	CRA-2019		LHS_IMP	
	N = 44		N = 44	
OrderIndex	Value	Probability	Value	Prob
1	-2.0098	0.0227	-2.0098	0
2	-1.4885	0.0455	-1.4885	0.023256
3	-1.3031	0.0682	-1.3031	0.046512
4	-1.0158	0.0909	-1.0158	0.069767
5	-0.9475	0.1136	-0.9475	0.093023
6	-0.8003	0.1364	-0.8003	0.116279
7	-0.7203	0.1591	-0.7203	0.139535
8	-0.7103	0.1818	-0.7103	0.162791

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9	-0.6458	0.2045	-0.6458	0.186047
10	-0.6103	0.2273	-0.6103	0.209302
11	-0.6103	0.25	-0.6103	0.232558
12	-0.5612	0.2727	-0.5612	0.255814
13	-0.5603	0.2955	-0.5603	0.27907
14	-0.5552	0.3182	-0.5552	0.302326
15	-0.5403	0.3409	-0.5403	0.325581
16	-0.5203	0.3636	-0.5203	0.348837
17	-0.4645	0.3864	-0.4645	0.372093
18	-0.4252	0.4091	-0.4252	0.395349
19	-0.4192	0.4318	-0.4192	0.418605
20	-0.4041	0.4545	-0.4041	0.44186
21	-0.3303	0.4773	-0.3303	0.465116
22	-0.0996	0.5	-0.0996	0.488372
23	-0.0803	0.5227	-0.0803	0.511628
24	0.0297	0.5455	0.0297	0.534884
25	0.1597	0.5682	0.1597	0.55814
26	0.2697	0.5909	0.2697	0.581395
27	0.2897	0.6136	0.2897	0.604651
28	0.3919	0.6364	0.3919	0.627907
29	0.4597	0.6591	0.4597	0.651163
30	0.6797	0.6818	0.6797	0.674419
31	0.6897	0.7045	0.6897	0.697674
32	0.734	0.7273	0.734	0.72093
33	0.7497	0.75	0.7497	0.744186
34	0.774	0.7727	0.774	0.767442
35	0.7873	0.7955	0.7873	0.790698
36	0.789	0.8182	0.789	0.813953
37	0.8085	0.8409	0.8085	0.837209
38	0.8228	0.8636	0.8228	0.860465
39	0.864	0.8864	0.864	0.883721
40	0.8897	0.9091	0.8897	0.906977
41	1.1567	0.9318	1.1567	0.930233

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42	1.2526	0.9545	1.2526	0.953488
43	1.2953	0.9773	1.2953	0.976744
44	1.4266	1	1.4266	1

Table 5. GLOBAL:PBRINE. Cumulative probability distributions for CRA-2019 and LHS_IMP.

	GLOBAL:PBRINE			
	CRA-2019		LHS_IMP	
	N = 54		N = 55	
OrderIndex	Value	Probability	Value	Prob
1	0.04	0.002	0.04	0
2	0.05	0.004	0.04	0.002
3	0.06	0.006	0.05	0.004
4	0.07	0.014	0.06	0.006
5	0.08	0.023	0.07	0.014
6	0.09	0.043	0.08	0.023
7	0.1	0.08	0.09	0.043
8	0.11	0.109	0.1	0.08
9	0.12	0.139	0.11	0.109
10	0.13	0.185	0.12	0.139
11	0.14	0.223	0.13	0.185
12	0.15	0.264	0.14	0.223
13	0.16	0.294	0.15	0.264
14	0.17	0.33	0.16	0.294
15	0.18	0.363	0.17	0.33
16	0.19	0.385	0.18	0.363
17	0.2	0.414	0.19	0.385
18	0.21	0.429	0.2	0.414
19	0.22	0.455	0.21	0.429
20	0.23	0.478	0.22	0.455
21	0.24	0.487	0.23	0.478
22	0.25	0.512	0.24	0.487
23	0.26	0.533	0.25	0.512

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24	0.27	0.546	0.26	0.533
25	0.28	0.563	0.27	0.546
26	0.29	0.577	0.28	0.563
27	0.3	0.593	0.29	0.577
28	0.31	0.609	0.3	0.593
29	0.32	0.633	0.31	0.609
30	0.33	0.653	0.32	0.633
31	0.34	0.673	0.33	0.653
32	0.35	0.689	0.34	0.673
33	0.36	0.713	0.35	0.689
34	0.37	0.735	0.36	0.713
35	0.38	0.759	0.37	0.735
36	0.39	0.774	0.38	0.759
37	0.4	0.796	0.39	0.774
38	0.41	0.825	0.4	0.796
39	0.42	0.851	0.41	0.825
40	0.43	0.875	0.42	0.851
41	0.44	0.89	0.43	0.875
42	0.45	0.908	0.44	0.89
43	0.46	0.927	0.45	0.908
44	0.47	0.939	0.46	0.927
45	0.48	0.953	0.47	0.939
46	0.49	0.964	0.48	0.953
47	0.5	0.976	0.49	0.964
48	0.51	0.982	0.5	0.976
49	0.52	0.986	0.51	0.982
50	0.53	0.993	0.52	0.986
51	0.54	0.997	0.53	0.993
52	0.55	0.998	0.54	0.997
53	0.56	0.999	0.55	0.998
54	0.57	1	0.56	0.999
55			0.57	1

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