Uncertainties in Organ Burdens Estimated from PAS (U)

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Introduction

In the 1990's the US Department of Energy conducted two internal dose intercomparisons[1,2]. In these intercomparisons participants were sent urine bioassay data and were asked to estimate intakes and committed effective dose equivalent (CEDE). While the intercomparisons gave an indication of the precision of the dose estimate, the accuracy[a] of the results could not be determined because *there was no right answer*, i.e., the "true" intake and CEDE were not known. Not only were these quantities not known, they are basically unknowable: for all intents and purposes, *intake* is a theoretical construct that can not be measured.

The Department of Energy is considering a third intercomparison in coordination with the United States Transuranium and Uranium Registry (USTUR). This intercomparison will be different than the previous two because they are going to send bioassay data from whole-body donors who have had complete autopsies. The "right" answer this time around will be the measured organ burdens. In other words, using the bioassay data, how well can I predict the organ burdens at the time of death? The advantage of this approach is that we now have a measurable, objective endpoint with which to compare different evaluations. James[3] et al. recently published just such an evaluation where they used the urine bioassay data from USTUR Case 0259 to calculate organ burdens. These burdens were subsequently compared to the observed organ burdens to assess the accuracy of their evaluation.

The individual described in USTUR Case 0259 had an inhalation intake of an insoluble ^{238}Pu ceramic aerosol. He died 6532 days later of cardiovascular disease. The observed and predicted urinary excretion from Case 0259 are shown in Figure 1. The data were evaluated using standard ICRP 66/67 biokinetic models with the exception that the solubility parameters were modified to account for the increasing solubility of the inhaled material over time. The complete specification of the model used here is given in Appendix A, which is the Mathcad worksheet used to perform the calculations.

Analytical uncertainties were not reported for the urinary excretion, so 2σ analytical uncertainties of ±50% are assumed[b]. An intake of 1.47×10^6 pCi was calculated from the urine data using the indicated models. The measured ^{238}Pu liver burden was reported as 137±4 Bq at 1σ (or 3703±108 pCi to the nearest pCi). The liver burden predicted from the intake is 2953 pCi (to the nearest pCi).

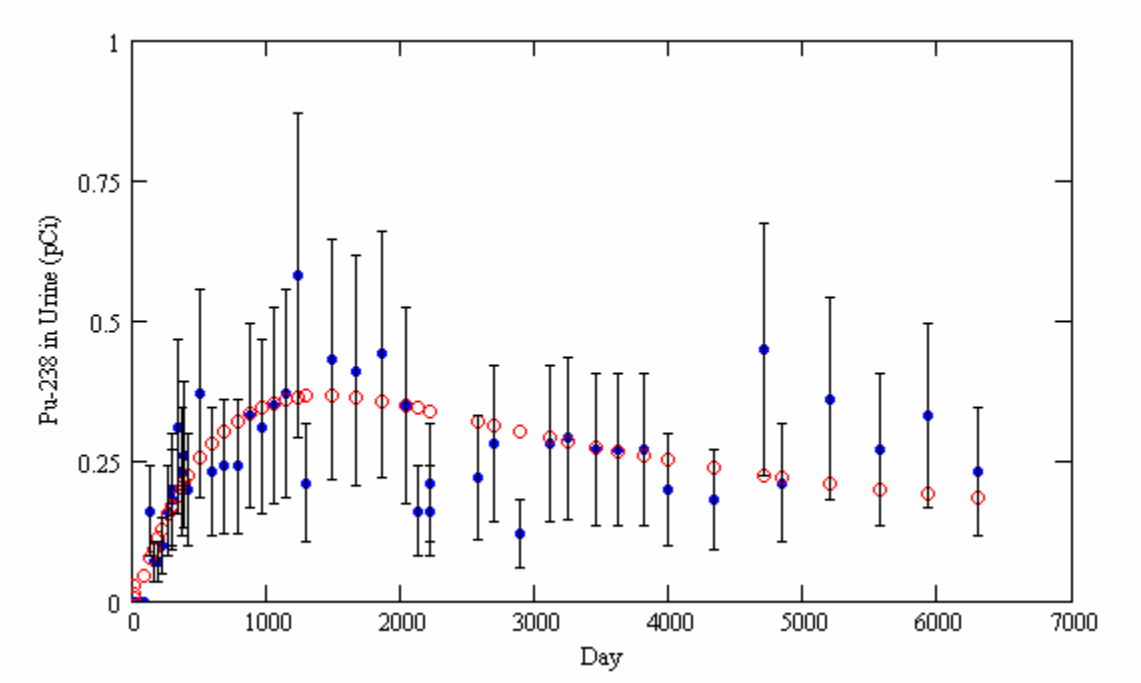
At first glance, the predicted liver burden does not appear to agree with the observed liver burden. However, to make any definitive statements we need to estimate the uncertainty in the predicted liver burden. For example, if we could say that the predicted liver burden was 2953±100 pCi at 1σ, then we might claim that the predicted and observed burdens do not agree, i.e., there is a bias in the predicted burden. On the other hand, if the predicted burden was 2953±1000 pCi at 1σ, then we might say that the low precision of the predicted burden does not make it possible to detect any bias. In summary, to have an *accurate* estimate of an organ

[a] In this discussion we will assume that the accuracy of a dose estimate is a function of its precision (how well can the result be reproduced) and its bias (how close is the result to the "true" dose).

[b] These uncertainties, which are considered to be a reasonable estimate of the total propagated uncertainty, are presented to help the reader judge how close the observed points are to the predicted line.

burden we need negligible *bias* between the predicted and observed burdens. To assess bias, we need a level of *precision* that is commensurate with the level of bias we seek to detect.

Figure 1. Observed urinary excretion of ^{238}Pu with ±50% uncertainties (solid dot with error bars) and the predicted urinary excretion (open dots).



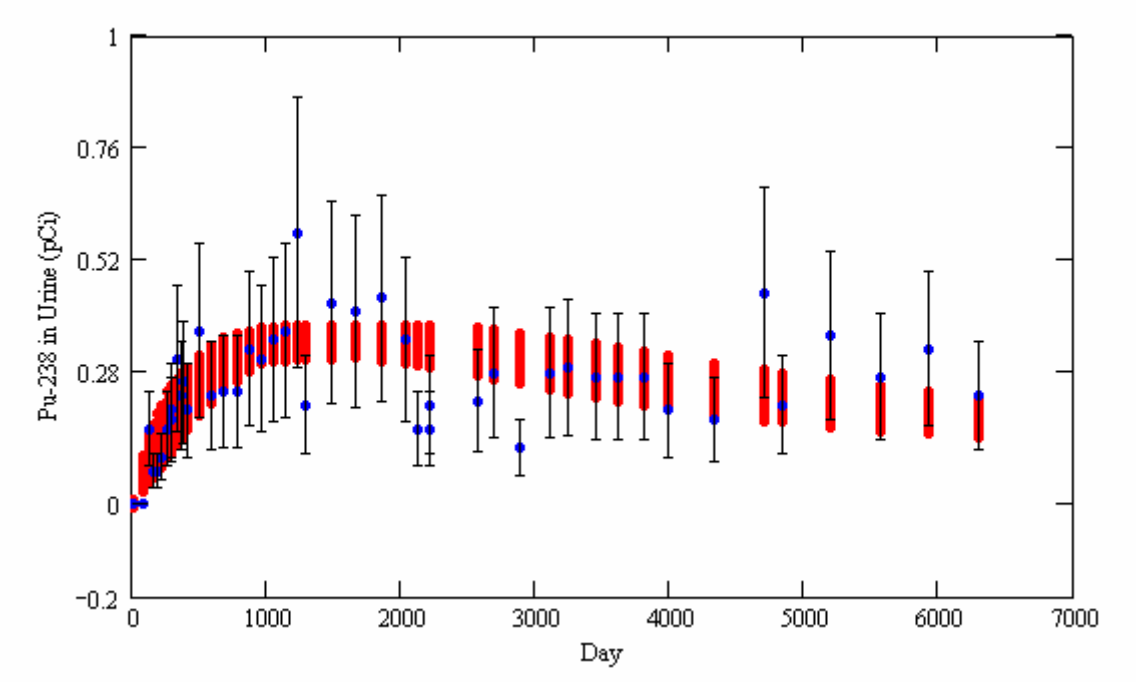
How would one go about calculating the uncertainty in a predicted organ burden? Bolch and other researchers at the University of Florida[4,5,6] have been using Monte Carlo methods to estimate the uncertainty in respiratory tract doses given the inhalation intake. In their approach they establish statistical distributions for each parameter in the ICRP 66 Human Respiratory Tract Model (HRTM). In a particular trial, a value of each parameter is drawn from its distribution and the respiratory tract doses from a unit intake are calculated with these parameters. This process is repeated for hundreds or thousands of trials until dose distributions are produced for each tissue of the respiratory tract.

Going from an intake to a dose is referred to as a solution in the "forward" direction. The solution in the "backward" direction is the calculation of intakes and ultimately organ burdens from bioassay data. Bolch's approach can be applied to the backward problem to generate a distribution of predicted organ burdens from a specific set of urinary excretion data:

observed urine data → select parameters of biokinetic model → calculate burdens

The results of this process being applied to Case 0259 with 1000 different biokinetic models are shown in Figure 2, where the predicted urinary excretion forms bands. The calculation is documented in Appendix B.

Figure 2. Observed urinary excretion of ^{238}Pu with ±50% uncertainties (solid dot with error bars) and the predicted urinary excretion (solid bars) for 1000 different biokinetic models.



To calculate the 1000 different biokinetic models only the deposition fractions and translocation rate constants in the HRTM were varied (according the Bolch's method). The parameters of the ICRP 67 systemic model were held constant[a]. The excretion fractions from each model were fit to the observed data using a weighted least-squares fit where the variance in the observed excretion is assumed to be proportional to the predicted excretion.

The 1000 predicted liver burdens and the observed liver burden are shown in Figure 3. The mean predicted liver burden is 2842±125 pCi (4.4% relative standard deviation) with a maximum of 3303 pCi and a minimum of 2309 pCi. The uncertainty in the predicted liver burden shown here is not the total uncertainty in the predicted liver burden but rather is the component of the total uncertainty that is caused by variability in the HRTM. The rather small uncertainty in the predicted liver burden makes the bias of -23% clearly visible. James attempted to reduce this bias by adjusting several parameters of the systemic model. The results of his efforts are shown in Figure 4. The calculations using the "tweaked" model are documented in Appendix C. Tweaking the systemic model reduced the bias to 8.4% while leaving the relative standard deviation largely unaffected at 3.9%.

If the uncertainty in the systemic biokinetic model had been incorporated into this calculation and the uncertainty in the predicted liver burden became excessively large (±100% for example), efforts to reduce any perceived bias by tweaking the model would be unwarranted.

[a] Because Bolch did not address the variability of systemic parameters in his work.

Figure 3. Liver burdens calculated with 1000 different biokinetic models. The solid line is the observed liver burden. Note that the standard parameters for the systemic model were used.

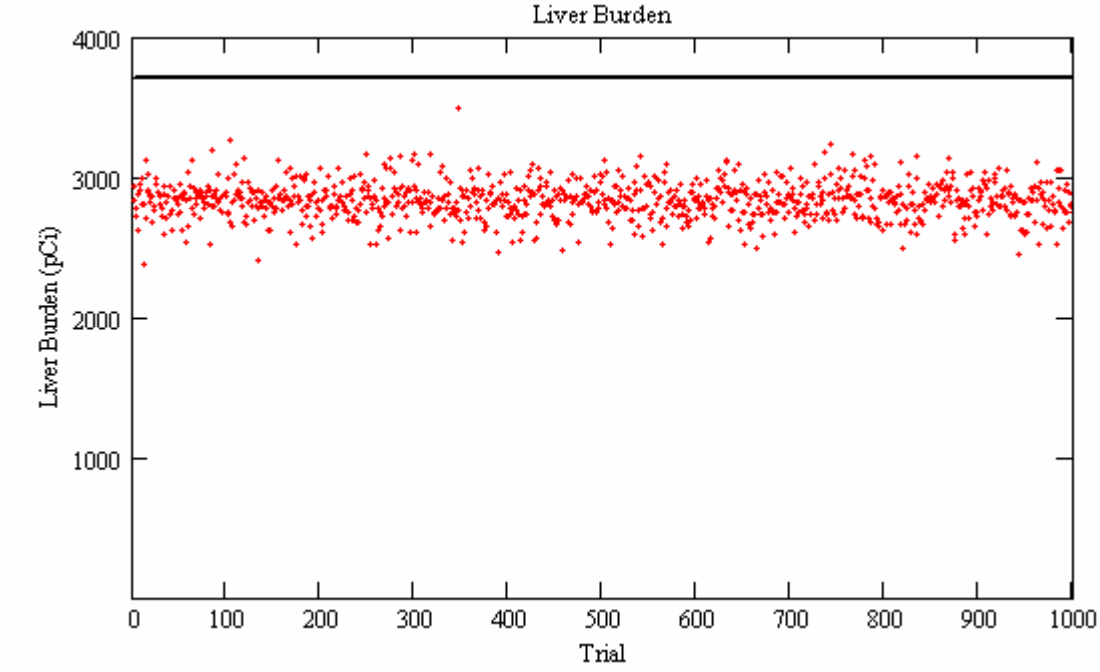
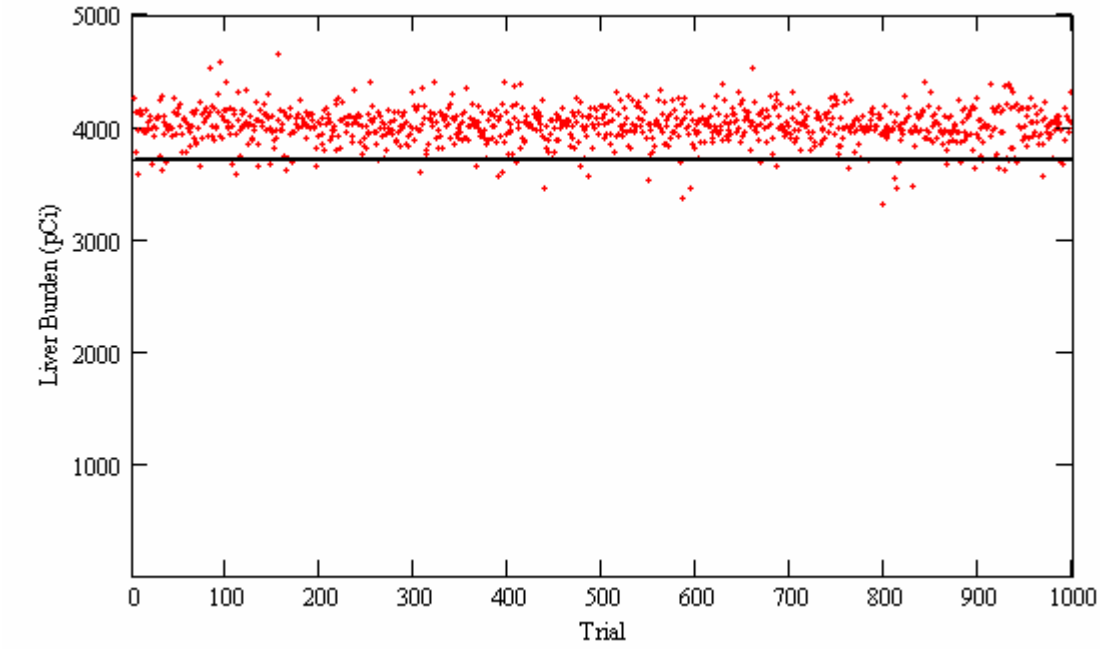


Figure 4. Liver burdens calculated with 1000 different biokinetic models. The solid line is the observed liver burden. Note that the parameters for the systemic model were modified in an effort to reduce the bias.



How should all of this be interpreted? Well, I selected a biokinetic model to evaluate the urinary excretion of Case 0259 with the express purpose of calculating the liver burden at the time of death. I really don't know if I have selected the "right" model for Case 0259, so I am interested in knowing how far off I could be if I picked the "wrong" model. In other words, I am interested in knowing how sensitive the predicted liver burden is to normal variations in the HRTM. In the case examined here, the predicted liver burden appears to be relatively insensitive to normal variations in the HRTM. If the liver burden calculated from urinary excretion had been extremely sensitive to normal variations in the HRTM, then urine bioassay would have to be considered unsuitable for calculating liver burdens[a].

Personal Air Samplers

The biokinetic models for plutonium dictate that the fraction of an intake excreted in the urine on any given day is quite small. For example, in the case of USTUR 0259, roughly 10^{-7} of the intake is excreted in the urine per day. In comparison, a personal air sampler (PAS) filter might be expected to capture around 0.25 of the intake. Thus, a PAS measurement is orders of magnitude more sensitive than a urine measurement. This means that (for plutonium) a PAS will have a much lower minimum detectable dose (MDD) than a urine bioassay, a concept discussed in detail by Skrable[7] et al. Thus, the strength of the PAS is that it is independent of the plutonium biokinetic model, which makes it very sensitive. However, once we have measurable urinary excretion (and other types of bioassay data) and detection of the intake is no longer an issue, this strength of PAS can become a weakness. The reasons for this will be discussed next.

By defining the "correct" answer to be the measured organ burden, the proposed bioassay intercomparison may provide a more meaningful measure of the accuracy of our internal dose evaluation methods. This approach also suggests an interesting way of looking at PAS. Discussions about the use of PAS versus bioassay frequently generate animated debates over which is more accurate and which is more sensitive. These debates are seldom resolved, with both camps left unmoved by the other's arguments. The problem here seems to be that *there is no right answer*. The classic example of this is to ask whether PAS or bioassay gives a more accurate estimate of intake. An *inhalation intake* is the quantity of material that passes through the nostrils into the body. For all intents and purposes *intake* is a theoretical construct that can not be measured. This means that *intake* should not be used to compare PAS and bioassay because there is no empirical result with which to compare our predictions.

A PAS measures the concentration of material (like ^{238}Pu) in the air it samples. An intake is typically calculated from a PAS measurement using something like the following:

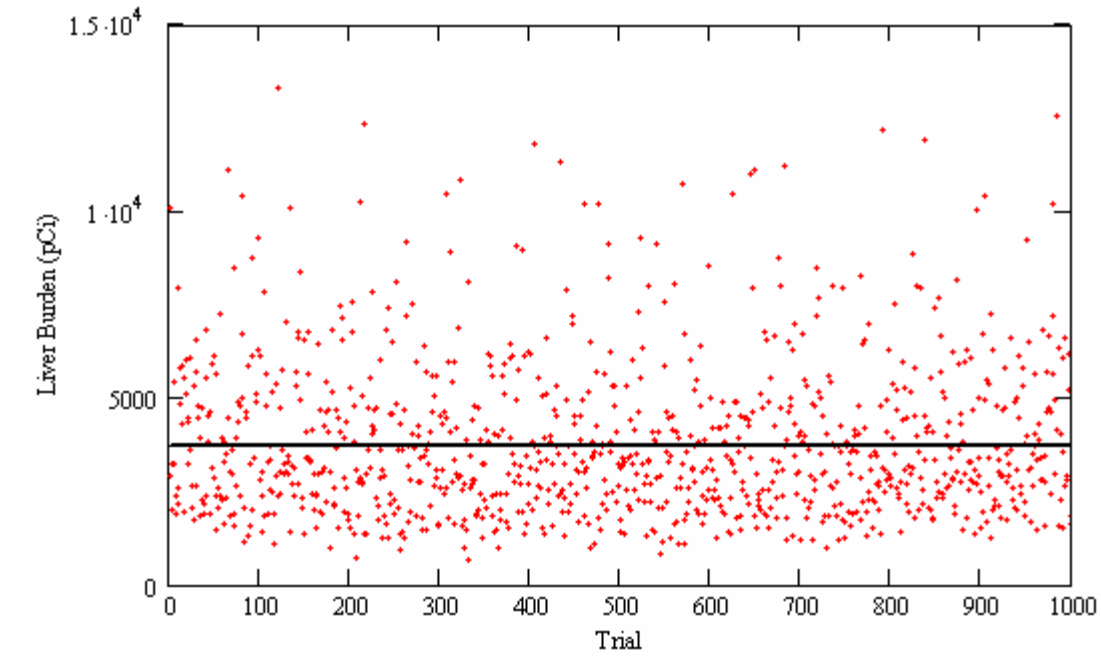
- The activity of plutonium on the PAS filter is quantified.
- This activity is multiplied by the ratio **R** of the breathing rate of the person to the flow rate of the PAS, e.g., R = (20 liters/minute) / (4 liters/min) = 5, to give the intake.

[a] Assuming of course that there was some other method that was better.

For example, assume[a] that the PAS filter for Case 0259 had on it 3.462×10^5 pCi of ^{238}Pu. The intake would then be calculated to be 5 times this, or 1.731×10^6 pCi. This calculation does not address the possibility that the concentration of plutonium in the air sampled by the PAS may not be the same as the concentration in the air breathed by the person, i.e., the PAS may not be a "representative" sampler, or that the breathing rate of the person may deviate from 20 liters/minute. Ignoring these issues for a moment, feeding this intake through the same 1000 biokinetic models used to evaluate the urinary excretion yields the plot in Figure 5.

As shown in Appendix D, the mean predicted liver burden is 3703±2010 pCi (54% relative standard deviation) with a maximum of 12840 pCi and a minimum of 627 pCi. As before, the uncertainty in the predicted liver burden shown here is not the total uncertainty in the predicted liver burden but rather is the component of the total uncertainty that is caused by variability in the HRTM. The rather attractive bias of 0.0% is completely negated by the extremely large uncertainty in the predicted liver burden. In other words, the mean predicted liver burden is very inaccurate even though it has no bias because it has poor precision. This situation cannot be improved simply by "tweaking" parameters of the biokinetic model as was done before.

Figure 5. The liver burdens predicted from the 1000 different biokinetic models and the constant intake of 1.731×10^6 pCi. The solid line is the observed liver burden.



The problem here is that the liver burden predicted from a given intake (like that indicated from a PAS measurement) is relatively sensitive to normal variations in the HRTM. Paradoxically, the liver burden calculated from a PAS measurement is very sensitive to changes in the HRTM

[a] James et al. did not report any PAS measurements for this individual. For this discussion, we can choose just about any reasonable value for the PAS measurement because we are focusing on the precision of the predicted organ burden, which is primarily a function of the biokinetic model and not the actual value of the PAS measurement.

because the PAS measurement itself has no connection whatsoever with the HRTM. A simple example can be used to illustrate this.

First, assume that we fit the observed urine data with urinary excretion fractions calculated with the standard HRTM, calculate the intake, and finally calculate the liver burden. Now, assume that a modified HRTM sends half of the normal amount of plutonium to the urine, i.e., the urinary excretion fractions are reduced by a factor of two. When we fit the observed urinary excretion with the modified excretion fractions, the intake will be twice as large as the intake calculated with the standard model. However, the predicted urinary excretion and liver burden will be the essentially the same as those calculated with the standard model. In other words, because the observed urinary excretion and observed liver burden are directly related through the model, a liver burden calculated from the urinary excretion is relatively insensitive to changes in the parameters of the HRTM. On the other hand, because a PAS is completely independent of the HRTM, any changes in its parameters are propagated to changes in the predicted urinary excretion and liver burden.

Non-representative PAS

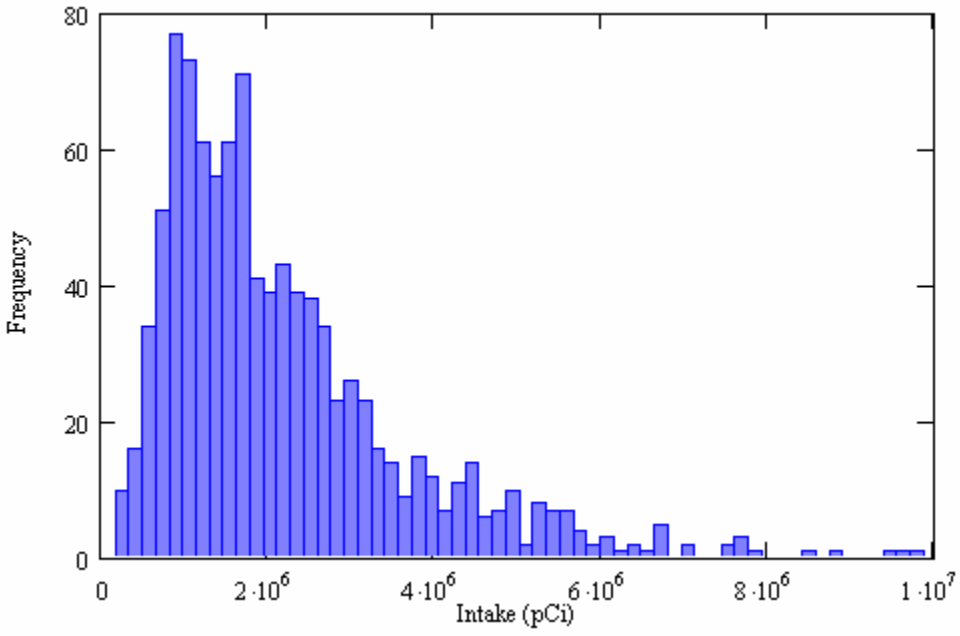
The calculations presented above do not address the possibility that the concentration of plutonium in the air sampled by the PAS may not be the same as the concentration in the air breathed by the person, i.e., the PAS may not be a "representative" sampler[a]. The ratio of the "true intake"[b] to the intake calculated from a PAS measurement is referred to here as the *PAS ratio*. The distribution of the PAS ratio can be estimated from published studies of air concentrations measured simultaneously by PAS on the left and right lapels. The PAS ratios estimated from three such studies[8,9,10] are presented in Appendix E. Based on the data presented in these studies, the PAS ratio used here is assumed to be lognormally distributed with a geometric mean μ_g of 1.0 and a geometric standard deviation σ_g of 2.0.

Given a unit intake estimated from PAS, a distribution of true intakes something like that shown in Figure 6 will result. The distribution depicted in Figure 6 has 99% of the PAS ratios in the range of 0.17 to 6.0. This means that 99% of the time the true intake could range from approximately 6 to 1/6 times the intake estimated from the PAS as a result of variability in the air concentration of the aerosol. Note that the variability in R, which is a function of the variability in the breathing rate of the individual and the sampling rate of the PAS, may not be fully accounted for in this calculation. Incorporating this additional variability into the calculation, as shown in Appendix F, more than doubles the relative standard deviation of the predicted liver burden to over 100%.

[a] The uncertainty in a PAS measurement is typically synonymous with the analytical uncertainty associated with counting the PAS filter. This uncertainty alone does not provide a meaningful picture of the uncertainty in the organ burden estimated from a PAS measurement.

[b] The quantity of material that actually goes into the person's nose is referred to as the "true intake" to differentiate it from the intake inferred from the PAS measurement.

Figure 6. A histogram of true intakes calculated from a PAS measurements after applying the PAS ratio.



Conclusions

Three major concepts discussed in this paper are:

1) The level of agreement between predicted and observed organs burdens is taken to be the measure of the accuracy of an internal dose assessment method. Using the organ burden "gold standard" allows one to objectively compare different assessment methodologies like PAS and bioassay.

2) The methods developed by Bolch et al. permit one to examine the natural variability in the respiratory track deposition fractions and translocation rates and the effects this variability has on urinary excretion and organ burdens.

3) The ratio of simultaneous PAS measurements made on the left and right lapel (the "PAS ratio") can be used to estimate the degree to which a single PAS measurement may not be representative of what a person inhales.

Using these techniques, we estimated the uncertainty in a ^{238}Pu liver burden predicted from a single PAS measurement and from 48 urinary excretion measurements. The uncertainties for the burdens estimated from urine data reflect only the variability in the parameters of the respiratory tract. There are other sources of variability, such as the variability in the systemic biokinetics and urinary excretion, that have not been accounted for here. The uncertainties in the burdens estimated from the PAS measurement reflect the variability caused by non-representative sampling in addition to the variability in the respiratory tract parameters. There are other sources of variability, such as variability in the person's breathing rate, that have not been accounted for here. Approximately ½ of the uncertainties for burdens calculated from the PAS measurement are from the variability in the respiratory tract parameters and ½ are from non-representative

sampling. It is worth noting that the uncertainties here are in all likelihood much smaller than the uncertainties that would be calculated if all sources of variability were included in the evaluation.

In summary, this study shows that an organ burden estimated from a PAS measurement is much more sensitive to variability in the respiratory tract biokinetic model than is an organ burden estimated from repetitive urine bioassay measurements. This conclusion may not be applicable to isolated measurements of urinary excretion rate combined with an unknown intake scenario (i.e., the dreaded "routine positive urine bioassay").

In this study we have seen uncertainties in organ burdens predicted from PAS measurements to be on the order of ± 200% at 2σ. The results of this study suggest that organ burdens predicted from PAS measurements (especially for acute exposures) can have large uncertainties – so large in fact that these measurements might be considered to be qualitative rather than quantitative *for the purpose of calculating organ burdens and dose*. However, this potential issue can be ignored for situations where the intakes are large enough to be of interest yet are too small to be detected and quantified with urine bioassay.

Even though this study only examines one case, we feel that it supports the following recommendations concerning the use of PAS and bioassay for materials like plutonium:

- PAS should be used to monitor for low-level (especially chronic) exposures where bioassay is unreliable.
- PAS measurements should be used to trigger special bioassay programs.
- If and when reliable bioassay data are available, the PAS measurements should assume a supporting role like area air monitoring data and nasal smears, and the bioassay data should be used as primary input for calculating dose.
- Agreement between PAS and bioassay is welcome when it occurs, but it should not be expected nor demanded.

The last two conclusions echo NUREG/CR-4033[11]:

"Breathing-zone air sampling and bioassay have been identified as suitable for assessing "actual exposure" of individuals. Although they play similar roles, this does not mean that there is a general equivalence or fixed relationship between these methods. It is usually not possible to accurately estimate uptake or internal dose, even from an accurate exposure estimate. It is also not possible to accurately estimate previous exposure from bioassay measurement."

References

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[3] A. C. James, R. E. Filipy, J. J. Russell, J. F. McInroy *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled $^{238}PuO_2$ Ceramic Particles* Health Physics 84(1):2-33; 2003.

[4] Wesley E. Bolch, Eduardo B. Farfan, CH Huh, Thomas E. Huston, and W. Emmett Bolch *Influences of Parameter Uncertainties within the ICRP-66 Respiratory Tract Model: Particle Deposition* Health Physics 81:378-394-435; 2001.

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Appendix A

Evaluation of USTUR Case 0259

Evalvuation of USTUR Case 0259 from data presented by A. C. James et al. *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled Pu238 Oxide Ceramic Particles* Health Physics 84(1):2-33:2003.

Define global constants.

$\lambda := 0$ Radioactive decay constant.

$nCi \equiv 37 \cdot Bq$ $pCi \equiv 10^{-3} \cdot nCi$ $aCi \equiv 10^{-9} \cdot nCi$ $dpm \equiv \frac{pCi}{2.22}$ $mrem \equiv 10^{-5} \cdot Sv$

$ORIGIN \equiv 1$

The compartments in the model are assigned numbers to clarify their use in the arrays to be defined.

Respiratory tract compartments.

AI1 := 1	bb1 := 4	BB1 := 7	ET2 := 10	LNet := 13
AI2 := 2	bb2 := 5	BB2 := 8	ETseq := 11	LNth := 14
AI3 := 3	bbseq := 6	BBseq := 9	ET1 := 12	

Transformed respiratory tract compartments.

TAI1 := 15	Tbb1 := 18	TBB1 := 21	TET2 := 24	TLNth := 27
TAI2 := 16	Tbb2 := 19	TBB2 := 22	TETseq := 25	
TAI3 := 17	Tbbseq := 20	TBBseq := 23	TLNet := 26	

GI tract compartments and feces.

S := 28 SI := 29 ULI := 30 LLI := 31

Systemic compartments of the ICRP 67 plutonium model.

blood := 32	ST0 := 35	CV := 38	TV := 41	OKT := 44	nads := 47	feces := 49
LIV1 := 33	ST1 := 36	CS := 39	TS := 42	UP := 45	ENV := 48	urine := 50
LIV2 := 34	ST2 := 37	CM := 40	TM := 43	UBC := 46		

Initial content of the compartments for a 5 μm AMAD aerosol. Any content not explicitly given has a value of zero.

$$\begin{pmatrix} q0_{AI1} \\ q0_{AI2} \\ q0_{AI3} \\ q0_{bb1} \\ q0_{bb2} \\ q0_{bbseq} \\ q0_{BB1} \\ q0_{BB2} \\ q0_{BBseq} \\ q0_{ET2} \\ q0_{ETseq} \\ q0_{ET1} \end{pmatrix} := \begin{pmatrix} 1.596 \cdot 10^{-2} \\ 3.191 \cdot 10^{-2} \\ 5.319 \cdot 10^{-3} \\ 6.569 \cdot 10^{-3} \\ 4.384 \cdot 10^{-3} \\ 7.721 \cdot 10^{-5} \\ 1.171 \cdot 10^{-2} \\ 5.921 \cdot 10^{-3} \\ 1.243 \cdot 10^{-4} \\ 3.989 \cdot 10^{-1} \\ 1.996 \cdot 10^{-4} \\ 3.385 \cdot 10^{-1} \end{pmatrix} \qquad q0_{urine} := 0$$

Define rate constants. All rate constants are in units of 1/days and modifications are highlighted in yellow.

Absorption rate constants inferred from bioassay data by James et al. These are the only parameters in the biokinetic model that are modified.

$s_p \equiv 10^{-6}$ $s_{pt} \equiv 0.00189$ $s_t \equiv 0.000257$

Define transfer rate constants for the respiratory tract compartments.

$k_{AI1,bb1} := 0.02$ $k_{bb2,BB1} := 0.03$ $k_{ETseq,LNet} := 0.001$

$k_{AI1,blood} := s_p$ $k_{bb2,blood} := s_p$ $k_{ETseq,blood} := s_p$

$k_{AI1,TAI1} := s_{pt}$ $k_{bb2,Tbb2} := s_{pt}$ $k_{ETseq,TETseq} := s_{pt}$

$k_{AI2,bb1} := 0.001$ $k_{BB1,ET2} := 10$ $k_{BBseq,LNth} := 0.01$

$k_{AI2,blood} := s_p$ $k_{BB1,blood} := s_p$ $k_{BBseq,blood} := s_p$

$k_{AI2,TAI2} := s_{pt}$ $k_{BB1,TBB1} := s_{pt}$ $k_{BBseq,TBBseq} := s_{pt}$

$k_{AI3,bb1} := 0.0001$ $k_{BB2,ET2} := 0.03$ $k_{bbseq,LNth} := 0.01$

$k_{AI3,LNth} := 0.00002$ $k_{BB2,blood} := s_p$ $k_{bbseq,blood} := s_p$

$k_{AI3,blood} := s_p$ $k_{BB2,TBB2} := s_{pt}$ $k_{bbseq,Tbbseq} := s_{pt}$

$k_{AI3,TAI3} := s_{pt}$ $k_{ET2,S} := 100$ $k_{LNth,TLNth} := s_{pt}$

$k_{bb1,BB1} := 2$ $k_{ET2,blood} := s_p$ $k_{LNet,blood} := s_p$

$k_{bb1,blood} := s_p$ $k_{ET2,TET2} := s_{pt}$ $k_{LNet,TLNet} := s_{pt}$

$k_{bb1,Tbb1} := s_{pt}$ $k_{ET1,ENV} := 1$ $k_{LNth,blood} := s_p$

Define transfer rate constants for the transformed respiratory tract compartments.

$k_{TAI1,Tbb1} := k_{AI1,bb1}$ $k_{TBB2,TET2} := k_{BB2,ET2}$

$k_{TAI1,blood} := s_t$ $k_{TBB2,blood} := s_t$

$k_{TAI2,Tbb1} := k_{AI2,bb1}$ $k_{TET2,S} := k_{ET2,S}$

$k_{TAI2,blood} := s_t$ $k_{TET2,blood} := s_t$

$k_{TAI3,Tbb1} := k_{AI3,bb1}$ $k_{TETseq,TLNet} := k_{ETseq,LNet}$

$k_{TAI3,TLNth} := k_{AI3,LNth}$ $k_{TETseq,blood} := s_t$

$k_{TAI3,blood} := s_t$ $k_{TBBseq,TLNth} := k_{BBseq,LNth}$

$k_{Tbb1,TBB1} := k_{bb1,BB1}$ $k_{TBBseq,blood} := s_t$

$k_{Tbb1,blood} := s_t$ $k_{Tbbseq,TLNth} := k_{bbseq,LNth}$

$k_{Tbb2,TBB1} := k_{bb2,BB1}$ $k_{Tbbseq,blood} := s_t$

$k_{Tbb2,blood} := s_t$ $k_{TLNet,blood} := s_t$

$k_{TBB1,TET2} := k_{BB1,ET2}$ $k_{TLNth,blood} := s_t$ $k_{TBB1,blood} := s_t$

Define transfer rate constants for the systemic compartments.

$k_{blood,LIV1} := 0.1941$ $k_{blood,ST2} := 0.0129$ $k_{CS,CM} := 0.0000821$

$k_{blood,CS} := 0.1294$ $k_{ST0,blood} := 0.693$ $k_{TV,TM} := 0.000493$

$k_{blood,TS} := 0.1941$ $k_{UP,UBC} := 0.01386$ $k_{CV,CM} := 0.0000821$

$k_{blood,UBC} := 0.0129$ $k_{OKT,blood} := 0.00139$ $k_{CM,blood} := 0.0076$

$k_{blood,UP} := 0.00647$ $k_{ST1,blood} := 0.000475$ $k_{TM,blood} := 0.0076$

$k_{blood,OKT} := 0.00323$ $k_{ST1,UBC} := 0.000475$ $k_{LIV1,LIV2} := 0.00177$

$k_{blood,ULI} := 0.0129$ $k_{ST2,blood} := 0.000019$ $k_{LIV1,SI} := 0.000133$

$k_{blood,nads} := 0.00023$ $k_{TS,TV} := 0.000247$ $k_{LIV2,blood} := 0.000211$

$k_{blood,ST0} := 0.2773$ $k_{TS,TM} := 0.000493$ $k_{nads,blood} := 0.00019$

$k_{blood,ST1} := 0.0806$ $k_{CS,CV} := 0.0000411$ $k_{UBC,urine} := 12$

Define transfer rate constants for the GI tract.

$f_1 := 1 \cdot 10^{-5}$ $k_{S,SI} := 24$ $k_{SI,ULI} := 6$ $k_{SI,blood} := \frac{k_{SI,ULI} \cdot f_1}{1 - f_1}$ $k_{ULI,LLI} := \frac{24}{13}$ $k_{LLI,feces} := 1$

Calculate the total removal rate constants

$$\text{total}(k,\lambda) := \left| \begin{array}{l} K \leftarrow k \\ \text{for } comp \in 1..\text{cols}(k) \\ \quad \left| \begin{array}{l} K_{comp,comp} \leftarrow 0 \\ \text{for } j \in 1..\text{cols}(k) \\ \quad K_{comp,comp} \leftarrow K_{comp,comp} + k_{comp,j} \text{ if } comp \neq j \\ K_{comp,comp} \leftarrow -\left(K_{comp,comp} + \lambda\right) \end{array} \right. \\ K \end{array} \right.$$

$k_{urine,urine} := 0$

$k := \text{total}(k,\lambda)$

Calculate the coefficients and rate constants for the retention functions.

$$\text{coeff}(k,q0) := \left| \begin{array}{l} q0 \leftarrow \text{submatrix}(q0,1,\text{rows}(k),1,1) \\ V \leftarrow \text{eigenvecs}\left(k^{T}\right) \\ M \leftarrow \text{lsolve}(V,q0) \\ \text{for } j \in 1..\text{cols}(k) \\ \quad \text{for } i \in 1..\text{cols}(k) \\ \quad\quad C_{i,j} \leftarrow V_{i,j} \cdot M_j \\ C \end{array} \right.$$

$\gamma := \text{eigenvals}\left(k^{T}\right)$

$C := \text{coeff}(k, q0)$

$$q(t, comp) := \sum_{i=1}^{cols(k)} C_{comp,i} \cdot \exp\left[\left(\gamma_i\right) \cdot t\right]$$

Define urinary excretion function

$$\lambda := \frac{\ln(2)}{3.203 \times 10^{4}}$$

$87.7 \cdot yr = 3.203 \times 10^{4}\,day$

$e_u(t) := (q(t, urine) - q(t-1, urine)) \cdot e^{-\lambda \cdot t}$ This function defines the Pu excreted in urine between day t-1 and day t.

Evaluate USTUR 259 Case

$$\begin{pmatrix} t \\ e_{obs} \end{pmatrix} :=$$

2	0
3	0
4	0
76	0
123	0.16
150	0.07
186	0.07
209	0.1
264	0.16
283	0.18

$e_{obs} := e_{obs} \cdot pCi$

$i := 1..48$

$T_d := 6532$ number of days from intake to death

Calculate the Pu-238 intake, predicted urinary excretion, and predicted organ burdens

$$I := \frac{\sum_{i=1}^{48} e_{obs_i}}{\sum_{i=1}^{48} e_u(t_i)} \qquad I = 1.473 \times 10^6 \text{ pCi} \qquad I = 5.451 \times 10^4 \text{ Bq}$$

$$q_{lung} := I \cdot \left(\sum_{i=AI1}^{BBseq} q(T_d, i) \cdot e^{-\lambda \cdot T_d} + \sum_{i=TAI1}^{TBBseq} q(T_d, i) \cdot e^{-\lambda \cdot T_d} \right)$$

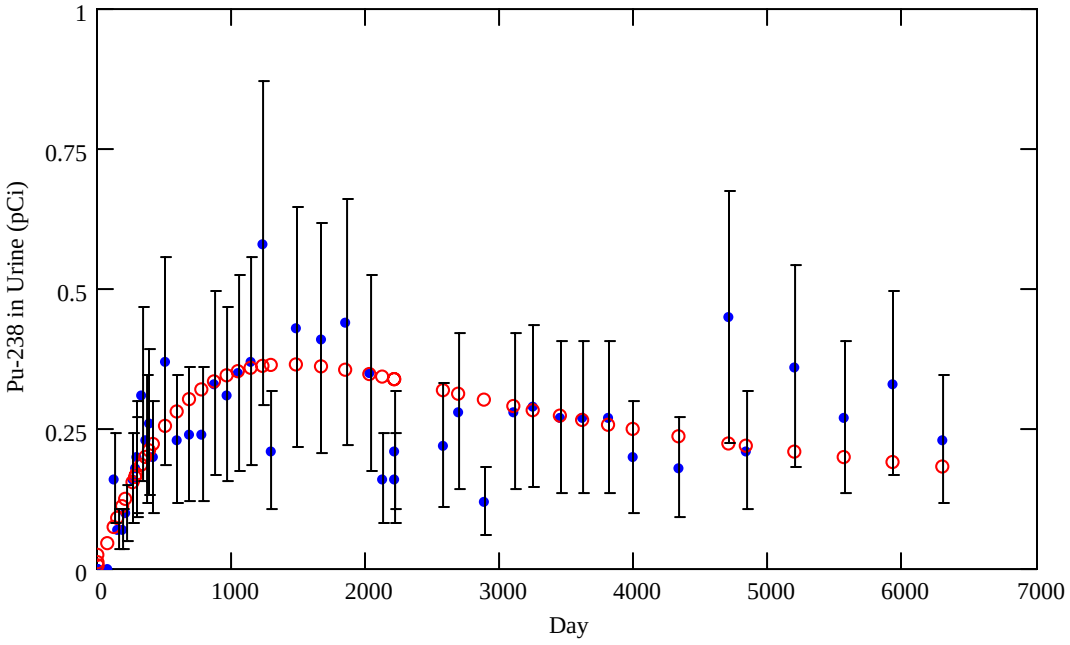
$$q_{bone} := I \cdot \left(\sum_{i=CV}^{TM} q(T_d, i) \cdot e^{-\lambda \cdot T_d} \right)$$

$$q_{liv} := I \cdot \left[\left(q(T_d, LIV1) + q(T_d, LIV2) \right) \cdot e^{-\lambda \cdot T_d} \right]$$

$$e_{exp_i} := e_u(t_i) \cdot I$$

$$\varepsilon_{high_i} := e_{obs_i} + 0.5 \cdot e_{obs_i}$$

$$\varepsilon_{low_i} := e_{obs_i} - 0.5 \cdot e_{obs_i}$$



Liver Autopsy Data	Lung Autopsy Data	Bone Autopsy Data
$137 \cdot Bq = 3.703 \times 10^{3}\,pCi$	$20.9 \cdot Bq = 5.649 \times 10^{2}\,pCi$	$104 \cdot Bq = 2.811 \times 10^{3}\,pCi$
+/-		+/-
$4 \cdot Bq = 1.081 \times 10^{2}\,pCi$	$q_{lung} = 683\,pCi$	$1 \cdot Bq = 2.703 \times 10^{1}\,pCi$
$q_{liv} = 2953\,pCi$		$q_{bone} = 4140\,pCi$

Appendix B

Evaluation of USTUR Case 0259 with Uncertainties

Evaluation of USTUR Case 0259 from data presented by A. C. James et al. *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled Pu238 Oxide Ceramic Particles* Health Physics 84(1):2-33:2003. Uncertainties from **urine bioassay** are calculated in this worksheet.

ORIGIN ≡ 1 nCi ≡ 37·Bq pCi ≡ 10^{-3}·nCi μCi ≡ 10^{6}·pCi

The compartments in the model are assigned numbers to clarify their use in the arrays to be defined.

AI1 := 1	bb1 := 4	BB1 := 7	ET2 := 10			
AI2 := 2	bb2 := 5	BB2 := 8	ETseq := 11	LNth := 13		
AI3 := 3	bbseq := 6	BBseq := 9	LNet := 12	ET1 := 14		
TAI1 := 15	Tbb1 := 18	TBB1 := 21	TET2 := 24			
TAI2 := 16	Tbb2 := 19	TBB2 := 22	TETseq := 25			
TAI3 := 17	Tbbseq := 20	TBBseq := 23	TLNet := 26	TLNth := 27		
S := 28	SI := 29	ULI := 30	LLI := 31			
blood := 32	ST0 := 35	CV := 38	TV := 41	OKT := 44	nads := 47	
LIV1 := 33	ST1 := 36	CS := 39	TS := 42	UP := 45	ENV := 48	urine := 50
LIV2 := 34	ST2 := 37	CM := 40	TM := 43	UBC := 46	feces := 49	

Deposition parameters calculated with LUDUC. These 1000 values assume 5 μm AMAD, a density of 10 g/cc, and light exercise.

$$\begin{pmatrix} DF_{ET1} \\ DF_{ET2} \\ DF_{BB} \\ DF_{bb} \\ DF_{AI} \\ Fs_{BB} \\ Fs_{bb} \end{pmatrix} :=$$

0.3824307	0.3618683	0.0215043	0.0164575	0.1045146	0.5605827	0.6211035
0.4117763	0.4768381	0.0114585	0.0026248	0.0302902	0.6252462	0.6516554
0.2854435	0.3096401	0.0181279	0.0122373	0.0555491	0.6261812	0.6701694
0.3640713	0.3770601	0.0147265	0.0030048	0.0242068	0.5873427	0.6121804
0.3614031	0.3861653	0.0118707	0.0123206	0.0990075	0.6184139	0.6778674
0.3513172	0.4606443	0.0220846	0.0085090	0.0468516	0.3974973	0.4262016
0.4115148	0.5665783	0.0158309	0.0067313	0.0294167	0.5511362	0.5840935
0.3544650	0.3765788	0.0050744	0.0052642	0.0232554	0.5171263	0.5598844
0.3327872	0.5143833	0.0092004	0.0052477	0.0305225	0.4724866	0.5001576
0.2299703	0.3362615	0.0111267	0.0288326	0.0861704	0.5291479	0.6004671

The function returns the deposition fractions in each compartment using the m^{th} row of the LUDUC parameter matrix. The geometric standard deviations are those given by Bolch et al, *Influences of Parameter Uncertainties within the ICRP 66 Respiratory Tract Model: Particle Deposition* Health Physics (81 (4):378-394; 2001. Any content not explicitly given has a value of zero.

$$\text{DepositionFractions}(m) := \left| \begin{array}{l} q0_{urine} \leftarrow 0 \\ q0_{AI1} \leftarrow \text{rlnorm}(1, \ln(0.3), \ln(1.10))_1 \cdot DF_{AI_m} \\ q0_{AI3} \leftarrow 0.1 \cdot DF_{AI_m} \\ q0_{AI2} \leftarrow DF_{AI_m} - q0_{AI1} - q0_{AI3} \\ q0_{bbseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{bb_m} \\ q0_{bb2} \leftarrow Fs_{bb_m} \cdot DF_{bb_m} \\ q0_{bb1} \leftarrow DF_{bb_m} - q0_{bbseq} - q0_{bb2} \\ q0_{BBseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{BB_m} \\ q0_{BB2} \leftarrow Fs_{BB_m} \cdot DF_{BB_m} \\ q0_{BB1} \leftarrow DF_{BB_m} - q0_{BBseq} - q0_{BB2} \\ q0_{ETseq} \leftarrow \text{rlnorm}(1, \ln(0.0005), \ln(1.73))_1 \cdot DF_{ET2_m} \\ q0_{ET2} \leftarrow DF_{ET2_m} - q0_{ETseq} \\ q0_{ET1} \leftarrow DF_{ET1_m} \\ q0 \end{array} \right.$$

Define transfer rate constants for the respiratory tract. The geometric standard deviations are those given by Bolch et al.

$\kappa_{lung}(k) :=$

$f_r \leftarrow -0.1566707$

$s_r \leftarrow 0.001891$

$s_s \leftarrow 0.000257$

$s_t \leftarrow s_s$

$s_{pt} \leftarrow (1 - f_r) \cdot (s_r - s_t)$

$s_p \leftarrow s_r - s_{pt}$

$k_{AI1,bb1} \leftarrow 0.02$

$k_{AI2,bb1} \leftarrow rlnorm(1, ln(0.001), ln(1.41))_1$

$k_{AI3,bb1} \leftarrow rlnorm(1, ln(0.0001), ln(1.73))_1$

$k_{AI3,LNth} \leftarrow rlnorm(1, ln(0.00002), ln(1.41))_1$

$k_{bb1,BB1} \leftarrow rlnorm(1, ln(2), ln(1.41))_1$

$k_{bb2,BB1} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{BB1,ET2} \leftarrow rlnorm(1, ln(10), ln(1.22))_1$

$k_{BB2,ET2} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{ET2,S} \leftarrow rlnorm(1, ln(100), ln(1.73))_1$

$k_{ET1,ENV} \leftarrow rlnorm(1, ln(1), ln(1.73))_1$

$k_{ETseq,LNet} \leftarrow rlnorm(1, ln(0.001), ln(1.73))_1$

$k_{BBseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

$k_{bbseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

for $i \in AI1 .. LNth$

  for $j \in AI1 .. LNth$

    $k_{i+14,j+14} \leftarrow k_{i,j}$

$k_{TET2,S} \leftarrow k_{ET2,S}$

for $i \in AI1 .. LNth$

  $k_{i,i+14} \leftarrow s_{pt}$

  $k_{i,blood} \leftarrow s_p$

for $i \in TAI1 .. TLNth$

  $k_{i,blood} \leftarrow s_t$

k

Define transfer rate constants for the systemic compartments and GI tract. For lack of better information, the geometric standard deviations are assumed to be equal to the constant α, which is assumed to equal 1.001 here. This results in basically a deterministic (point) estimate of the parameters.

$$\kappa_{sys1}(k) := \begin{| } k_{blood,\,LIV1} \leftarrow rlnorm(1, ln(0.1941), ln(\alpha))_1 \\ k_{blood,\,CS} \leftarrow rlnorm(1, ln(0.1294), ln(\alpha))_1 \\ k_{blood,\,TS} \leftarrow rlnorm(1, ln(0.1941), ln(\alpha))_1 \\ k_{blood,\,UBC} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k_{blood,\,UP} \leftarrow rlnorm(1, ln(0.00647), ln(\alpha))_1 \\ k_{blood,\,OKT} \leftarrow rlnorm(1, ln(0.00323), ln(\alpha))_1 \\ k_{blood,\,ULI} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k_{blood,\,nads} \leftarrow rlnorm(1, ln(0.00023), ln(\alpha))_1 \\ k_{blood,\,ST0} \leftarrow rlnorm(1, ln(0.2773), ln(\alpha))_1 \\ k_{blood,\,ST1} \leftarrow rlnorm(1, ln(0.0806), ln(\alpha))_1 \\ k_{blood,\,ST2} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k \end{|}$$

$$\kappa_{sys2}(k) := \begin{| } k_{ST0,\,blood} \leftarrow rlnorm(1, ln(0.693), ln(\alpha))_1 \\ k_{OKT,\,blood} \leftarrow rlnorm(1, ln(0.00139), ln(\alpha))_1 \\ k_{ST1,\,blood} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{ST2,\,blood} \leftarrow rlnorm(1, ln(0.000019), ln(\alpha))_1 \\ k_{CM,\,blood} \leftarrow rlnorm(1, ln(0.0076), ln(\alpha))_1 \\ k_{TM,\,blood} \leftarrow rlnorm(1, ln(0.0076), ln(\alpha))_1 \\ k_{LIV2,\,blood} \leftarrow rlnorm(1, ln(0.000211), ln(\alpha))_1 \\ k_{nads,\,blood} \leftarrow rlnorm(1, ln(0.00019), ln(\alpha))_1 \\ k \end{|}$$

$$\kappa_{sys3}(k) := \begin{| k_{UP,UBC} \leftarrow rlnorm(1, ln(0.01386), ln(\alpha))_1 \\ k_{ST1,UBC} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{TS,TV} \leftarrow rlnorm(1, ln(0.000247), ln(\alpha))_1 \\ k_{TS,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CS,CV} \leftarrow rlnorm(1, ln(0.0000411), ln(\alpha))_1 \\ k_{CS,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{TV,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CV,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{LIV1,LIV2} \leftarrow rlnorm(1, ln(0.00177), ln(\alpha))_1 \\ k_{LIV1,SI} \leftarrow rlnorm(1, ln(0.000133), ln(\alpha))_1 \\ k_{UBC,urine} \leftarrow rlnorm(1, ln(12), ln(\alpha))_1 \\ k |$$

$$\kappa_{GI}(k) := \begin{| f_1 \leftarrow 10^{-7} \\ k_{S,SI} \leftarrow rlnorm(1, ln(24), ln(\alpha))_1 \\ k_{SI,ULI} \leftarrow rlnorm(1, ln(6), ln(\alpha))_1 \\ k_{SI,blood} \leftarrow \frac{k_{SI,ULI} \cdot f_1}{1 - f_1} \\ k_{ULI,LLI} \leftarrow rlnorm\left(1, ln\left(\frac{24}{13}\right), ln(\alpha)\right)_1 \\ k_{LLI,feces} \leftarrow rlnorm(1, ln(1), ln(\alpha))_1 \\ k |$$

Calculate the total removal rate constants

$$total(k, \lambda) := \begin{| K \leftarrow k \\ \text{for } comp \in 1..cols(k) \\ \quad \begin{| K_{comp,comp} \leftarrow 0 \\ \quad \text{for } j \in 1..cols(k) \\ \quad\quad K_{comp,comp} \leftarrow K_{comp,comp} + k_{comp,j} \text{ if } comp \neq j \\ \quad K_{comp,comp} \leftarrow -(K_{comp,comp} + \lambda) \\ K |$$

This function creates a complete rate constant matrix.

$$\text{RateMatrix}(k) := \left| \begin{array}{l} k \leftarrow \kappa_{lung}(k) \\ k \leftarrow \kappa_{sys1}(k) \\ k \leftarrow \kappa_{sys2}(k) \\ k \leftarrow \kappa_{sys3}(k) \\ k \leftarrow \kappa_{GI}(k) \\ k \leftarrow \text{total}(k, 0) \\ k \end{array} \right.$$

Calculate the coefficients and rate constants for the retention functions.

$$\text{coeff}(k, q0) := \left| \begin{array}{l} q0 \leftarrow \text{submatrix}(q0, 1, \text{rows}(k), 1, 1) \\ V \leftarrow \text{eigenvecs}\left(k^{T}\right) \\ M \leftarrow \text{lsolve}(V, q0) \\ \text{for } j \in 1 .. \text{cols}(k) \\ \quad \text{for } i \in 1 .. \text{cols}(k) \\ \quad\quad C_{i,j} \leftarrow V_{i,j} \cdot M_{j} \\ C \end{array} \right.$$

$$q(t, comp, C, \gamma) := \sum_{i=1}^{\text{rows}(\gamma)} C_{comp,i} \cdot e^{\left[-(\gamma_i) \cdot t\right]}$$

Urinary excretion data for USTUR 0259. Time t is in days and observed urinary excretion e_{obs} is in pCi per day.

$$\begin{pmatrix} t \\ e_{obs} \end{pmatrix} :=$$

2	0
3	0
4	0
76	0
123	0.16
150	0.07
186	0.07
209	0.1
264	0.16
283	0.18

$$\lambda := \frac{\ln(2)}{\left(3.203 \times 10^{4}\right)}$$ decay constant for Pu-238

$\alpha \equiv 1.001$ σ_g for systemic parameters

$T_d := 6532$ number of days from intake to death

$$i := 1 .. \text{rows}(e_{obs})$$

This function calculates the organ burdens of interest, intake, and urinary excretion for a given vector of initial compartment contents *q0*.

$$\text{Results}(q0) := \left| \begin{array}{l} k_{urine,\,urine} \leftarrow 0 \\ \text{for } i \in 1..urine \\ \quad \text{for } j \in 1..urine \\ \quad\quad k_{i,\,j} \leftarrow 0 \\ k \leftarrow \text{RateMatrix}(k) \\ \gamma \leftarrow \text{eigenvals}\left(k^{T}\right) \\ C \leftarrow \text{coeff}(k, q0) \\ q_{lung} \leftarrow \sum_{i=AI1}^{BBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} + \sum_{i=TAI1}^{TBBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{bone} \leftarrow \sum_{i=CV}^{TM} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{liv} \leftarrow \left(q\left(T_d, LIV1, C, \gamma\right) + q\left(T_d, LIV2, C, \gamma\right)\right) \cdot e^{-\lambda \cdot T_d} \\ q_{urine} \leftarrow q\left(T_d, urine, C, \gamma\right) \\ \text{for } j \in 1..\text{rows}(t) \\ \quad e_{exp_j} \leftarrow \left[q\left(t_j, urine, C, \gamma\right) - q\left[\left(t_j - 1\right), urine, C, \gamma\right]\right] \cdot e^{-\lambda \cdot t_j} \\ I \leftarrow \dfrac{\sum_{i=1}^{\text{rows}(t)} e_{obs_i}}{\sum_{i=1}^{\text{rows}(t)} e_{exp_i}} \\ \begin{pmatrix} I \\ e_{exp} \\ q_{liv} \\ q_{bone} \\ q_{lung} \\ q_{urine} \end{pmatrix} \end{array} \right.$$

$N := 1000$

$m := 1..N$

All of the functions defined above are executed below and the results assigned to the matrix A. Note that in Mathcad a function can return only one parameter, which may be a rather complex matrix as in this case.

$$A := \left| \begin{array}{l} \text{for } m \in 1..N \\ \quad A_m \leftarrow \text{Results}(\text{DepositionFractions}(m)) \\ A \end{array} \right.$$

To make things clearer, the relevant parts of A are assigned to matrices with more meaningful names.

$\text{Intake}_m := (A_m)_1$ The 1000 intakes calculated from iterative fits to the urine data in units of pCi.

$\text{IRF}_m := (A_m)_2$ The 24-hour incremental urinary excretion fractions for Pu-238.

$q_{\text{urine}_m} := \text{Intake}_m \cdot (A_m)_6$ The total amount of stable plutonium excreted to the urine compartment over 6532 days.

$q_{\text{bone}_m} := \text{Intake}_m \cdot (A_m)_4$ The skeletal burdens in pCi at 6532 days after intake.

$q_{\text{liv}_m} := \text{Intake}_m \cdot (A_m)_3$ The liver burdens in pCi at 6532 days after intake.

$q_{\text{lung}_m} := \text{Intake}_m \cdot (A_m)_5$ The lung burdens in pCi at 6532 days after intake.

Intakes Calculated from Urine Data

$\text{mean}(\text{Intake}) = 1.731 \times 10^6$

$\text{stdev}(\text{Intake}) = 9.397 \times 10^5$

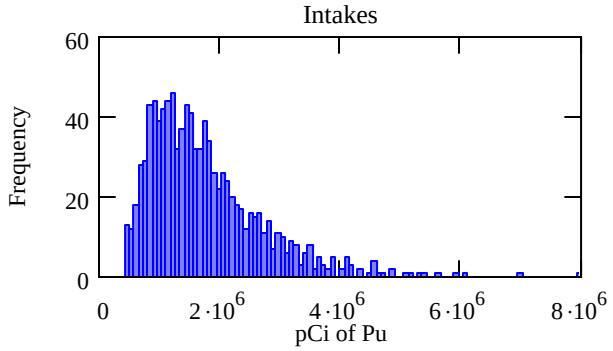
$\max(\text{Intake}) = 7.992 \times 10^6$

$\min(\text{Intake}) = 4.046 \times 10^5$

$\frac{\text{stdev}(\text{Intake})}{\text{mean}(\text{Intake})} = 5.427 \times 10^{-1}$

$\text{Intake}_{\text{mean}} := \text{mean}(\text{Intake})$

$G := \text{histogram}(100, \text{Intake})$



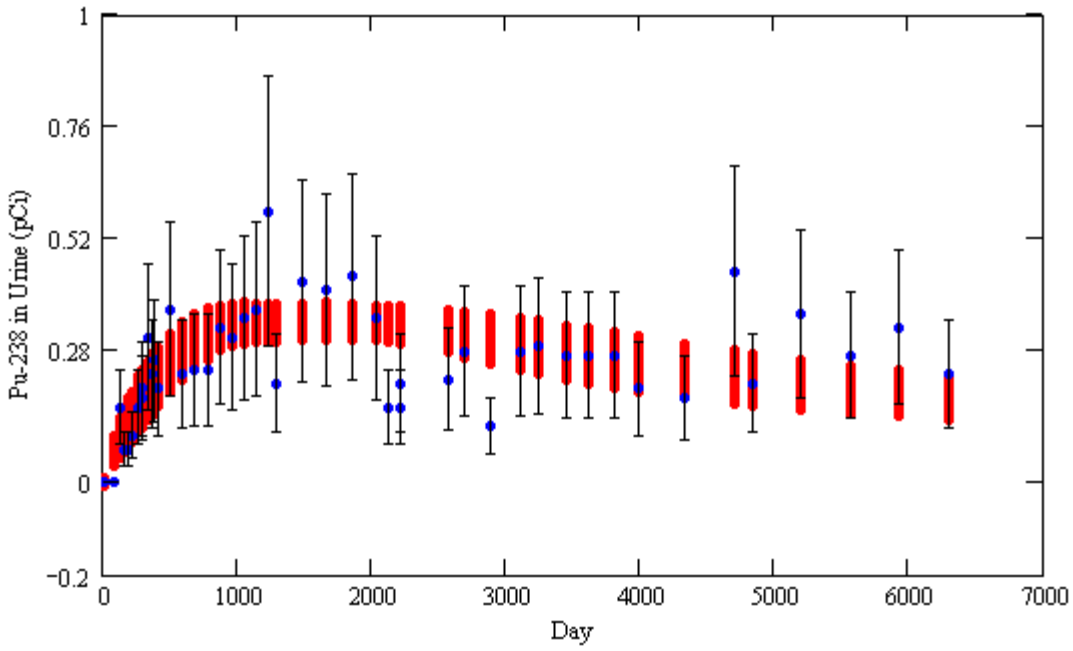
Urinary Excretion

$j := 1 .. N$

$i := 1 .. 48$

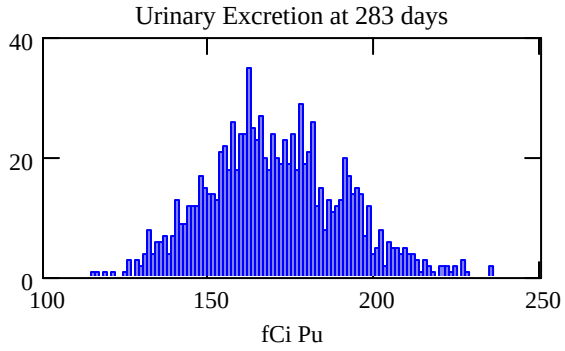
$$e_{exp_{j,i}} := Intake_j \cdot \left(IRF_j\right)_i$$

$$\varepsilon_{high_i} := e_{obs_i} + 0.5 \cdot e_{obs_i} \qquad \varepsilon_{low_i} := e_{obs_i} - 0.5 \cdot e_{obs_i}$$

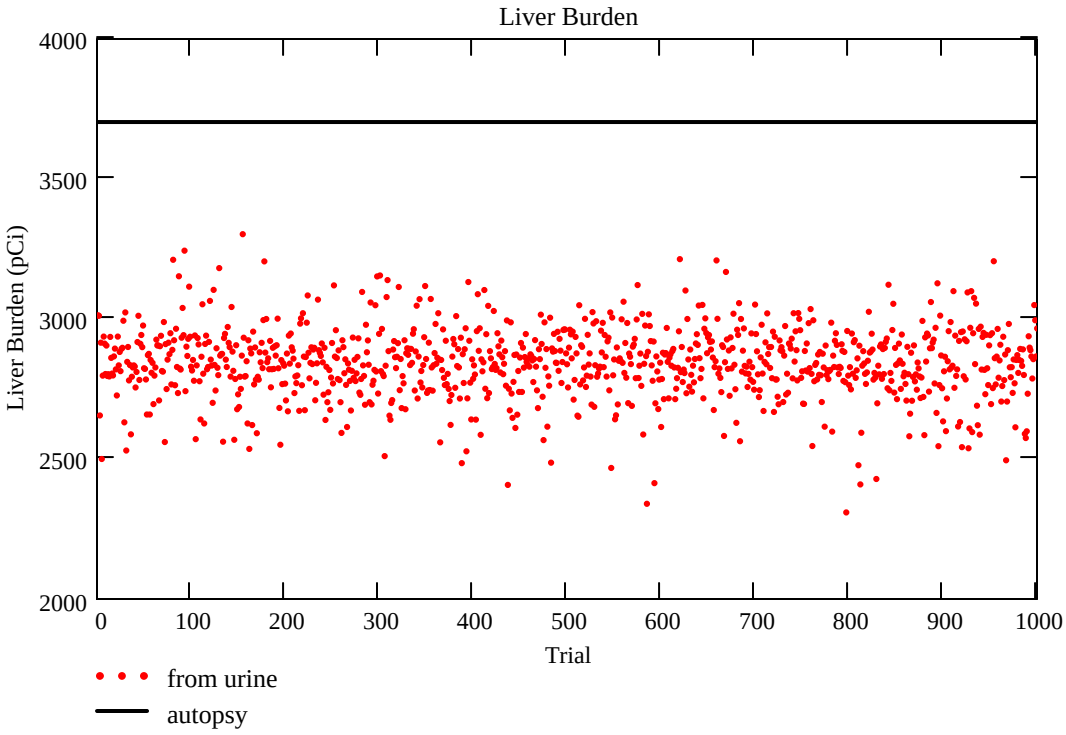


The uncertainties in the observed urinary excretion are arbitrarily set to +/-50% of the observed value.

$$G := histogram\left(100, e_{exp}^{\langle 10 \rangle} \cdot 1000\right)$$



Liver



Liver Autopsy Data

$137 \cdot Bq = 3.703 \times 10^{3}\ pCi$

+/-

$4 \cdot Bq = 1.081 \times 10^{2}\ pCi$

$\text{mean}(q_{liv}) = 2.842 \times 10^{3}$

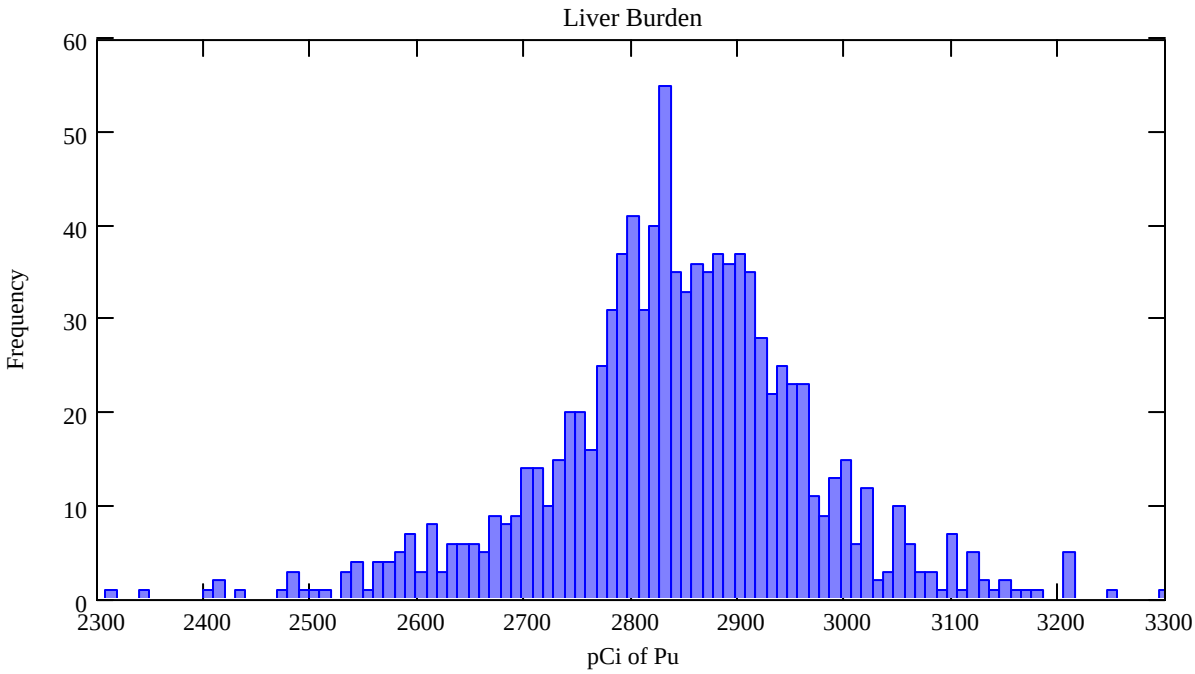
$\text{stdev}(q_{liv}) = 1.247 \times 10^{2}$

$\max(q_{liv}) = 3.303 \times 10^{3}$

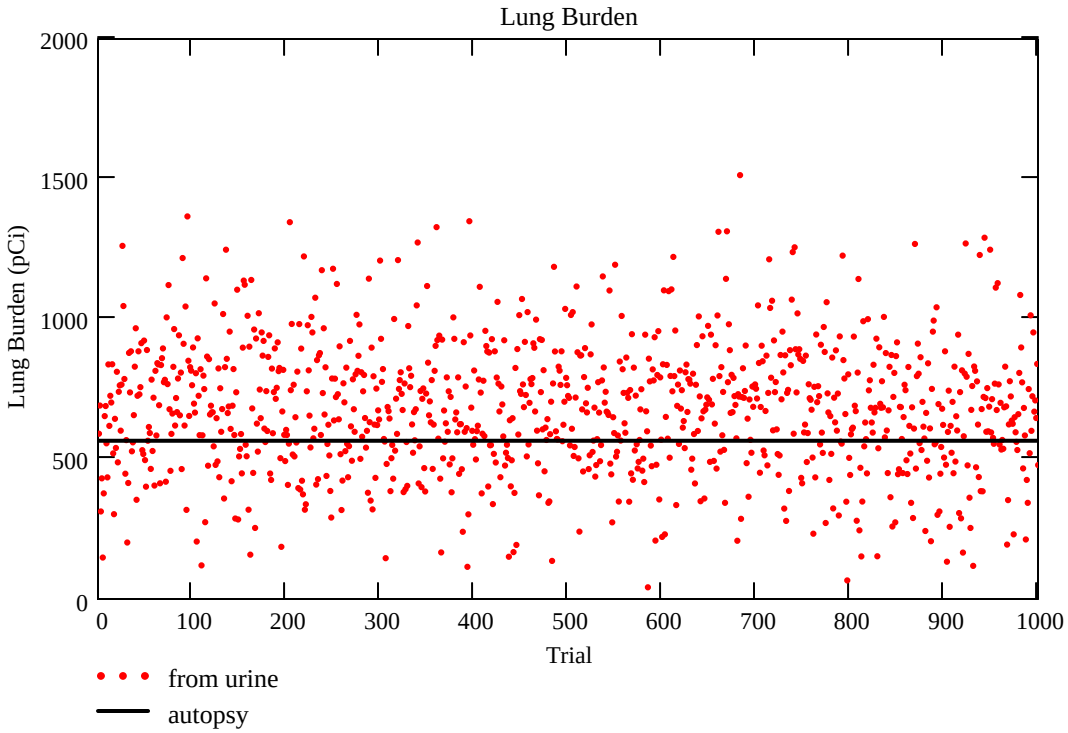
$\min(q_{liv}) = 2.309 \times 10^{3}$

$\frac{\text{stdev}(q_{liv})}{\text{mean}(q_{liv})} = 4.388 \times 10^{-2}$

$G := \text{histogram}(100, q_{liv})$



Lung



Lung Autopsy Data

$20.9 \cdot Bq = 5.649 \times 10^{2}\ pCi$

$\text{mean}(q_{lung}) = 6.796 \times 10^{2}$

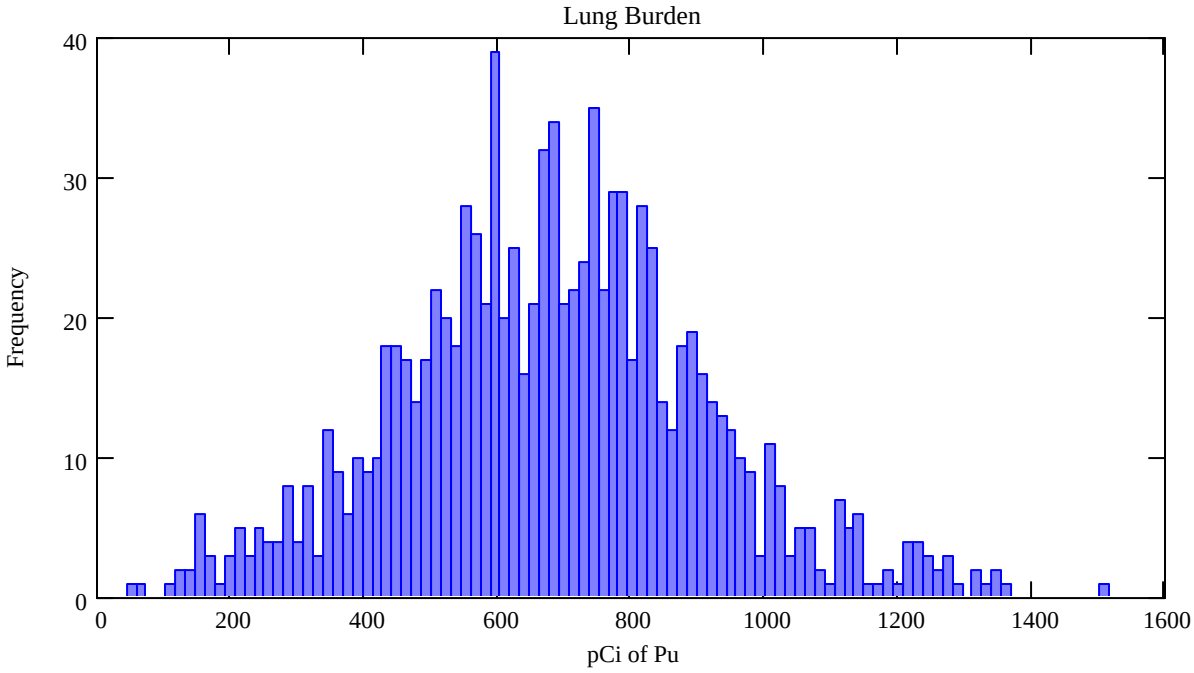
$\text{stdev}(q_{lung}) = 2.296 \times 10^{2}$

$\max(q_{lung}) = 1.514 \times 10^{3}$

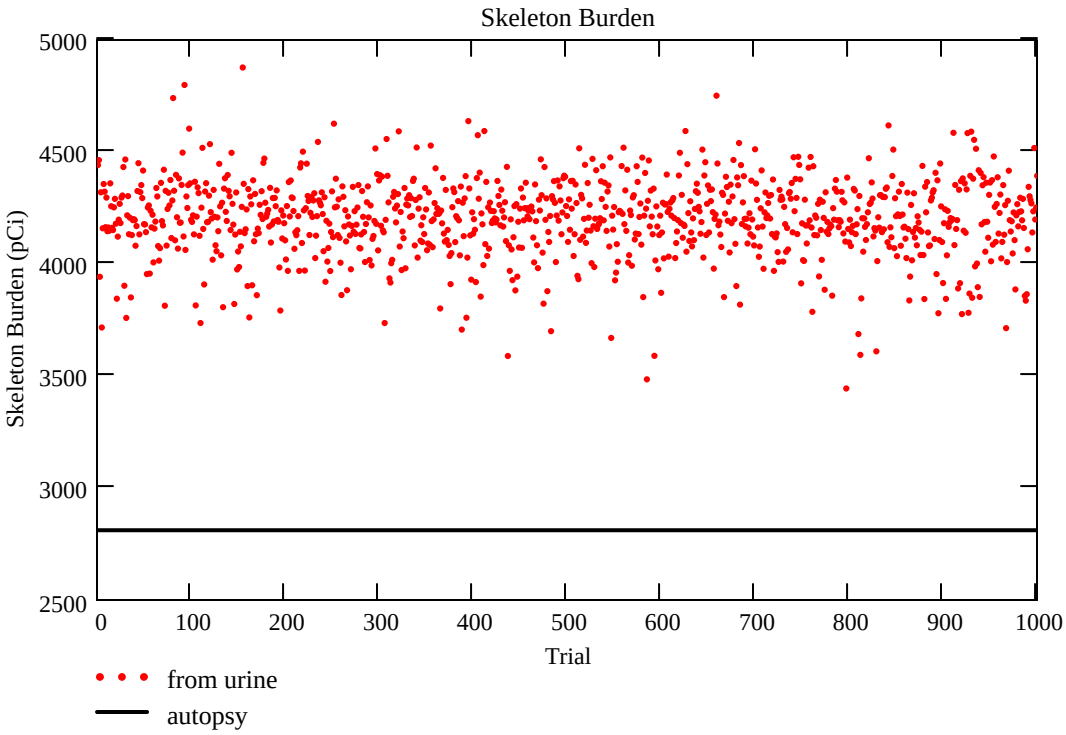
$\min(q_{lung}) = 4.125 \times 10^{1}$

$$\frac{\text{stdev}(q_{lung})}{\text{mean}(q_{lung})} = 3.379 \times 10^{-1}$$

$G := \text{histogram}(100, q_{lung})$



Skeleton (including all marrow)



Bone Autopsy Data

$104 \cdot Bq = 2.811 \times 10^{3}\ pCi$

+/-

$1 \cdot Bq = 2.703 \times 10^{1}\ pCi$

$\text{mean}(q_{bone}) = 4.201 \times 10^{3}$

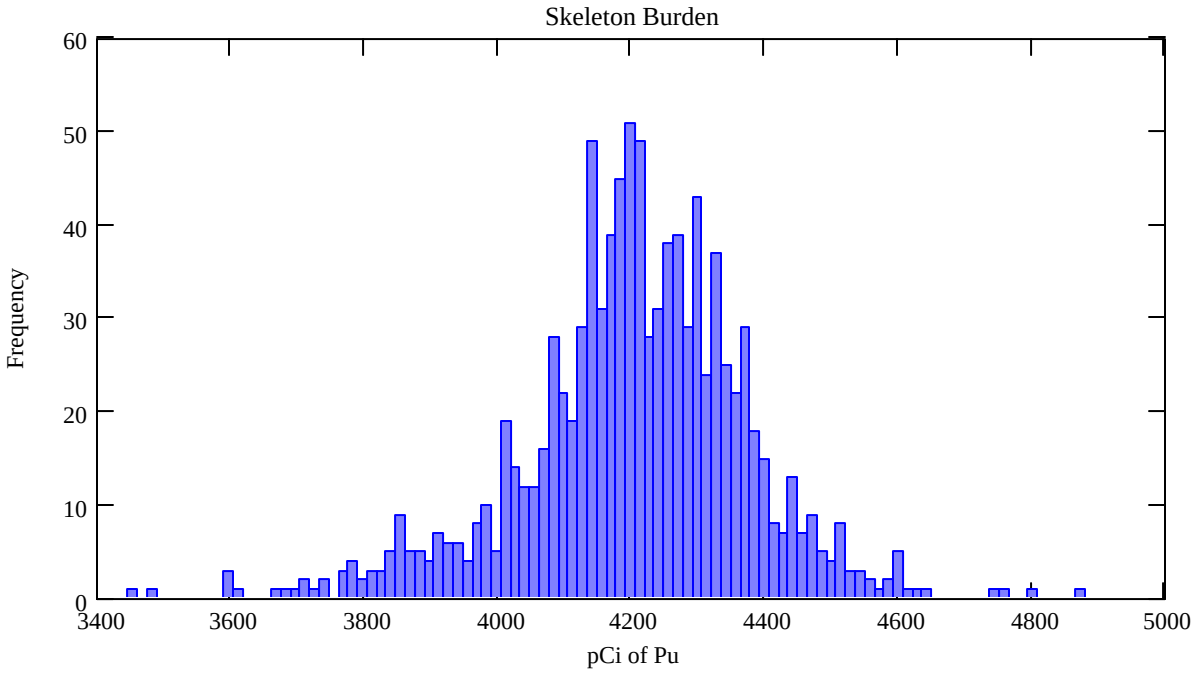
$\text{stdev}(q_{bone}) = 1.709 \times 10^{2}$

$\max(q_{bone}) = 4.877 \times 10^{3}$

$\min(q_{bone}) = 3.444 \times 10^{3}$

$\frac{\text{stdev}(q_{bone})}{\text{mean}(q_{bone})} = 4.069 \times 10^{-2}$

$G := \text{histogram}(100, q_{bone})$



Appendix C

Evaluation of USTUR Case 0259 with Uncertainties

Evaluation of USTUR Case 0259 from data presented by A. C. James et al. *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled Pu238 Oxide Ceramic Particles* Health Physics 84(1):2-33:2003.
Uncertainties from **urine bioassay** are calculated in this worksheet.

ORIGIN ≡ 1 nCi ≡ 37·Bq pCi ≡ 10^{-3}·nCi μCi ≡ 10^{6}·pCi

The compartments in the model are assigned numbers to clarify their use in the arrays to be defined.

AI1 := 1	bb1 := 4	BB1 := 7	ET2 := 10			
AI2 := 2	bb2 := 5	BB2 := 8	ETseq := 11	LNth := 13		
AI3 := 3	bbseq := 6	BBseq := 9	LNet := 12	ET1 := 14		
TAI1 := 15	Tbb1 := 18	TBB1 := 21	TET2 := 24			
TAI2 := 16	Tbb2 := 19	TBB2 := 22	TETseq := 25			
TAI3 := 17	Tbbseq := 20	TBBseq := 23	TLNet := 26	TLNth := 27		
S := 28	SI := 29	ULI := 30	LLI := 31			
blood := 32	ST0 := 35	CV := 38	TV := 41	OKT := 44	nads := 47	
LIV1 := 33	ST1 := 36	CS := 39	TS := 42	UP := 45	ENV := 48	urine := 50
LIV2 := 34	ST2 := 37	CM := 40	TM := 43	UBC := 46	feces := 49	

Deposition parameters calculated with LUDUC. These 1000 values assume 5 μm AMAD, a density of 10 g/cc, and light exercise.

$$\begin{pmatrix} DF_{ET1} \\ DF_{ET2} \\ DF_{BB} \\ DF_{bb} \\ DF_{AI} \\ Fs_{BB} \\ Fs_{bb} \end{pmatrix} :=$$

0.3824307	0.3618683	0.0215043	0.0164575	0.1045146	0.5605827	0.6211035
0.4117763	0.4768381	0.0114585	0.0026248	0.0302902	0.6252462	0.6516554
0.2854435	0.3096401	0.0181279	0.0122373	0.0555491	0.6261812	0.6701694
0.3640713	0.3770601	0.0147265	0.0030048	0.0242068	0.5873427	0.6121804
0.3614031	0.3861653	0.0118707	0.0123206	0.0990075	0.6184139	0.6778674
0.3513172	0.4606443	0.0220846	0.0085090	0.0468516	0.3974973	0.4262016
0.4115148	0.5665783	0.0158309	0.0067313	0.0294167	0.5511362	0.5840935
0.3544650	0.3765788	0.0050744	0.0052642	0.0232554	0.5171263	0.5598844
0.3327872	0.5143833	0.0092004	0.0052477	0.0305225	0.4724866	0.5001576
0.2299703	0.3362615	0.0111267	0.0288326	0.0861704	0.5291479	0.6004671

The function returns the deposition fractions in each compartment using the m^{th} row of the LUDUC parameter matrix. The geometric standard deviations are those given by Bolch et al, *Influences of Parameter Uncertainties within the ICRP 66 Respiratory Tract Model: Particle Deposition* Health Physics (81 (4):378-394; 2001. Any content not explicitly given has a value of zero.

$$\text{DepositionFractions}(m) := \left| \begin{array}{l} q0_{urine} \leftarrow 0 \\ q0_{AI1} \leftarrow \text{rlnorm}(1, \ln(0.3), \ln(1.10))_1 \cdot DF_{AI_m} \\ q0_{AI3} \leftarrow 0.1 \cdot DF_{AI_m} \\ q0_{AI2} \leftarrow DF_{AI_m} - q0_{AI1} - q0_{AI3} \\ q0_{bbseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{bb_m} \\ q0_{bb2} \leftarrow Fs_{bb_m} \cdot DF_{bb_m} \\ q0_{bb1} \leftarrow DF_{bb_m} - q0_{bbseq} - q0_{bb2} \\ q0_{BBseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{BB_m} \\ q0_{BB2} \leftarrow Fs_{BB_m} \cdot DF_{BB_m} \\ q0_{BB1} \leftarrow DF_{BB_m} - q0_{BBseq} - q0_{BB2} \\ q0_{ETseq} \leftarrow \text{rlnorm}(1, \ln(0.0005), \ln(1.73))_1 \cdot DF_{ET2_m} \\ q0_{ET2} \leftarrow DF_{ET2_m} - q0_{ETseq} \\ q0_{ET1} \leftarrow DF_{ET1_m} \\ q0 \end{array} \right.$$

Define transfer rate constants for the respiratory tract. The geometric standard deviations are those given by Bolch et al.

$\kappa_{lung}(k) :=$

$f_r \leftarrow -0.1566707$

$s_r \leftarrow 0.001891$

$s_s \leftarrow 0.000257$

$s_t \leftarrow s_s$

$s_{pt} \leftarrow (1 - f_r)\cdot(s_r - s_t)$

$s_p \leftarrow s_r - s_{pt}$

$k_{AI1,bb1} \leftarrow 0.02$

$k_{AI2,bb1} \leftarrow rlnorm(1, ln(0.001), ln(1.41))_1$

$k_{AI3,bb1} \leftarrow rlnorm(1, ln(0.0001), ln(1.73))_1$

$k_{AI3,LNth} \leftarrow rlnorm(1, ln(0.00002\cdot 1.55), ln(1.41))_1$

$k_{bb1,BB1} \leftarrow rlnorm(1, ln(2), ln(1.41))_1$

$k_{bb2,BB1} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{BB1,ET2} \leftarrow rlnorm(1, ln(10), ln(1.22))_1$

$k_{BB2,ET2} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{ET2,S} \leftarrow rlnorm(1, ln(100), ln(1.73))_1$

$k_{ET1,ENV} \leftarrow rlnorm(1, ln(1), ln(1.73))_1$

$k_{ETseq,LNet} \leftarrow rlnorm(1, ln(0.001), ln(1.73))_1$

$k_{BBseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

$k_{bbseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

for $i \in AI1 .. LNth$

  for $j \in AI1 .. LNth$

    $k_{i+14,j+14} \leftarrow k_{i,j}$

$k_{TET2,S} \leftarrow k_{ET2,S}$

for $i \in AI1 .. LNth$

  $k_{i,i+14} \leftarrow s_{pt}$

  $k_{i,blood} \leftarrow s_p$

for $i \in TAI1 .. TLNth$

  $k_{i,blood} \leftarrow s_t$

k

Define transfer rate constants for the systemic compartments and GI tract. For lack of better information, the geometric standard deviations are assumed to be equal to the constant α, which is assumed to equal 1.001 here. This results in basically a deterministic (point) estimate of the parameters. Also, note that modifications per James et al. are implemented here.

$$\kappa_{sys1}(k) := \left| \begin{array}{l} k_{blood,\,LIV1} \leftarrow rlnorm\left(1, \ln(0.1941 \cdot 1.412), \ln(\alpha)\right)_1 \\ k_{blood,\,CS} \leftarrow rlnorm\left(1, \ln(0.1294 \cdot 0.420), \ln(\alpha)\right)_1 \\ k_{blood,\,TS} \leftarrow rlnorm\left(1, \ln(0.1941 \cdot 1.425), \ln(\alpha)\right)_1 \\ k_{blood,\,UBC} \leftarrow rlnorm\left(1, \ln(0.0129 \cdot 1.12), \ln(\alpha)\right)_1 \\ k_{blood,\,UP} \leftarrow rlnorm\left(1, \ln(0.00647 \cdot 1.12), \ln(\alpha)\right)_1 \\ k_{blood,\,OKT} \leftarrow rlnorm\left(1, \ln(0.00323), \ln(\alpha)\right)_1 \\ k_{blood,\,ULI} \leftarrow rlnorm\left(1, \ln(0.0129), \ln(\alpha)\right)_1 \\ k_{blood,\,nads} \leftarrow rlnorm\left(1, \ln(0.00023), \ln(\alpha)\right)_1 \\ k_{blood,\,ST0} \leftarrow rlnorm\left(1, \ln(0.2773), \ln(\alpha)\right)_1 \\ k_{blood,\,ST1} \leftarrow rlnorm\left(1, \ln(0.0806), \ln(\alpha)\right)_1 \\ k_{blood,\,ST2} \leftarrow rlnorm\left(1, \ln(0.0129), \ln(\alpha)\right)_1 \\ k \end{array} \right.$$

$$\kappa_{sys2}(k) := \left| \begin{array}{l} k_{ST0,\,blood} \leftarrow rlnorm\left(1, \ln(0.693), \ln(\alpha)\right)_1 \\ k_{OKT,\,blood} \leftarrow rlnorm\left(1, \ln(0.00139), \ln(\alpha)\right)_1 \\ k_{ST1,\,blood} \leftarrow rlnorm\left(1, \ln(0.000475), \ln(\alpha)\right)_1 \\ k_{ST2,\,blood} \leftarrow rlnorm\left(1, \ln(0.000019), \ln(\alpha)\right)_1 \\ k_{CM,\,blood} \leftarrow rlnorm\left(1, \ln(0.0076), \ln(\alpha)\right)_1 \\ k_{TM,\,blood} \leftarrow rlnorm\left(1, \ln(0.0076), \ln(\alpha)\right)_1 \\ k_{LIV2,\,blood} \leftarrow rlnorm\left(1, \ln(0.000211), \ln(\alpha)\right)_1 \\ k_{nads,\,blood} \leftarrow rlnorm\left(1, \ln(0.00019), \ln(\alpha)\right)_1 \\ k \end{array} \right.$$

$$\kappa_{sys3}(k) := \begin{| k_{UP,UBC} \leftarrow rlnorm(1, ln(0.01386), ln(\alpha))_1 \\ k_{ST1,UBC} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{TS,TV} \leftarrow rlnorm(1, ln(0.000247), ln(\alpha))_1 \\ k_{TS,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CS,CV} \leftarrow rlnorm(1, ln(0.0000411), ln(\alpha))_1 \\ k_{CS,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{TV,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CV,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{LIV1,LIV2} \leftarrow rlnorm(1, ln(0.00177), ln(\alpha))_1 \\ k_{LIV1,SI} \leftarrow rlnorm(1, ln(0.000133), ln(\alpha))_1 \\ k_{UBC,urine} \leftarrow rlnorm(1, ln(12), ln(\alpha))_1 \\ k |$$

$$\kappa_{GI}(k) := \begin{| f_1 \leftarrow 10^{-7} \\ k_{S,SI} \leftarrow rlnorm(1, ln(24), ln(\alpha))_1 \\ k_{SI,ULI} \leftarrow rlnorm(1, ln(6), ln(\alpha))_1 \\ k_{SI,blood} \leftarrow \frac{k_{SI,ULI} \cdot f_1}{1 - f_1} \\ k_{ULI,LLI} \leftarrow rlnorm\left(1, ln\left(\frac{24}{13}\right), ln(\alpha)\right)_1 \\ k_{LLI,feces} \leftarrow rlnorm(1, ln(1), ln(\alpha))_1 \\ k |$$

Calculate the total removal rate constants

$$total(k, \lambda) := \begin{| K \leftarrow k \\ \text{for } comp \in 1..cols(k) \\ \quad \begin{| K_{comp,comp} \leftarrow 0 \\ \quad \text{for } j \in 1..cols(k) \\ \quad\quad K_{comp,comp} \leftarrow K_{comp,comp} + k_{comp,j} \text{ if } comp \neq j \\ \quad K_{comp,comp} \leftarrow -(K_{comp,comp} + \lambda) \\ K |$$

This function creates a complete rate constant matrix.

$$\text{RateMatrix}(k) := \begin{array}{l} k \leftarrow \kappa_{lung}(k) \\ k \leftarrow \kappa_{sys1}(k) \\ k \leftarrow \kappa_{sys2}(k) \\ k \leftarrow \kappa_{sys3}(k) \\ k \leftarrow \kappa_{GI}(k) \\ k \leftarrow \text{total}(k, 0) \\ k \end{array}$$

Calculate the coefficients and rate constants for the retention functions.

$$\text{coeff}(k, q0) := \begin{array}{l} q0 \leftarrow \text{submatrix}(q0, 1, \text{rows}(k), 1, 1) \\ V \leftarrow \text{eigenvecs}\left(k^{T}\right) \\ M \leftarrow \text{lsolve}(V, q0) \\ \text{for } j \in 1..\text{cols}(k) \\ \quad \text{for } i \in 1..\text{cols}(k) \\ \quad\quad C_{i,j} \leftarrow V_{i,j} \cdot M_{j} \\ C \end{array}$$

$$q(t, comp, C, \gamma) := \sum_{i=1}^{\text{rows}(\gamma)} C_{comp,i} \cdot e^{\left[-(\gamma_i) \cdot t\right]}$$

Urinary excretion data for USTUR 0259. Time t is in days and observed urinary excretion e_{obs} is in pCi per day.

$$\begin{pmatrix} t \\ e_{obs} \end{pmatrix} :=$$

2	0
3	0
4	0
76	0
123	0.16
150	0.07
186	0.07
209	0.1
264	0.16
283	0.18

$$\lambda := \frac{\ln(2)}{\left(3.203 \times 10^{4}\right)}$$ decay constant for Pu-238

$\alpha \equiv 1.001$ σ_g for systemic parameters

$T_d := 6532$ number of days from intake to death

$$i := 1..\text{rows}(e_{obs})$$

This function calculates the organ burdens of interest, intake, and urinary excretion for a given vector of initial compartment contents *q0*.

$$\text{Results}(q0) := \left| \begin{array}{l} k_{urine,\,urine} \leftarrow 0 \\ \text{for } i \in 1..urine \\ \quad \text{for } j \in 1..urine \\ \quad\quad k_{i,\,j} \leftarrow 0 \\ k \leftarrow \text{RateMatrix}(k) \\ \gamma \leftarrow \text{eigenvals}\left(k^{T}\right) \\ C \leftarrow \text{coeff}(k, q0) \\ q_{lung} \leftarrow \sum_{i=AI1}^{BBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} + \sum_{i=TAI1}^{TBBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{bone} \leftarrow \sum_{i=CV}^{TM} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{liv} \leftarrow \left(q\left(T_d, LIV1, C, \gamma\right) + q\left(T_d, LIV2, C, \gamma\right)\right) \cdot e^{-\lambda \cdot T_d} \\ q_{urine} \leftarrow q\left(T_d, urine, C, \gamma\right) \\ \text{for } j \in 1..rows(t) \\ \quad e_{exp_j} \leftarrow \left[q\left(t_j, urine, C, \gamma\right) - q\left[\left(t_j - 1\right), urine, C, \gamma\right]\right] \cdot e^{-\lambda \cdot t_j} \\ I \leftarrow \dfrac{\sum_{i=1}^{rows(t)} e_{obs_i}}{\sum_{i=1}^{rows(t)} e_{exp_i}} \\ \begin{pmatrix} I \\ e_{exp} \\ q_{liv} \\ q_{bone} \\ q_{lung} \\ q_{urine} \end{pmatrix} \end{array} \right.$$

$N := 1000$

$m := 1..N$

All of the functions defined above are executed below and the results assigned to the matrix A. Note that in Mathcad a function can return only one parameter, which may be a rather complex matrix as in this case.

$$A := \left| \begin{array}{l} \text{for } m \in 1..N \\ \quad A_m \leftarrow \text{Results}(\text{DepositionFractions}(m)) \\ A \end{array} \right.$$

To make things clearer, the relevant parts of A are assigned to matrices with more meaningful names.

$\text{Intake}_m := (A_m)_1$ The 1000 intakes calculated from iterative fits to the urine data in units of pCi.

$\text{IRF}_m := (A_m)_2$ The 24-hour incremental urinary excretion fractions for Pu-238.

$q_{\text{urine}_m} := \text{Intake}_m \cdot (A_m)_6$ The total amount of stable plutonium excreted to the urine compartment over 6532 days.

$q_{\text{bone}_m} := \text{Intake}_m \cdot (A_m)_4$ The skeletal burdens in pCi at 6532 days after intake.

$q_{\text{liv}_m} := \text{Intake}_m \cdot (A_m)_3$ The liver burdens in pCi at 6532 days after intake.

$q_{\text{lung}_m} := \text{Intake}_m \cdot (A_m)_5$ The lung burdens in pCi at 6532 days after intake.

Intakes Calculated from Urine Data

$\text{mean}(\text{Intake}) = 1.790 \times 10^6$

$\text{stdev}(\text{Intake}) = 9.710 \times 10^5$

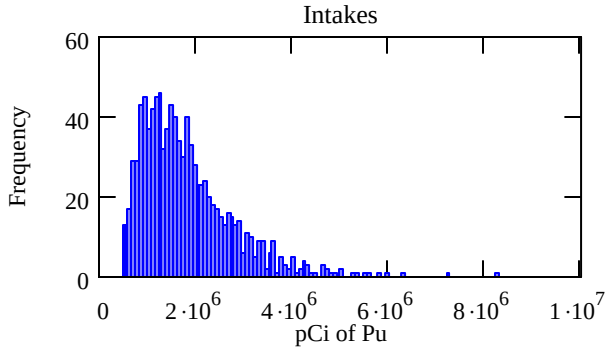
$\max(\text{Intake}) = 8.277 \times 10^6$

$\min(\text{Intake}) = 4.185 \times 10^5$

$\frac{\text{stdev}(\text{Intake})}{\text{mean}(\text{Intake})} = 5.424 \times 10^{-1}$

$\text{Intake}_{\text{mean}} := \text{mean}(\text{Intake})$

$G := \text{histogram}(100, \text{Intake})$



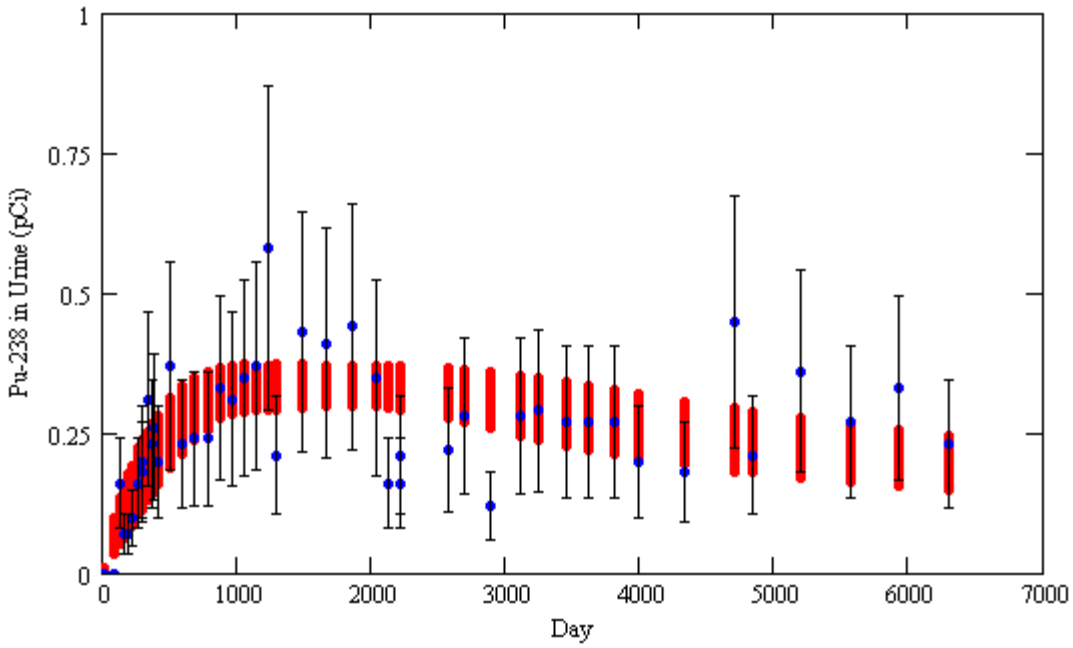
Urinary Excretion

$j := 1 .. N$

$i := 1 .. 48$

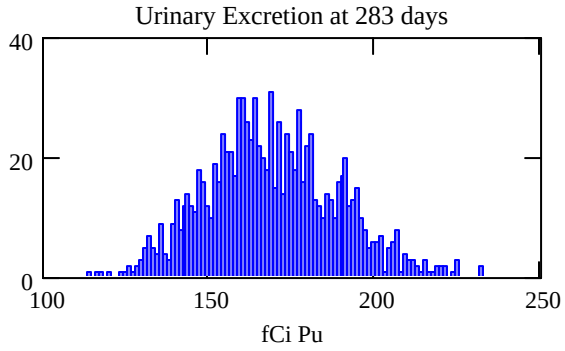
$e_{exp_{j,i}} := Intake_j \cdot \left(IRF_j\right)_i$

$\varepsilon_{high_i} := e_{obs_i} + 0.5 \cdot e_{obs_i}$ $\varepsilon_{low_i} := e_{obs_i} - 0.5 \cdot e_{obs_i}$

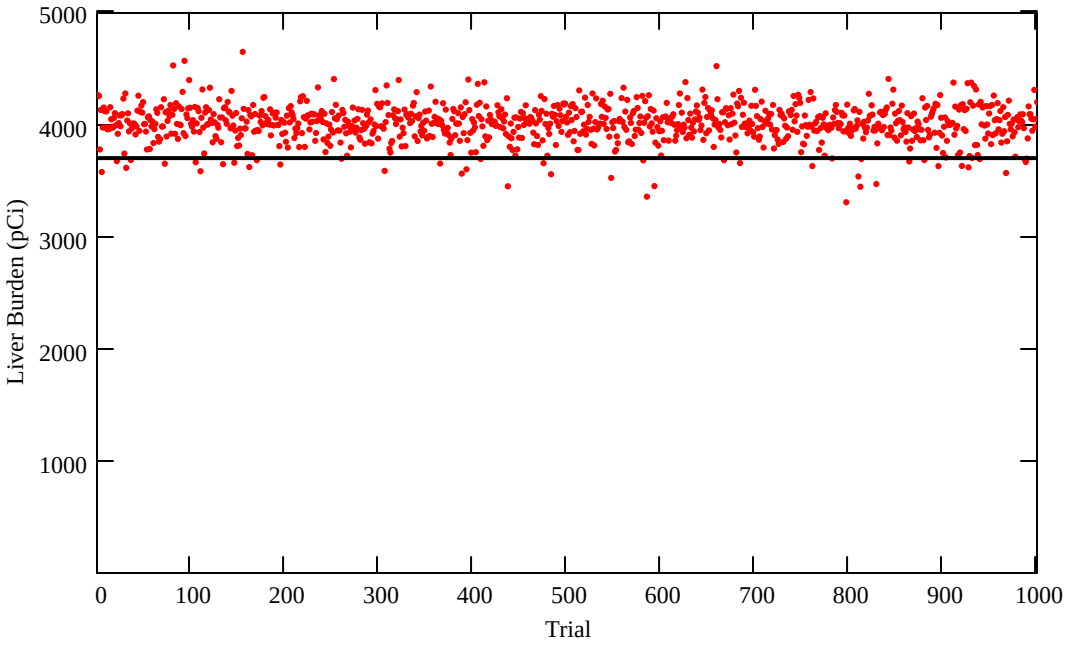


The uncertainties in the observed urinary excretion are arbitrarily set to +/-50% of the observed value.

$G := histogram\left(100, e_{exp}^{\langle 10 \rangle} \cdot 1000\right)$



Liver



Liver Autopsy Data

$137 \cdot Bq = 3.703 \times 10^{3}\ pCi$

+/-

$4 \cdot Bq = 1.081 \times 10^{2}\ pCi$

$\text{mean}(q_{liv}) = 4.013 \times 10^{3}$

$\text{stdev}(q_{liv}) = 1.581 \times 10^{2}$

$\max(q_{liv}) = 4.652 \times 10^{3}$

$\min(q_{liv}) = 3.310 \times 10^{3}$

$\frac{\text{stdev}(q_{liv})}{\text{mean}(q_{liv})} = 3.940 \times 10^{-2}$

$\max(q_{liv}) = 4.652 \times 10^{3}$

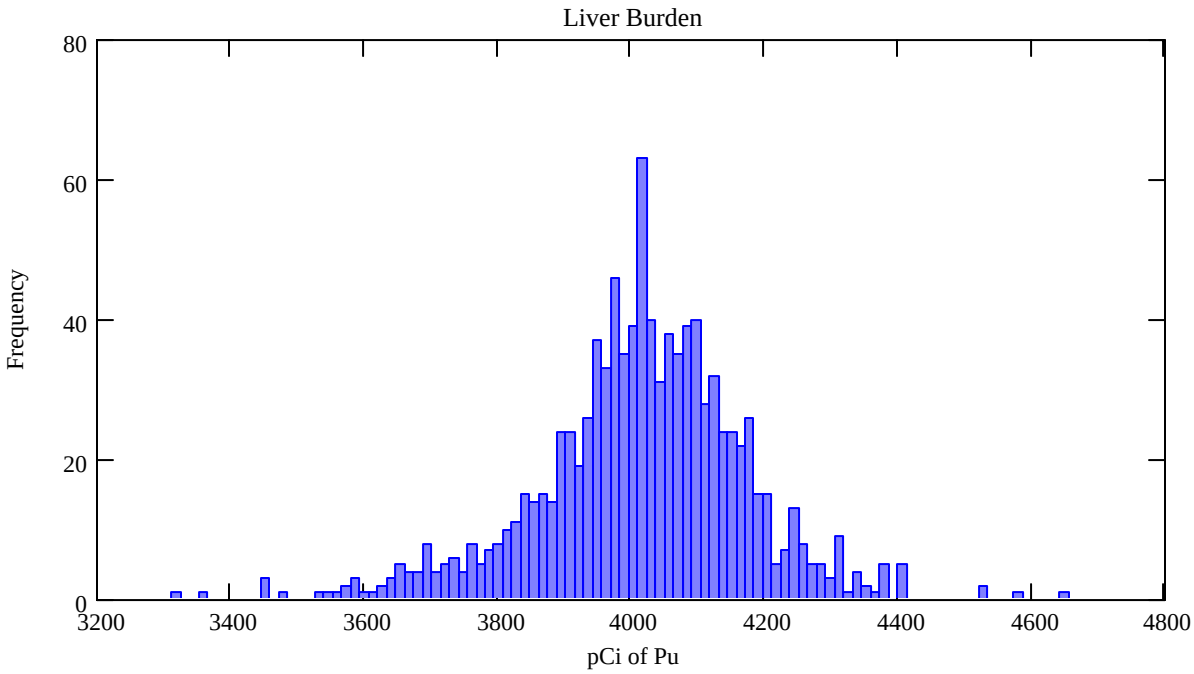
$\min(q_{liv}) = 3.310 \times 10^{3}$

$r_i := \frac{q_{liv_i}}{3703}$

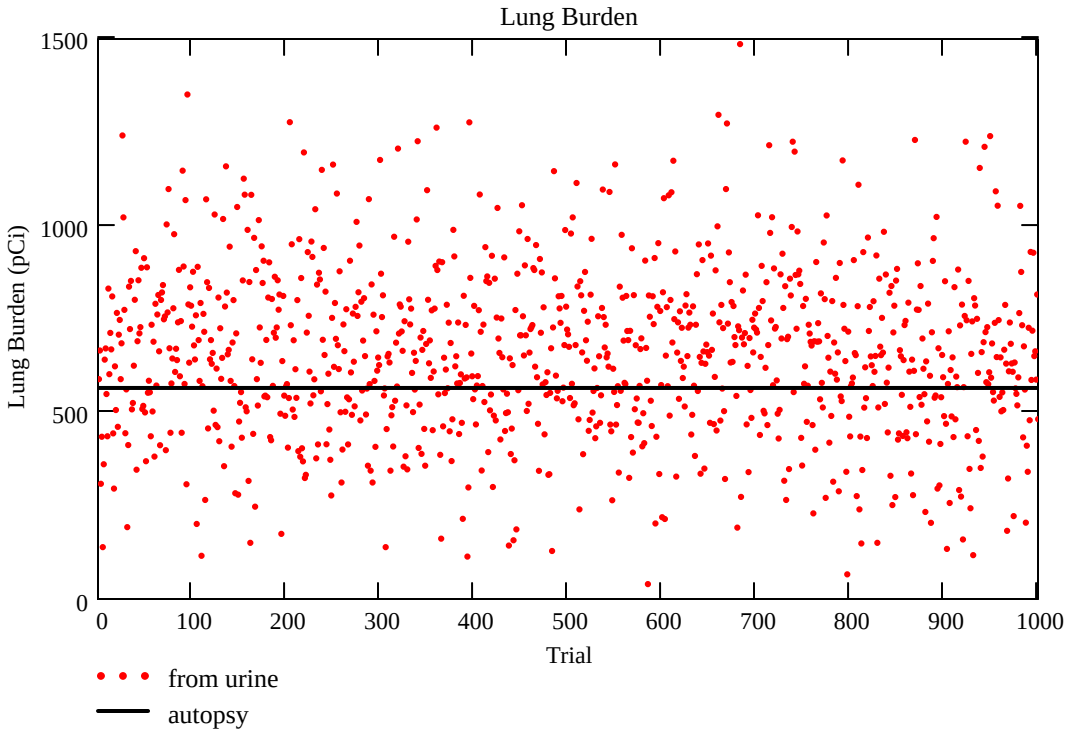
$\text{mean}(r) = 1.085$

$\frac{\text{stdev}(r)}{\text{mean}(r)} = 3.966 \times 10^{-2}$

$G := \text{histogram}(100, q_{liv})$



Lung



Lung Autopsy Data

$20.9 \cdot Bq = 5.649 \times 10^{2}\ pCi$

$\text{mean}(q_{lung}) = 6.549 \times 10^{2}$

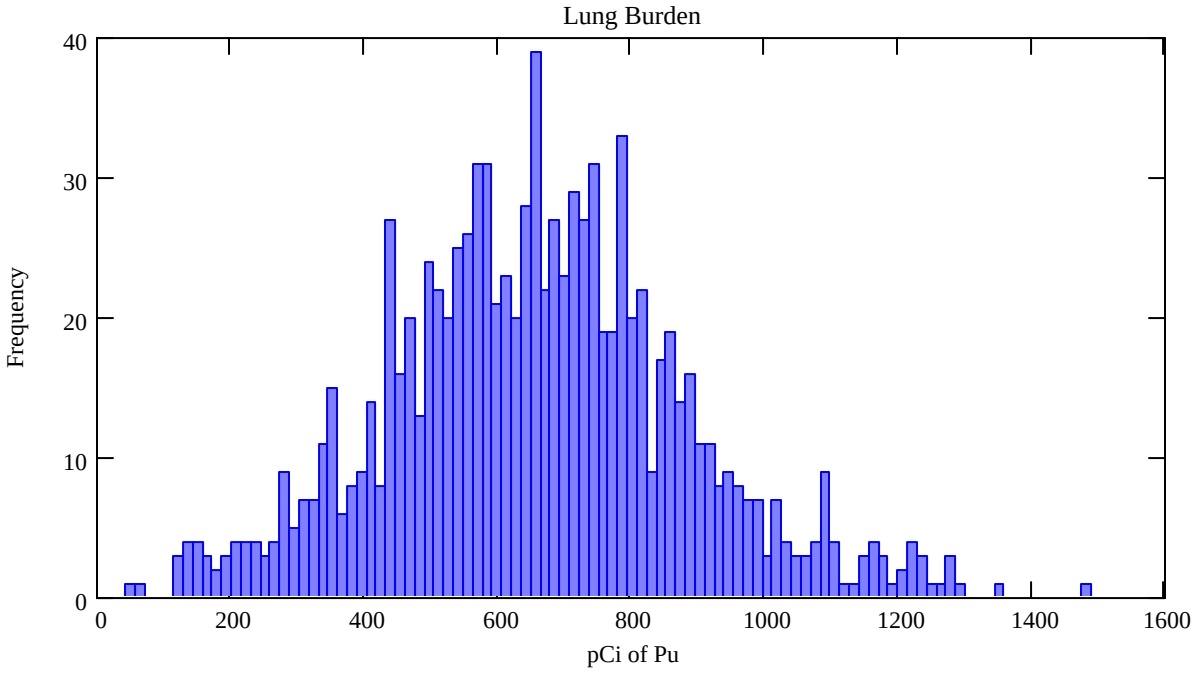
$\text{stdev}(q_{lung}) = 2.232 \times 10^{2}$

$\max(q_{lung}) = 1.486 \times 10^{3}$

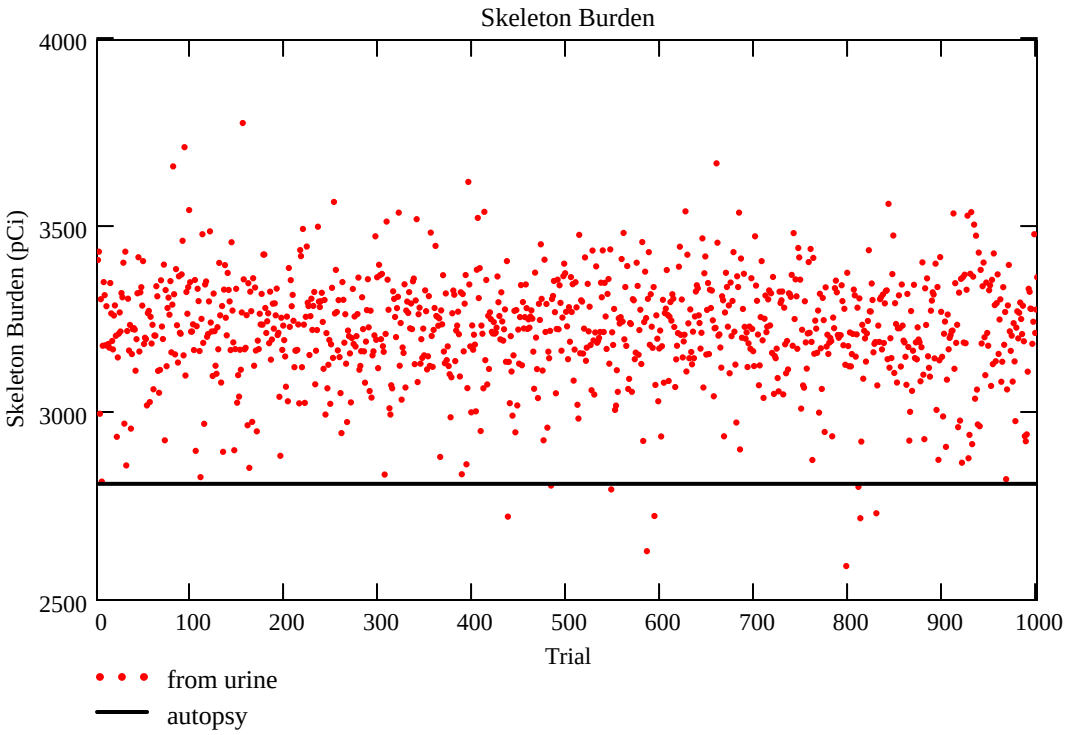
$\min(q_{lung}) = 3.946 \times 10^{1}$

$$\frac{\text{stdev}(q_{lung})}{\text{mean}(q_{lung})} = 3.409 \times 10^{-1}$$

$G := \text{histogram}(100, q_{lung})$



Skeleton (including all marrow)



Bone Autopsy Data

$104 \cdot Bq = 2.811 \times 10^{3}\ pCi$

+/-

$1 \cdot Bq = 2.703 \times 10^{1}\ pCi$

$\text{mean}(q_{bone}) = 3.223 \times 10^{3}$

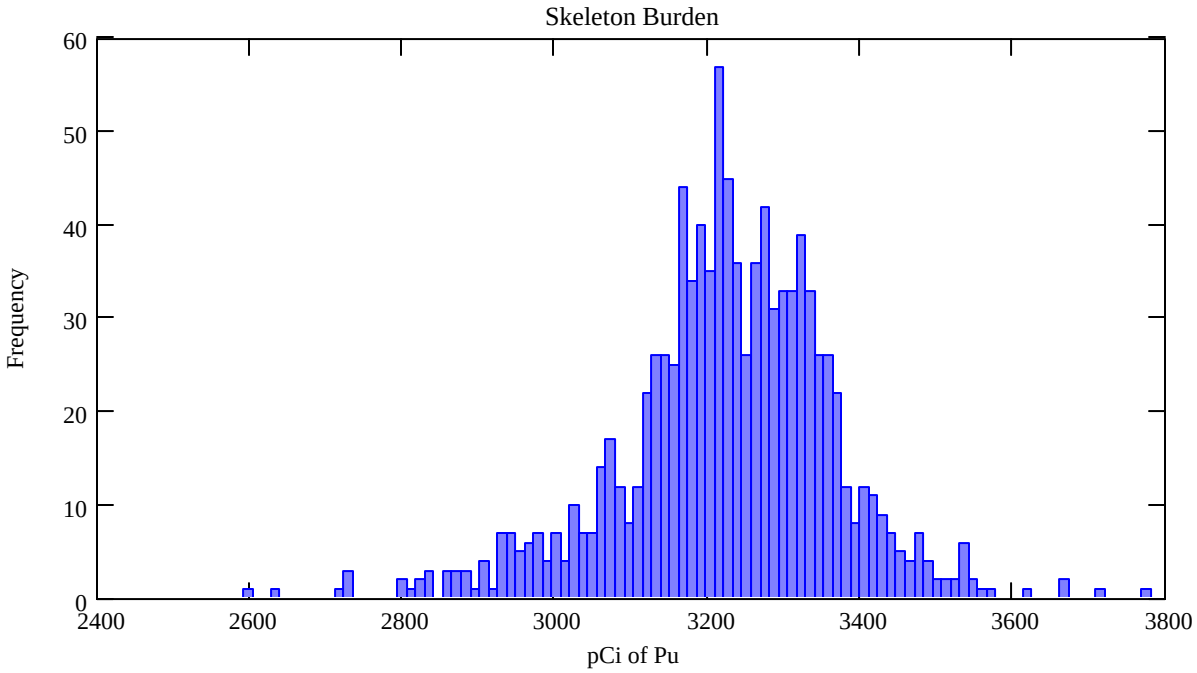
$\text{stdev}(q_{bone}) = 1.405 \times 10^{2}$

$\max(q_{bone}) = 3.777 \times 10^{3}$

$\min(q_{bone}) = 2.591 \times 10^{3}$

$\frac{\text{stdev}(q_{bone})}{\text{mean}(q_{bone})} = 4.361 \times 10^{-2}$

$G := \text{histogram}(100, q_{bone})$



Appendix D

Evaluation of USTUR Case 0259 with Uncertainties

Evaluation of USTUR Case 0259 from data presented by A. C. James et al. *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled Pu238 Oxide Ceramic Particles* Health Physics 84(1):2-33:2003. Uncertainties from **PAS** are calculated in this worksheet.

ORIGIN ≡ 1 nCi ≡ 37·Bq pCi ≡ 10^{-3}·nCi μCi ≡ 10^{6}·pCi

The compartments in the model are assigned numbers to clarify their use in the arrays to be defined.

AI1 := 1	bb1 := 4	BB1 := 7	ET2 := 10			
AI2 := 2	bb2 := 5	BB2 := 8	ETseq := 11	LNth := 13		
AI3 := 3	bbseq := 6	BBseq := 9	LNet := 12	ET1 := 14		
TAI1 := 15	Tbb1 := 18	TBB1 := 21	TET2 := 24			
TAI2 := 16	Tbb2 := 19	TBB2 := 22	TETseq := 25			
TAI3 := 17	Tbbseq := 20	TBBseq := 23	TLNet := 26	TLNth := 27		
S := 28	SI := 29	ULI := 30	LLI := 31			
blood := 32	ST0 := 35	CV := 38	TV := 41	OKT := 44	nads := 47	
LIV1 := 33	ST1 := 36	CS := 39	TS := 42	UP := 45	ENV := 48	urine := 50
LIV2 := 34	ST2 := 37	CM := 40	TM := 43	UBC := 46	feces := 49	

Deposition parameters calculated with LUDUC. These 1000 values assume 5 μm AMAD, a density of 10 g/cc, and light exercise.

$$\begin{pmatrix} DF_{ET1} \\ DF_{ET2} \\ DF_{BB} \\ DF_{bb} \\ DF_{AI} \\ Fs_{BB} \\ Fs_{bb} \end{pmatrix} :=$$

0.3824307	0.3618683	0.0215043	0.0164575	0.1045146	0.5605827	0.6211035
0.4117763	0.4768381	0.0114585	0.0026248	0.0302902	0.6252462	0.6516554
0.2854435	0.3096401	0.0181279	0.0122373	0.0555491	0.6261812	0.6701694
0.3640713	0.3770601	0.0147265	0.0030048	0.0242068	0.5873427	0.6121804
0.3614031	0.3861653	0.0118707	0.0123206	0.0990075	0.6184139	0.6778674
0.3513172	0.4606443	0.0220846	0.0085090	0.0468516	0.3974973	0.4262016
0.4115148	0.5665783	0.0158309	0.0067313	0.0294167	0.5511362	0.5840935
0.3544650	0.3765788	0.0050744	0.0052642	0.0232554	0.5171263	0.5598844
0.3327872	0.5143833	0.0092004	0.0052477	0.0305225	0.4724866	0.5001576
0.2299703	0.3362615	0.0111267	0.0288326	0.0861704	0.5291479	0.6004671

The function returns the deposition fractions in each compartment using the m^{th} row of the LUDUC parameter matrix. The geometric standard deviations are those given by Bolch et al, *Influences of Parameter Uncertainties within the ICRP 66 Respiratory Tract Model: Particle Deposition* Health Physics (81 (4):378-394; 2001. Any content not explicitly given has a value of zero.

$$\text{DepositionFractions}(m) := \left| \begin{array}{l} q0_{urine} \leftarrow 0 \\ q0_{AI1} \leftarrow \text{rlnorm}(1, \ln(0.3), \ln(1.10))_1 \cdot DF_{AI_m} \\ q0_{AI3} \leftarrow 0.1 \cdot DF_{AI_m} \\ q0_{AI2} \leftarrow DF_{AI_m} - q0_{AI1} - q0_{AI3} \\ q0_{bbseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{bb_m} \\ q0_{bb2} \leftarrow Fs_{bb_m} \cdot DF_{bb_m} \\ q0_{bb1} \leftarrow DF_{bb_m} - q0_{bbseq} - q0_{bb2} \\ q0_{BBseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{BB_m} \\ q0_{BB2} \leftarrow Fs_{BB_m} \cdot DF_{BB_m} \\ q0_{BB1} \leftarrow DF_{BB_m} - q0_{BBseq} - q0_{BB2} \\ q0_{ETseq} \leftarrow \text{rlnorm}(1, \ln(0.0005), \ln(1.73))_1 \cdot DF_{ET2_m} \\ q0_{ET2} \leftarrow DF_{ET2_m} - q0_{ETseq} \\ q0_{ET1} \leftarrow DF_{ET1_m} \\ q0 \end{array} \right.$$

Define transfer rate constants for the respiratory tract. The geometric standard deviations are those given by Bolch et al.

$\kappa_{lung}(k) :=$

$f_r \leftarrow -0.1566707$

$s_r \leftarrow 0.001891$

$s_s \leftarrow 0.000257$

$s_t \leftarrow s_s$

$s_{pt} \leftarrow (1 - f_r) \cdot (s_r - s_t)$

$s_p \leftarrow s_r - s_{pt}$

$k_{AI1,bb1} \leftarrow 0.02$

$k_{AI2,bb1} \leftarrow rlnorm(1, ln(0.001), ln(1.41))_1$

$k_{AI3,bb1} \leftarrow rlnorm(1, ln(0.0001), ln(1.73))_1$

$k_{AI3,LNth} \leftarrow rlnorm(1, ln(0.00002), ln(1.41))_1$

$k_{bb1,BB1} \leftarrow rlnorm(1, ln(2), ln(1.41))_1$

$k_{bb2,BB1} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{BB1,ET2} \leftarrow rlnorm(1, ln(10), ln(1.22))_1$

$k_{BB2,ET2} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{ET2,S} \leftarrow rlnorm(1, ln(100), ln(1.73))_1$

$k_{ET1,ENV} \leftarrow rlnorm(1, ln(1), ln(1.73))_1$

$k_{ETseq,LNet} \leftarrow rlnorm(1, ln(0.001), ln(1.73))_1$

$k_{BBseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

$k_{bbseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

for $i \in AI1 .. LNth$

  for $j \in AI1 .. LNth$

    $k_{i+14,j+14} \leftarrow k_{i,j}$

$k_{TET2,S} \leftarrow k_{ET2,S}$

for $i \in AI1 .. LNth$

  $k_{i,i+14} \leftarrow s_{pt}$

  $k_{i,blood} \leftarrow s_p$

for $i \in TAI1 .. TLNth$

  $k_{i,blood} \leftarrow s_t$

k

Define transfer rate constants for the systemic compartments and GI tract. For lack of better information, the geometric standard deviations are assumed to be equal to the constant α, which is assumed to equal 1.001 here. This results in basically a deterministic (point) estimate of the parameters.

$$\kappa_{sys1}(k) := \left| \begin{array}{l} k_{blood,\,LIV1} \leftarrow rlnorm(1, ln(0.1941), ln(\alpha))_1 \\ k_{blood,\,CS} \leftarrow rlnorm(1, ln(0.1294), ln(\alpha))_1 \\ k_{blood,\,TS} \leftarrow rlnorm(1, ln(0.1941), ln(\alpha))_1 \\ k_{blood,\,UBC} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k_{blood,\,UP} \leftarrow rlnorm(1, ln(0.00647), ln(\alpha))_1 \\ k_{blood,\,OKT} \leftarrow rlnorm(1, ln(0.00323), ln(\alpha))_1 \\ k_{blood,\,ULI} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k_{blood,\,nads} \leftarrow rlnorm(1, ln(0.00023), ln(\alpha))_1 \\ k_{blood,\,ST0} \leftarrow rlnorm(1, ln(0.2773), ln(\alpha))_1 \\ k_{blood,\,ST1} \leftarrow rlnorm(1, ln(0.0806), ln(\alpha))_1 \\ k_{blood,\,ST2} \leftarrow rlnorm(1, ln(0.0129), ln(\alpha))_1 \\ k \end{array} \right.$$

$$\kappa_{sys2}(k) := \left| \begin{array}{l} k_{ST0,\,blood} \leftarrow rlnorm(1, ln(0.693), ln(\alpha))_1 \\ k_{OKT,\,blood} \leftarrow rlnorm(1, ln(0.00139), ln(\alpha))_1 \\ k_{ST1,\,blood} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{ST2,\,blood} \leftarrow rlnorm(1, ln(0.000019), ln(\alpha))_1 \\ k_{CM,\,blood} \leftarrow rlnorm(1, ln(0.0076), ln(\alpha))_1 \\ k_{TM,\,blood} \leftarrow rlnorm(1, ln(0.0076), ln(\alpha))_1 \\ k_{LIV2,\,blood} \leftarrow rlnorm(1, ln(0.000211), ln(\alpha))_1 \\ k_{nads,\,blood} \leftarrow rlnorm(1, ln(0.00019), ln(\alpha))_1 \\ k \end{array} \right.$$

$$\kappa_{sys3}(k) := \begin{| k_{UP,UBC} \leftarrow rlnorm(1, ln(0.01386), ln(\alpha))_1 \\ k_{ST1,UBC} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{TS,TV} \leftarrow rlnorm(1, ln(0.000247), ln(\alpha))_1 \\ k_{TS,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CS,CV} \leftarrow rlnorm(1, ln(0.0000411), ln(\alpha))_1 \\ k_{CS,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{TV,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CV,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{LIV1,LIV2} \leftarrow rlnorm(1, ln(0.00177), ln(\alpha))_1 \\ k_{LIV1,SI} \leftarrow rlnorm(1, ln(0.000133), ln(\alpha))_1 \\ k_{UBC,urine} \leftarrow rlnorm(1, ln(12), ln(\alpha))_1 \\ k |$$

$$\kappa_{GI}(k) := \begin{| f_1 \leftarrow 10^{-7} \\ k_{S,SI} \leftarrow rlnorm(1, ln(24), ln(\alpha))_1 \\ k_{SI,ULI} \leftarrow rlnorm(1, ln(6), ln(\alpha))_1 \\ k_{SI,blood} \leftarrow \frac{k_{SI,ULI} \cdot f_1}{1 - f_1} \\ k_{ULI,LLI} \leftarrow rlnorm\left(1, ln\left(\frac{24}{13}\right), ln(\alpha)\right)_1 \\ k_{LLI,feces} \leftarrow rlnorm(1, ln(1), ln(\alpha))_1 \\ k |$$

Calculate the total removal rate constants

$$total(k, \lambda) := \begin{| K \leftarrow k \\ \text{for } comp \in 1..cols(k) \\ \quad \begin{| K_{comp,comp} \leftarrow 0 \\ \quad \text{for } j \in 1..cols(k) \\ \quad\quad K_{comp,comp} \leftarrow K_{comp,comp} + k_{comp,j} \text{ if } comp \neq j \\ \quad K_{comp,comp} \leftarrow -\left(K_{comp,comp} + \lambda\right) \\ K |$$

This function creates a complete rate constant matrix.

$$\text{RateMatrix}(k) := \begin{array}{l} k \leftarrow \kappa_{lung}(k) \\ k \leftarrow \kappa_{sys1}(k) \\ k \leftarrow \kappa_{sys2}(k) \\ k \leftarrow \kappa_{sys3}(k) \\ k \leftarrow \kappa_{GI}(k) \\ k \leftarrow \text{total}(k, 0) \\ k \end{array}$$

Calculate the coefficients and rate constants for the retention functions.

$$\text{coeff}(k, q0) := \begin{array}{l} q0 \leftarrow \text{submatrix}(q0, 1, \text{rows}(k), 1, 1) \\ V \leftarrow \text{eigenvecs}\left(k^{T}\right) \\ M \leftarrow \text{lsolve}(V, q0) \\ \text{for } j \in 1..\text{cols}(k) \\ \quad \text{for } i \in 1..\text{cols}(k) \\ \quad\quad C_{i,j} \leftarrow V_{i,j} \cdot M_{j} \\ C \end{array}$$

$$q(t, comp, C, \gamma) := \sum_{i=1}^{\text{rows}(\gamma)} C_{comp,i} \cdot e^{\left[\left(\gamma_i\right) \cdot t\right]}$$

Urinary excretion data for USTUR 0259. Time t is in days and observed urinary excretion e_{obs} is in pCi per day.

$$\begin{pmatrix} t \\ e_{obs} \end{pmatrix} :=$$

2	0
3	0
4	0
76	0
123	0.16
150	0.07
186	0.07
209	0.1
264	0.16
283	0.18

$$\lambda := \frac{\ln(2)}{\left(3.203 \times 10^{4}\right)}$$ decay constant for Pu-238

$\alpha \equiv 1.001$ σ_g for systemic parameters

$T_d := 6532$ number of days from intake to death

$$i := 1..\text{rows}\left(e_{obs}\right)$$

This function calculates the organ burdens of interest, intake, and urinary excretion for a given vector of initial compartment contents *q0*.

$$\text{Results}(q0) := \left| \begin{array}{l} k_{urine,urine} \leftarrow 0 \\ \text{for } i \in 1..urine \\ \quad \text{for } j \in 1..urine \\ \quad\quad k_{i,j} \leftarrow 0 \\ k \leftarrow \text{RateMatrix}(k) \\ \gamma \leftarrow \text{eigenvals}\left(k^{T}\right) \\ C \leftarrow \text{coeff}(k, q0) \\ q_{lung} \leftarrow \sum_{i=AI1}^{BBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} + \sum_{i=TAI1}^{TBBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{bone} \leftarrow \sum_{i=CV}^{TM} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{liv} \leftarrow \left(q\left(T_d, LIV1, C, \gamma\right) + q\left(T_d, LIV2, C, \gamma\right)\right) \cdot e^{-\lambda \cdot T_d} \\ q_{urine} \leftarrow q\left(T_d, urine, C, \gamma\right) \\ \text{for } j \in 1..\text{rows}(t) \\ \quad e_{exp_j} \leftarrow \left[q\left(t_j, urine, C, \gamma\right) - q\left[\left(t_j - 1\right), urine, C, \gamma\right]\right] \cdot e^{-\lambda \cdot t_j} \\ \begin{pmatrix} e_{exp} \\ q_{liv} \\ q_{bone} \\ q_{lung} \\ q_{urine} \end{pmatrix} \end{array} \right.$$

$$N := 1000$$

$$m := 1..N$$

All of the functions defined above are executed below and the results assigned to the matrix A. Note that in Mathcad a function can return only one parameter, which may be a rather complex matrix as in this case.

$$A := \left| \begin{array}{l} \text{for } m \in 1..N \\ \quad A_m \leftarrow \text{Results}(\text{DepositionFractions}(m)) \\ A \end{array} \right.$$

To make things clearer, the relevant parts of A are assigned to matrices with more meaningful names.

$\text{Intake} \equiv 1.731 \times 10^6$ The intake indicated by the PAS

$\text{IRF}_m := (A_m)_1$ The 24-hour incremental urinary excretion fractions for Pu-238.

$q_{\text{urine}_m} := \text{Intake} \cdot (A_m)_5$ The total amount of stable plutonium excreted to the urine compartment over 6532 days.

$q_{\text{bone}_m} := \text{Intake} \cdot (A_m)_3$ The skeletal burdens in pCi at 6532 days after intake.

$q_{\text{liv}_m} := \text{Intake} \cdot (A_m)_2$ The liver burdens in pCi at 6532 days after intake.

$q_{\text{lung}_m} := \text{Intake} \cdot (A_m)_4$ The lung burdens in pCi at 6532 days after intake.

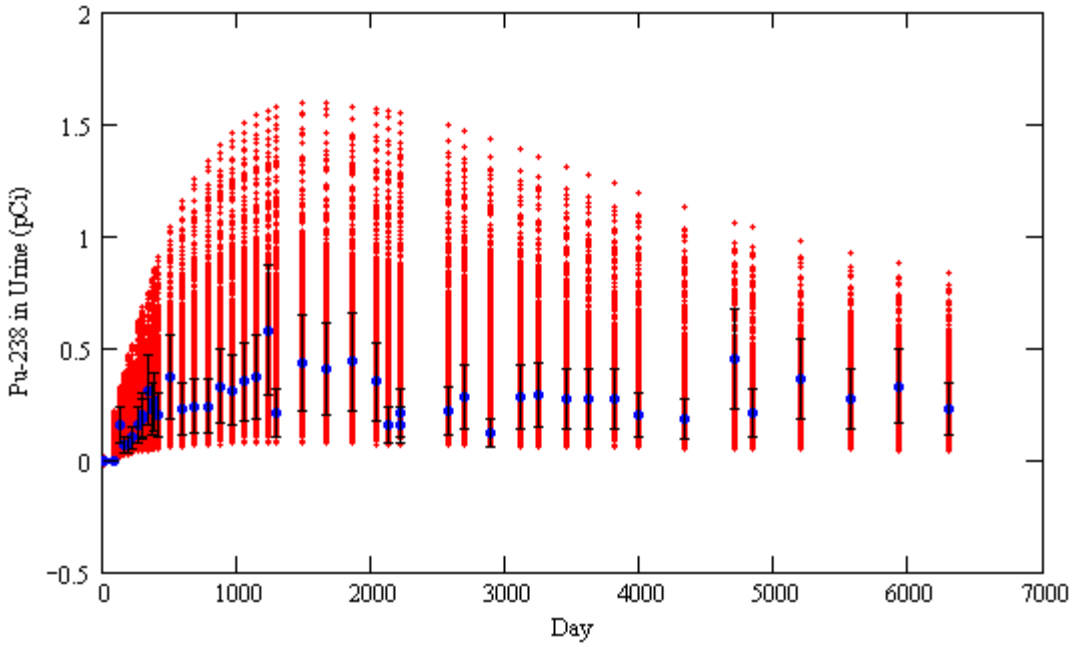
Urinary Excretion

$j := 1 .. N$

$i := 1 .. 48$

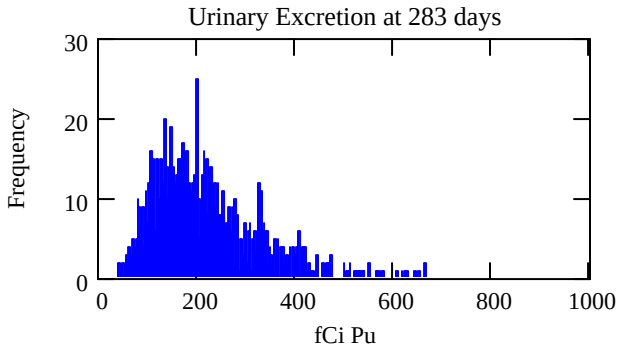
$e_{exp_{j,i}} := Intake \cdot \left(IRF_j\right)_i$

$\varepsilon_{high_i} := e_{obs_i} + 0.5 \cdot e_{obs_i}$ $\varepsilon_{low_i} := e_{obs_i} - 0.5 \cdot e_{obs_i}$



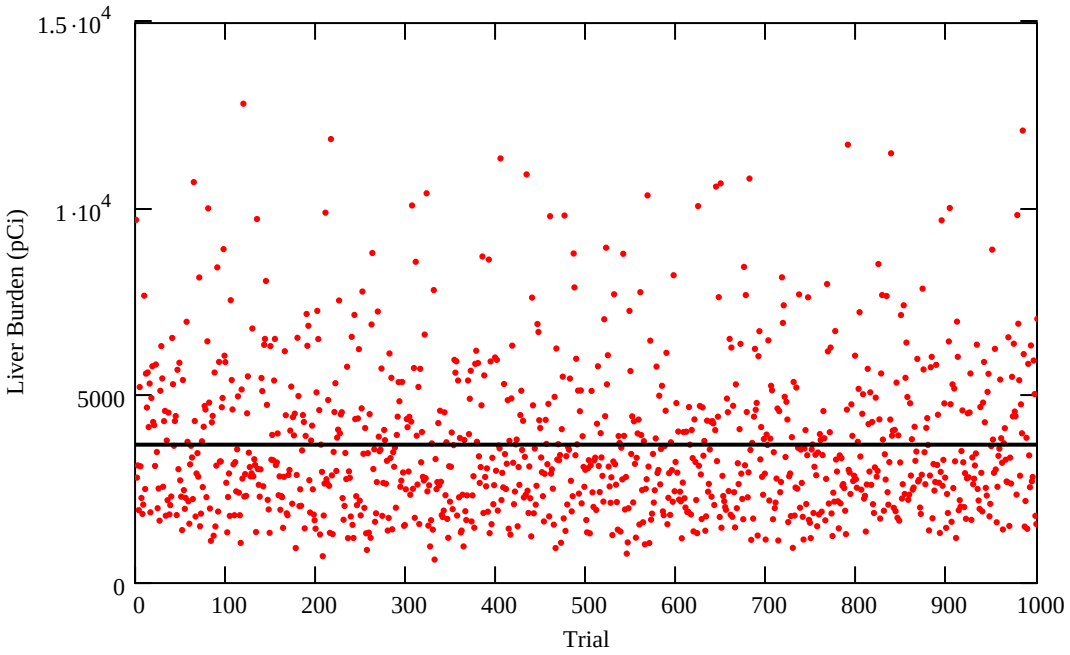
The uncertainties in the observed urinary excretion are arbitrarily set to +/-50% of the observed value.

$G := histogram\left(200, e_{exp}^{\langle 10 \rangle} \cdot 1000\right)$



Liver

The quantity q_{liv} is the liver burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Liver Autopsy Data

$137 \cdot Bq = 3.703 \times 10^{3}\ pCi$

+/-

$4 \cdot Bq = 1.081 \times 10^{2}\ pCi$

$\text{mean}(q_{liv}) = 3.703 \times 10^{3}$

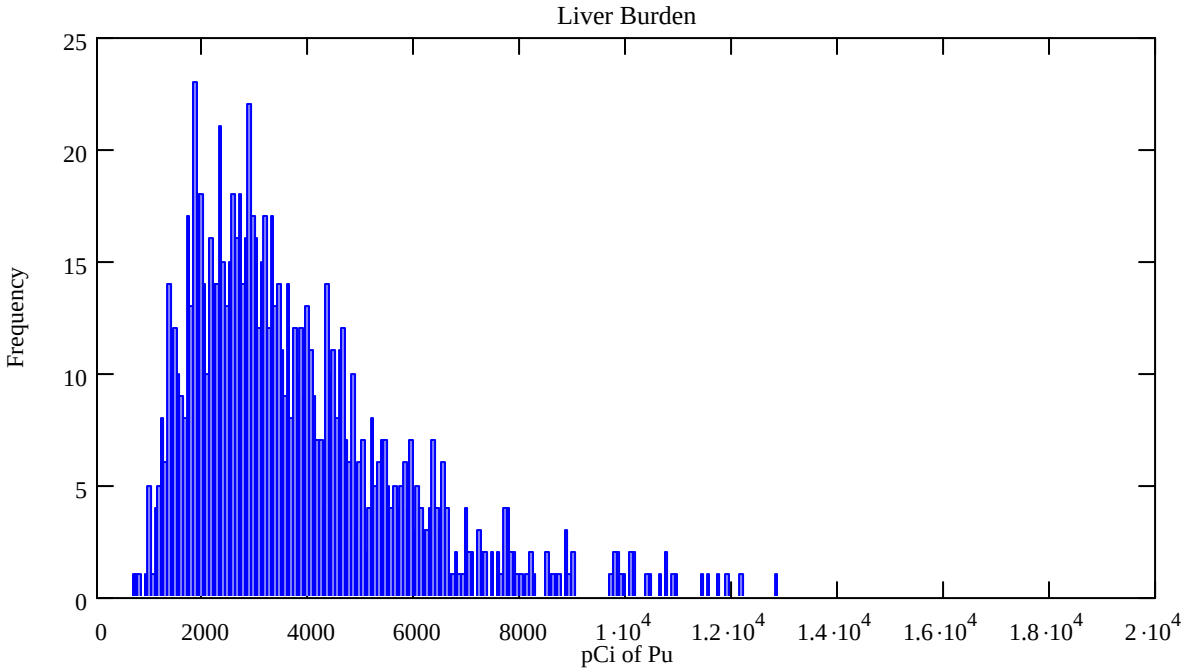
$\text{stdev}(q_{liv}) = 2.010 \times 10^{3}$

$\max(q_{liv}) = 1.284 \times 10^{4}$

$\min(q_{liv}) = 6.267 \times 10^{2}$

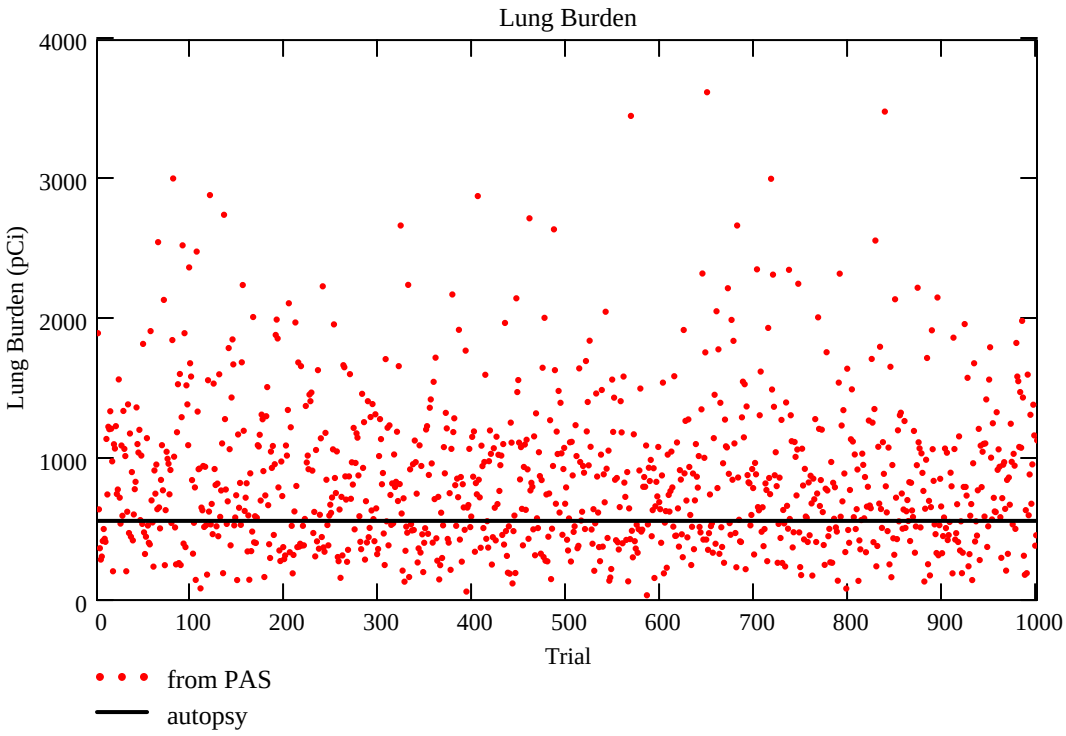
$\frac{\text{stdev}(q_{liv})}{\text{mean}(q_{liv})} = 5.428 \times 10^{-1}$

$G := \text{histogram}(200, q_{liv})$



Lung

The quantity q_{lung} is the lung burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Lung Autopsy Data

$20.9 \cdot Bq = 5.649 \times 10^{2}\ pCi$

$\text{mean}(q_{lung}) = 8.724 \times 10^{2}$

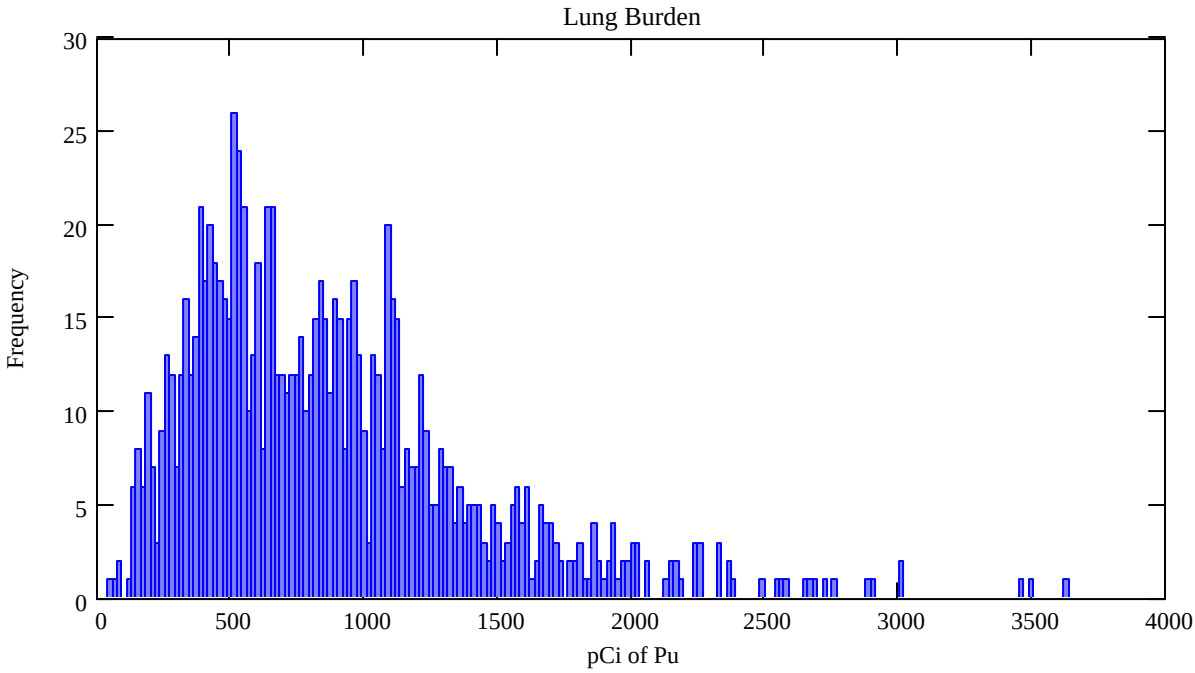
$\text{stdev}(q_{lung}) = 5.350 \times 10^{2}$

$\max(q_{lung}) = 3.626 \times 10^{3}$

$\min(q_{lung}) = 3.379 \times 10^{1}$

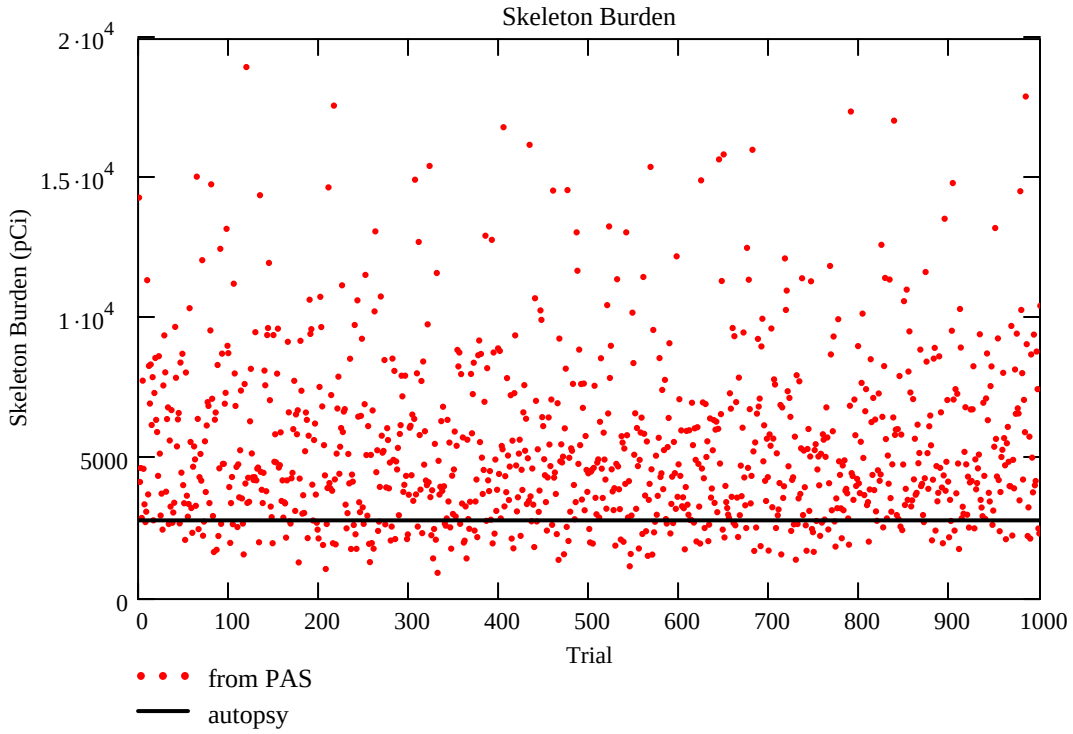
$$\frac{\text{stdev}(q_{lung})}{\text{mean}(q_{lung})} = 6.133 \times 10^{-1}$$

$G := \text{histogram}(200, q_{lung})$



Skeleton (including all marrow)

The quantity q_{bone} is the skeletal burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Bone Autopsy Data

$104 \cdot Bq = 2.811 \times 10^{3}\ pCi$

+/-

$1 \cdot Bq = 2.703 \times 10^{1}\ pCi$

$\text{mean}(q_{bone}) = 5.474 \times 10^{3}$

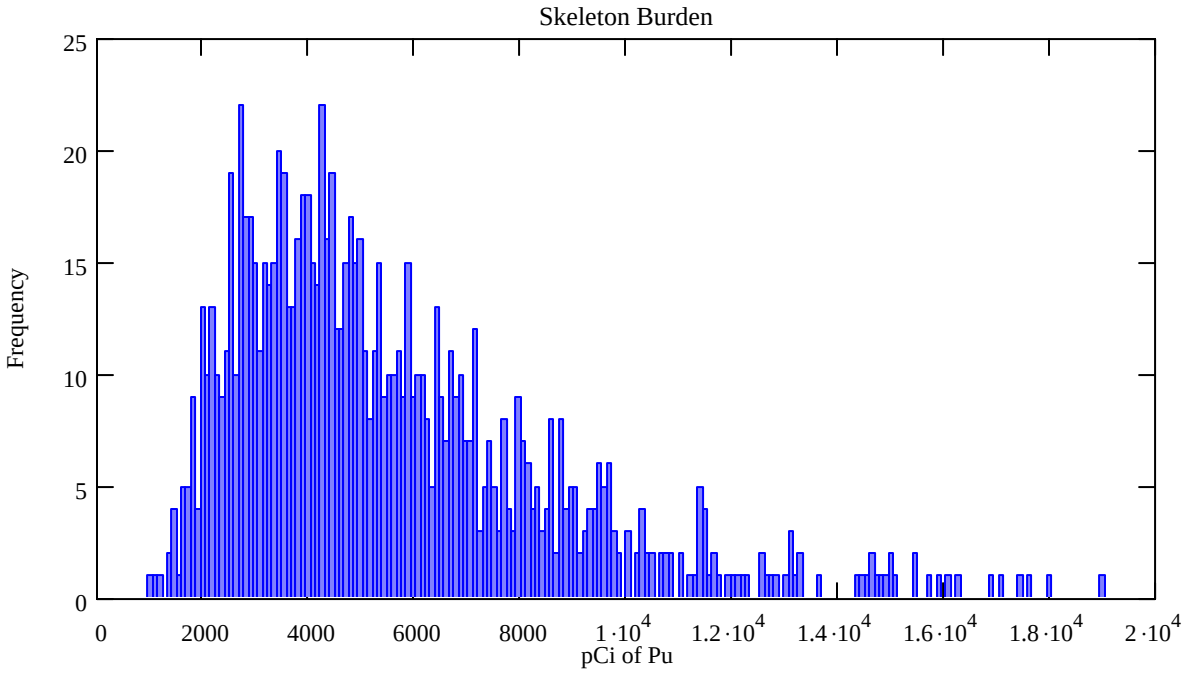
$\text{stdev}(q_{bone}) = 2.967 \times 10^{3}$

$\max(q_{bone}) = 1.900 \times 10^{4}$

$\min(q_{bone}) = 9.329 \times 10^{2}$

$\frac{\text{stdev}(q_{bone})}{\text{mean}(q_{bone})} = 5.421 \times 10^{-1}$

$G := \text{histogram}(200, q_{bone})$

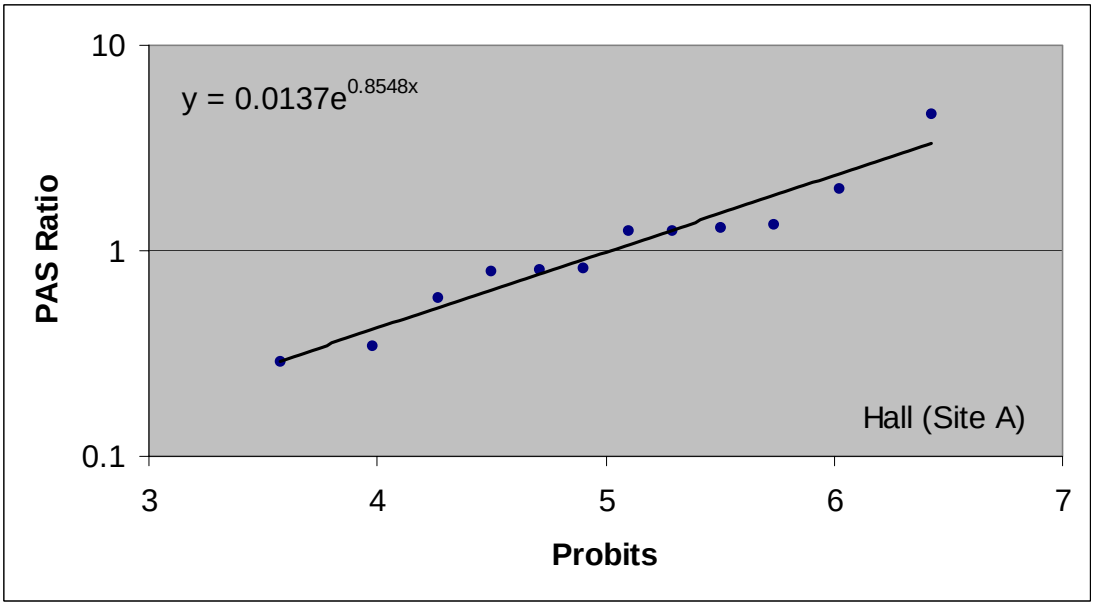


Empirical Estimates of PAS Ratio

The ***PAS ratio*** is defined to be the ratio of the concentration measured with one PAS to the concentration measured by another PAS. The PAS are typically located on the left and right lapels. The PAS ratio is taken to be a measure of the ratio between a "true" intake and the intake indicated by a single PAS worn on the lapel.

ORIGIN := 1 m := 1 .. 10000

Data from Sherry C. Hall, *Comparison of Right and Left Side Lapel Sampling Results*, Master's Thesis University of Alabama, Birmingham; April 25, 1991. Aerosol measured is nuisance dust in at a fire extinguisher manufacturer (Site A) and an iron foundry (Site B).



The geometric mean PAS ratio is

$$\mu_g := 0.0137 \cdot e^{0.8548 \cdot 5}$$

$$\mu_g = 0.984$$

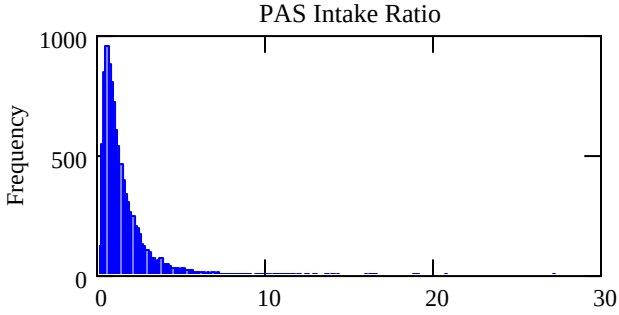
The geometric standard deviation is

$$\sigma_g := \frac{0.0137 \cdot e^{0.8548 \cdot 6}}{0.0137 \cdot e^{0.8548 \cdot 5}}$$

$$\sigma_g = 2.351$$

$$PAS_m := rlnorm\left(1, \ln(1), \ln\left(\sigma_g\right)\right)_1$$

$$G := histogram(200, PAS)$$

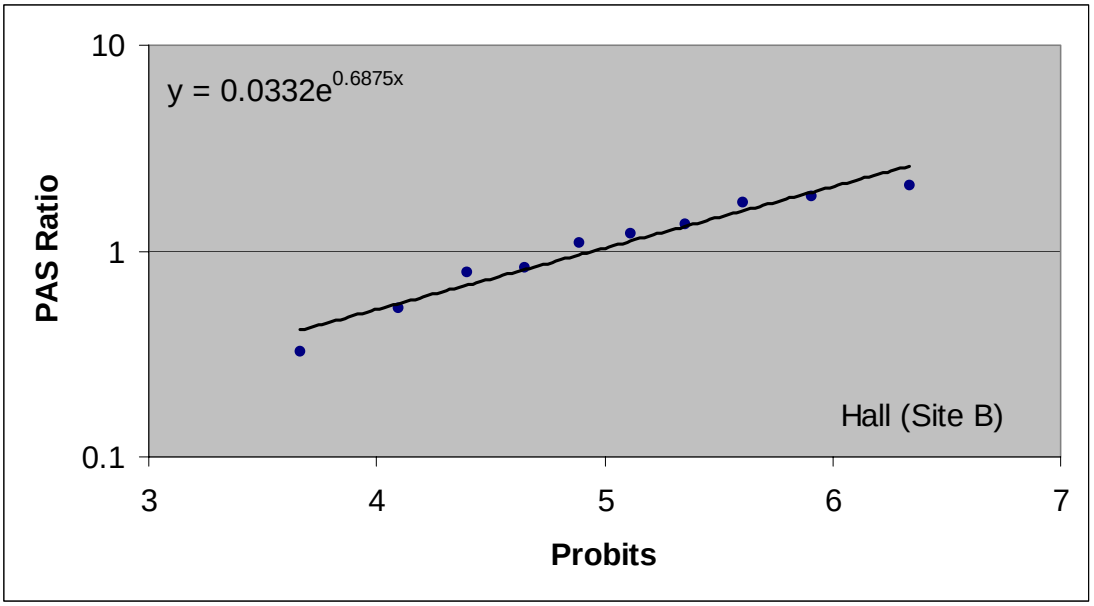


$max(PAS) = 27.11$

$min(PAS) = 0.06$

$$\mu_g \cdot \sigma_g^{2.58} = 8.927$$

$$\mu_g \cdot \sigma_g^{-2.58} = 0.108$$



The geometric mean PAS ratio is The geometric standard deviation is

$$\mu_g := 0.0332 \cdot e^{0.6875 \cdot 5}$$

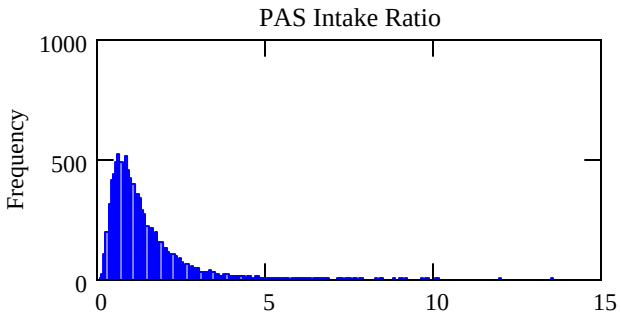
$$\mu_g = 1.033$$

$$\sigma_g := \frac{0.0332 \cdot e^{0.6875 \cdot 6}}{0.0332 \cdot e^{0.6875 \cdot 5}}$$

$$\sigma_g = 1.989$$

$$PAS_m := rlnorm\left(1, \ln(1), \ln\left(\sigma_g\right)\right)_1$$

$$G := histogram(200, PAS)$$

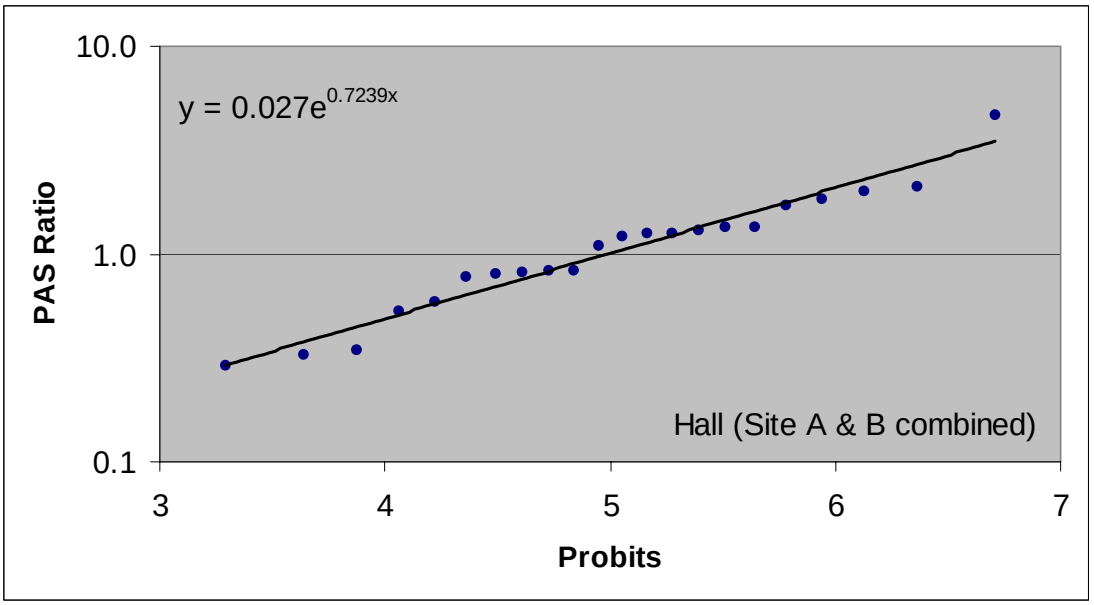


$$\max(PAS) = 13.45$$

$$\min(PAS) = 0.07$$

$$\mu_g \cdot \sigma_g^{2.58} = 6.086$$

$$\mu_g \cdot \sigma_g^{-2.58} = 0.175$$



The geometric mean PAS ratio is

$$\mu_g := 0.027 \cdot e^{0.7239 \cdot 5}$$

$$\mu_g = 1.008$$

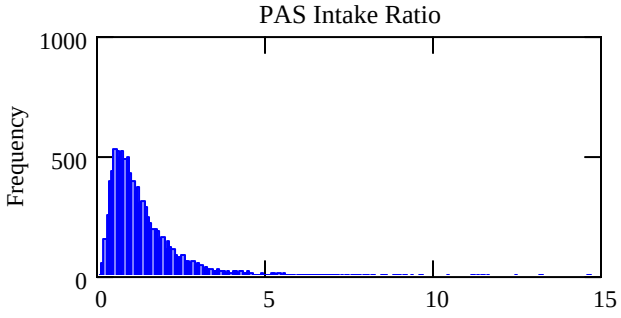
The geometric standard deviation is

$$\sigma_g := \frac{0.027 \cdot e^{0.7239 \cdot 6}}{0.027 \cdot e^{0.7239 \cdot 5}}$$

$$\sigma_g = 2.062$$

$$PAS_m := rlnorm\left(1, \ln(1), \ln\left(\sigma_g\right)\right)_1$$

$$G := histogram(200, PAS)$$



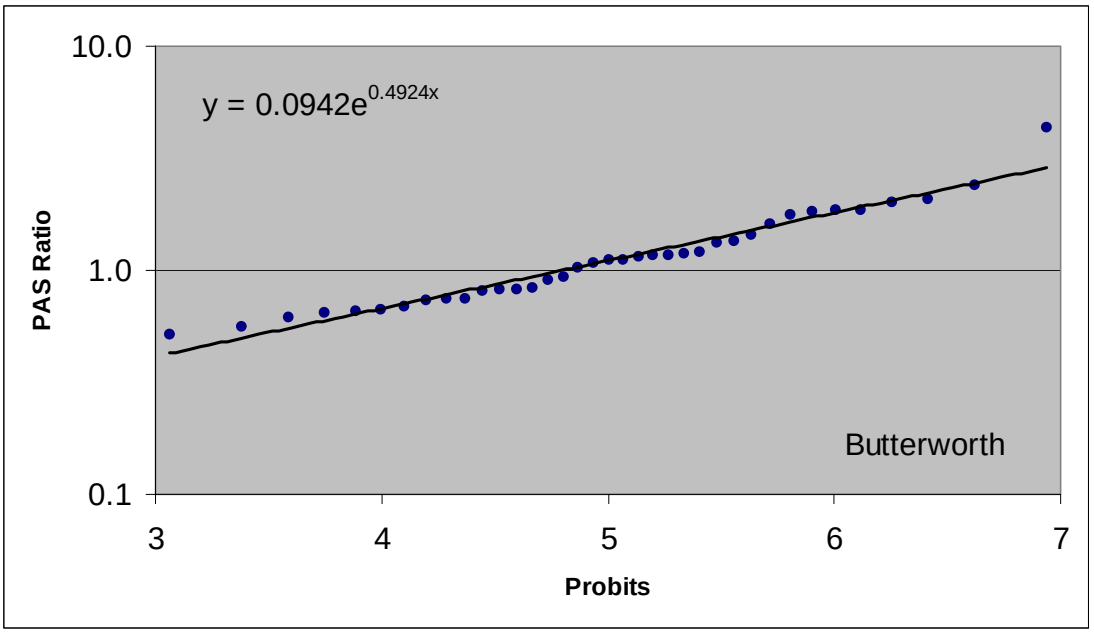
$$\max(PAS) = 14.62$$

$$\min(PAS) = 0.07$$

$$\mu_g \cdot \sigma_g^{2.58} = 6.522$$

$$\mu_g \cdot \sigma_g^{-2.58} = 0.156$$

Data from R. Butterworth and J. K. Donoghue, *Contribution of Activity Released from Protective Clothing to Air Contamination Measured by Personal Air Samplers*, Health Physics (18) 319-323; 1970. Aerosol measured was uranium dust.



The geometric mean PAS ratio is

$$\mu_g := 0.0942 \cdot e^{0.4924 \cdot 5}$$

$$\mu_g = 1.105$$

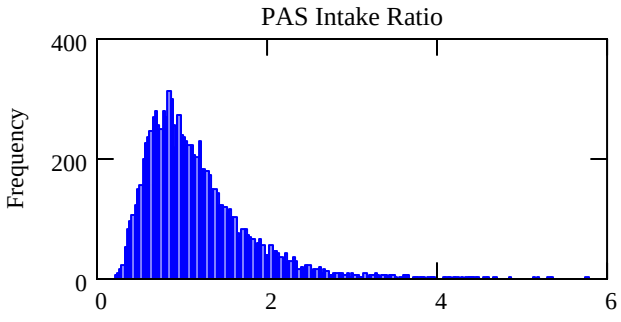
The geometric standard deviation is

$$\sigma_g := \frac{0.0942 \cdot e^{0.4924 \cdot 6}}{0.0942 \cdot e^{0.4924 \cdot 5}}$$

$$\sigma_g = 1.636$$

$$PAS_m := \text{rlnorm}\left(1, \ln(1), \ln\left(\sigma_g\right)\right)_1$$

$$G := \text{histogram}(200, PAS)$$



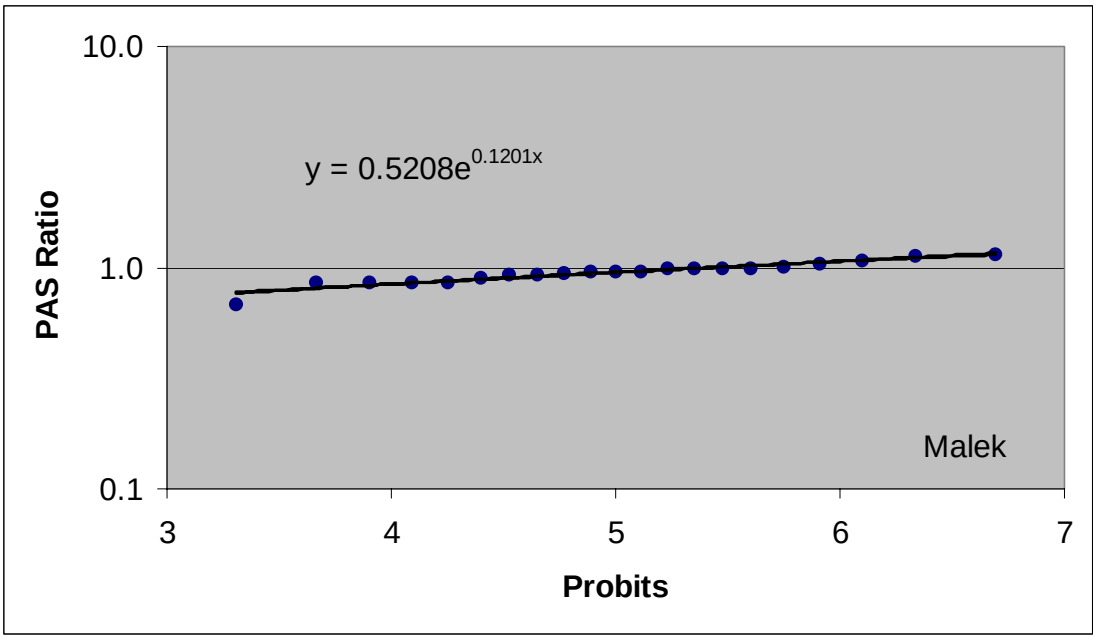
$$\max(PAS) = 5.75$$

$$\min(PAS) = 0.19$$

$$\mu_g \cdot \sigma_g^{2.58} = 3.936$$

$$\mu_g \cdot \sigma_g^{-2.58} = 0.31$$

Data from Ralph F. Malek, *Estimates of Inhalation Exposure to Styrene in the Reinforced Plastic Industry: Controlling Factors and Predictive Model*, Ph.D. thesis New York University, 1993. Styrene vapors were measured.



The geometric mean PAS ratio is

$$\mu_g := 0.5208 \cdot e^{0.1201 \cdot 5}$$

$$\mu_g = 0.949$$

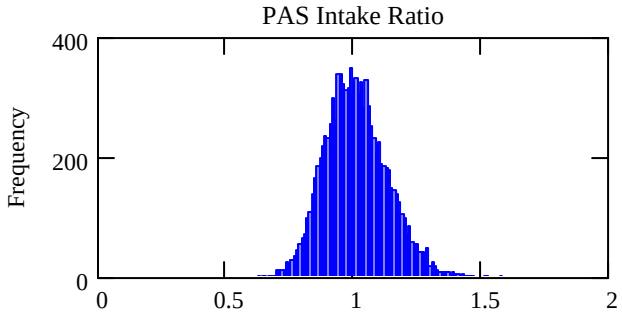
The geometric standard deviation is

$$\sigma_g := \frac{0.5208 \cdot e^{0.1201 \cdot 6}}{0.5208 \cdot e^{0.1201 \cdot 5}}$$

$$\sigma_g = 1.128$$

$$PAS_m := rlnorm\left(1, \ln(1), \ln\left(\sigma_g\right)\right)_1$$

$$G := histogram(200, PAS)$$



$$max(PAS) = 1.57$$

$$min(PAS) = 0.62$$

$$\mu_g \cdot \sigma_g^{2.58} = 1.294$$

$$\mu_g \cdot \sigma_g^{-2.58} = 0.696$$

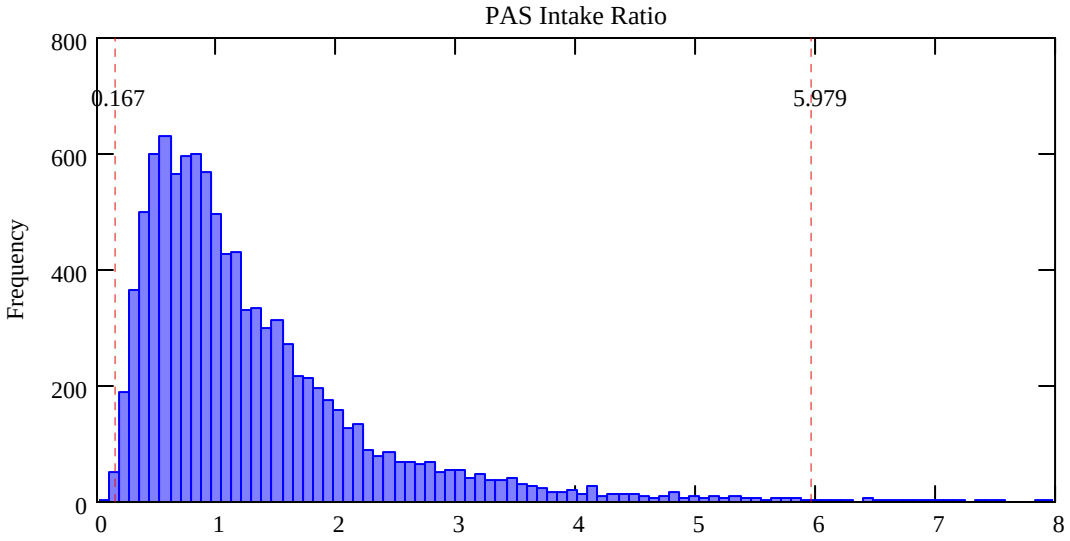
In all three studies, the cumulative distribution of the PAS ratios is adequately described with both normal and lognormal distributions. A lognormal distribution was chosen over the normal distribution because it precludes the generation of negative PAS ratios.

Based on the above data, a geometric mean of 1.0 and a geometric standard deviation of 2.0 are assumed for this study.

$\mu_g := 1$ $\sigma_g := 2$

$PAS_m := rlnorm(1, ln(1), ln(2))_1$

$G := histogram(200, PAS)$



max(PAS) = 16.41

min(PAS) = 0.07

$\mu_g \cdot \sigma_g^{2.58} = 5.979$

$\mu_g \cdot \sigma_g^{-2.58} = 0.167$

Appendix F

Evaluation of USTUR Case 0259 with Uncertainties

Evaluation of USTUR Case 0259 from data presented by A. C. James et al. *USTUR Case0259 Whole Body Donation: A Comprehensive Test of the Current ICRP Models for the Behavior of Inhaled Pu238 Oxide Ceramic Particles* Health Physics 84(1):2-33:2003. Uncertainties from **PAS** are calculated in this worksheet.

ORIGIN ≡ 1 nCi ≡ 37·Bq pCi ≡ 10^{-3}·nCi μCi ≡ 10^{6}·pCi

The compartments in the model are assigned numbers to clarify their use in the arrays to be defined.

AI1 := 1	bb1 := 4	BB1 := 7	ET2 := 10			
AI2 := 2	bb2 := 5	BB2 := 8	ETseq := 11	LNth := 13		
AI3 := 3	bbseq := 6	BBseq := 9	LNet := 12	ET1 := 14		
TAI1 := 15	Tbb1 := 18	TBB1 := 21	TET2 := 24			
TAI2 := 16	Tbb2 := 19	TBB2 := 22	TETseq := 25			
TAI3 := 17	Tbbseq := 20	TBBseq := 23	TLNet := 26	TLNth := 27		
S := 28	SI := 29	ULI := 30	LLI := 31			
blood := 32	ST0 := 35	CV := 38	TV := 41	OKT := 44	nads := 47	
LIV1 := 33	ST1 := 36	CS := 39	TS := 42	UP := 45	ENV := 48	urine := 50
LIV2 := 34	ST2 := 37	CM := 40	TM := 43	UBC := 46	feces := 49	

Deposition parameters calculated with LUDUC. These 1000 values assume 5 μm AMAD, a density of 10 g/cc, and light exercise.

$$\begin{pmatrix} DF_{ET1} \\ DF_{ET2} \\ DF_{BB} \\ DF_{bb} \\ DF_{AI} \\ Fs_{BB} \\ Fs_{bb} \end{pmatrix} :=$$

0.3824307	0.3618683	0.0215043	0.0164575	0.1045146	0.5605827	0.6211035
0.4117763	0.4768381	0.0114585	0.0026248	0.0302902	0.6252462	0.6516554
0.2854435	0.3096401	0.0181279	0.0122373	0.0555491	0.6261812	0.6701694
0.3640713	0.3770601	0.0147265	0.0030048	0.0242068	0.5873427	0.6121804
0.3614031	0.3861653	0.0118707	0.0123206	0.0990075	0.6184139	0.6778674
0.3513172	0.4606443	0.0220846	0.0085090	0.0468516	0.3974973	0.4262016
0.4115148	0.5665783	0.0158309	0.0067313	0.0294167	0.5511362	0.5840935
0.3544650	0.3765788	0.0050744	0.0052642	0.0232554	0.5171263	0.5598844
0.3327872	0.5143833	0.0092004	0.0052477	0.0305225	0.4724866	0.5001576
0.2299703	0.3362615	0.0111267	0.0288326	0.0861704	0.5291479	0.6004671

The function returns the deposition fractions in each compartment using the m^{th} row of the LUDUC parameter matrix. The geometric standard deviations are those given by Bolch et al, *Influences of Parameter Uncertainties within the ICRP 66 Respiratory Tract Model: Particle Deposition* Health Physics (81 (4):378-394; 2001. Any content not explicitly given has a value of zero.

$$
\begin{aligned}
&\text{DepositionFractions}(m) := \\
&\quad q0_{urine} \leftarrow 0 \\
&\quad q0_{AI1} \leftarrow \text{rlnorm}(1, \ln(0.3), \ln(1.10))_1 \cdot DF_{AI_m} \\
&\quad q0_{AI3} \leftarrow 0.1 \cdot DF_{AI_m} \\
&\quad q0_{AI2} \leftarrow DF_{AI_m} - q0_{AI1} - q0_{AI3} \\
&\quad q0_{bbseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{bb_m} \\
&\quad q0_{bb2} \leftarrow Fs_{bb_m} \cdot DF_{bb_m} \\
&\quad q0_{bb1} \leftarrow DF_{bb_m} - q0_{bbseq} - q0_{bb2} \\
&\quad q0_{BBseq} \leftarrow \text{rlnorm}(1, \ln(0.007), \ln(1.73))_1 \cdot DF_{BB_m} \\
&\quad q0_{BB2} \leftarrow Fs_{BB_m} \cdot DF_{BB_m} \\
&\quad q0_{BB1} \leftarrow DF_{BB_m} - q0_{BBseq} - q0_{BB2} \\
&\quad q0_{ETseq} \leftarrow \text{rlnorm}(1, \ln(0.0005), \ln(1.73))_1 \cdot DF_{ET2_m} \\
&\quad q0_{ET2} \leftarrow DF_{ET2_m} - q0_{ETseq} \\
&\quad q0_{ET1} \leftarrow DF_{ET1_m} \\
&\quad q0
\end{aligned}
$$

Define transfer rate constants for the respiratory tract. The geometric standard deviations are those given by Bolch et al.

$\kappa_{lung}(k) :=$

$f_r \leftarrow -0.1566707$

$s_r \leftarrow 0.001891$

$s_s \leftarrow 0.000257$

$s_t \leftarrow s_s$

$s_{pt} \leftarrow (1 - f_r) \cdot (s_r - s_t)$

$s_p \leftarrow s_r - s_{pt}$

$k_{AI1,bb1} \leftarrow 0.02$

$k_{AI2,bb1} \leftarrow rlnorm(1, ln(0.001), ln(1.41))_1$

$k_{AI3,bb1} \leftarrow rlnorm(1, ln(0.0001), ln(1.73))_1$

$k_{AI3,LNth} \leftarrow rlnorm(1, ln(0.00002), ln(1.41))_1$

$k_{bb1,BB1} \leftarrow rlnorm(1, ln(2), ln(1.41))_1$

$k_{bb2,BB1} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{BB1,ET2} \leftarrow rlnorm(1, ln(10), ln(1.22))_1$

$k_{BB2,ET2} \leftarrow rlnorm(1, ln(0.03), ln(1.73))_1$

$k_{ET2,S} \leftarrow rlnorm(1, ln(100), ln(1.73))_1$

$k_{ET1,ENV} \leftarrow rlnorm(1, ln(1), ln(1.73))_1$

$k_{ETseq,LNet} \leftarrow rlnorm(1, ln(0.001), ln(1.73))_1$

$k_{BBseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

$k_{bbseq,LNth} \leftarrow rlnorm(1, ln(0.01), ln(1.73))_1$

for $i \in AI1 .. LNth$

  for $j \in AI1 .. LNth$

    $k_{i+14,j+14} \leftarrow k_{i,j}$

$k_{TET2,S} \leftarrow k_{ET2,S}$

for $i \in AI1 .. LNth$

  $k_{i,i+14} \leftarrow s_{pt}$

  $k_{i,blood} \leftarrow s_p$

for $i \in TAI1 .. TLNth$

  $k_{i,blood} \leftarrow s_t$

k

Define transfer rate constants for the systemic compartments and GI tract. For lack of better information, the geometric standard deviations are assumed to be equal to the constant α, which is assumed to equal 1.001 here. This results in basically a deterministic (point) estimate of the parameters.

$$\kappa_{sys1}(k) := \left| \begin{array}{l} k_{blood,\,LIV1} \leftarrow rlnorm(1, \ln(0.1941), \ln(\alpha))_1 \\ k_{blood,\,CS} \leftarrow rlnorm(1, \ln(0.1294), \ln(\alpha))_1 \\ k_{blood,\,TS} \leftarrow rlnorm(1, \ln(0.1941), \ln(\alpha))_1 \\ k_{blood,\,UBC} \leftarrow rlnorm(1, \ln(0.0129), \ln(\alpha))_1 \\ k_{blood,\,UP} \leftarrow rlnorm(1, \ln(0.00647), \ln(\alpha))_1 \\ k_{blood,\,OKT} \leftarrow rlnorm(1, \ln(0.00323), \ln(\alpha))_1 \\ k_{blood,\,ULI} \leftarrow rlnorm(1, \ln(0.0129), \ln(\alpha))_1 \\ k_{blood,\,nads} \leftarrow rlnorm(1, \ln(0.00023), \ln(\alpha))_1 \\ k_{blood,\,ST0} \leftarrow rlnorm(1, \ln(0.2773), \ln(\alpha))_1 \\ k_{blood,\,ST1} \leftarrow rlnorm(1, \ln(0.0806), \ln(\alpha))_1 \\ k_{blood,\,ST2} \leftarrow rlnorm(1, \ln(0.0129), \ln(\alpha))_1 \\ k \end{array} \right.$$

$$\kappa_{sys2}(k) := \left| \begin{array}{l} k_{ST0,\,blood} \leftarrow rlnorm(1, \ln(0.693), \ln(\alpha))_1 \\ k_{OKT,\,blood} \leftarrow rlnorm(1, \ln(0.00139), \ln(\alpha))_1 \\ k_{ST1,\,blood} \leftarrow rlnorm(1, \ln(0.000475), \ln(\alpha))_1 \\ k_{ST2,\,blood} \leftarrow rlnorm(1, \ln(0.000019), \ln(\alpha))_1 \\ k_{CM,\,blood} \leftarrow rlnorm(1, \ln(0.0076), \ln(\alpha))_1 \\ k_{TM,\,blood} \leftarrow rlnorm(1, \ln(0.0076), \ln(\alpha))_1 \\ k_{LIV2,\,blood} \leftarrow rlnorm(1, \ln(0.000211), \ln(\alpha))_1 \\ k_{nads,\,blood} \leftarrow rlnorm(1, \ln(0.00019), \ln(\alpha))_1 \\ k \end{array} \right.$$

$$\kappa_{sys3}(k) := \begin{| k_{UP,UBC} \leftarrow rlnorm(1, ln(0.01386), ln(\alpha))_1 \\ k_{ST1,UBC} \leftarrow rlnorm(1, ln(0.000475), ln(\alpha))_1 \\ k_{TS,TV} \leftarrow rlnorm(1, ln(0.000247), ln(\alpha))_1 \\ k_{TS,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CS,CV} \leftarrow rlnorm(1, ln(0.0000411), ln(\alpha))_1 \\ k_{CS,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{TV,TM} \leftarrow rlnorm(1, ln(0.000493), ln(\alpha))_1 \\ k_{CV,CM} \leftarrow rlnorm(1, ln(0.0000821), ln(\alpha))_1 \\ k_{LIV1,LIV2} \leftarrow rlnorm(1, ln(0.00177), ln(\alpha))_1 \\ k_{LIV1,SI} \leftarrow rlnorm(1, ln(0.000133), ln(\alpha))_1 \\ k_{UBC,urine} \leftarrow rlnorm(1, ln(12), ln(\alpha))_1 \\ k |$$

$$\kappa_{GI}(k) := \begin{| f_1 \leftarrow 10^{-7} \\ k_{S,SI} \leftarrow rlnorm(1, ln(24), ln(\alpha))_1 \\ k_{SI,ULI} \leftarrow rlnorm(1, ln(6), ln(\alpha))_1 \\ k_{SI,blood} \leftarrow \frac{k_{SI,ULI} \cdot f_1}{1 - f_1} \\ k_{ULI,LLI} \leftarrow rlnorm\left(1, ln\left(\frac{24}{13}\right), ln(\alpha)\right)_1 \\ k_{LLI,feces} \leftarrow rlnorm(1, ln(1), ln(\alpha))_1 \\ k |$$

Calculate the total removal rate constants

$$total(k, \lambda) := \begin{| K \leftarrow k \\ \text{for } comp \in 1..cols(k) \\ \quad \begin{| K_{comp,comp} \leftarrow 0 \\ \quad \text{for } j \in 1..cols(k) \\ \quad\quad K_{comp,comp} \leftarrow K_{comp,comp} + k_{comp,j} \text{ if } comp \neq j \\ \quad K_{comp,comp} \leftarrow -\left(K_{comp,comp} + \lambda\right) \\ K |$$

This function creates a complete rate constant matrix.

$$\text{RateMatrix}(k) := \begin{| } k \leftarrow \kappa_{lung}(k) \\ k \leftarrow \kappa_{sys1}(k) \\ k \leftarrow \kappa_{sys2}(k) \\ k \leftarrow \kappa_{sys3}(k) \\ k \leftarrow \kappa_{GI}(k) \\ k \leftarrow \text{total}(k, 0) \\ k \end{|}$$

Calculate the coefficients and rate constants for the retention functions.

$$\text{coeff}(k, q0) := \begin{| } q0 \leftarrow \text{submatrix}(q0, 1, \text{rows}(k), 1, 1) \\ V \leftarrow \text{eigenvecs}\left(k^{T}\right) \\ M \leftarrow \text{lsolve}(V, q0) \\ \text{for } j \in 1 .. \text{cols}(k) \\ \quad \text{for } i \in 1 .. \text{cols}(k) \\ \quad\quad C_{i,j} \leftarrow V_{i,j} \cdot M_{j} \\ C \end{|}$$

$$q(t, comp, C, \gamma) := \sum_{i=1}^{\text{rows}(\gamma)} C_{comp,i} \cdot e^{\left[\left(\gamma_i\right) \cdot t\right]}$$

Urinary excretion data for USTUR 0259. Time t is in days and observed urinary excretion e_{obs} is in pCi per day.

$$\begin{pmatrix} t \\ e_{obs} \end{pmatrix} :=$$

2	0
3	0
4	0
76	0
123	0.16
150	0.07
186	0.07
209	0.1
264	0.16
283	0.18

$$\lambda := \frac{\ln(2)}{\left(3.203 \times 10^{4}\right)}$$ decay constant for Pu-238

$\alpha \equiv 1.001$ σ_g for systemic parameters

$T_d := 6532$ number of days from intake to death

$$i := 1 .. \text{rows}\left(e_{obs}\right)$$

This function calculates the organ burdens of interest, intake, and urinary excretion for a given vector of initial compartment contents *q0*.

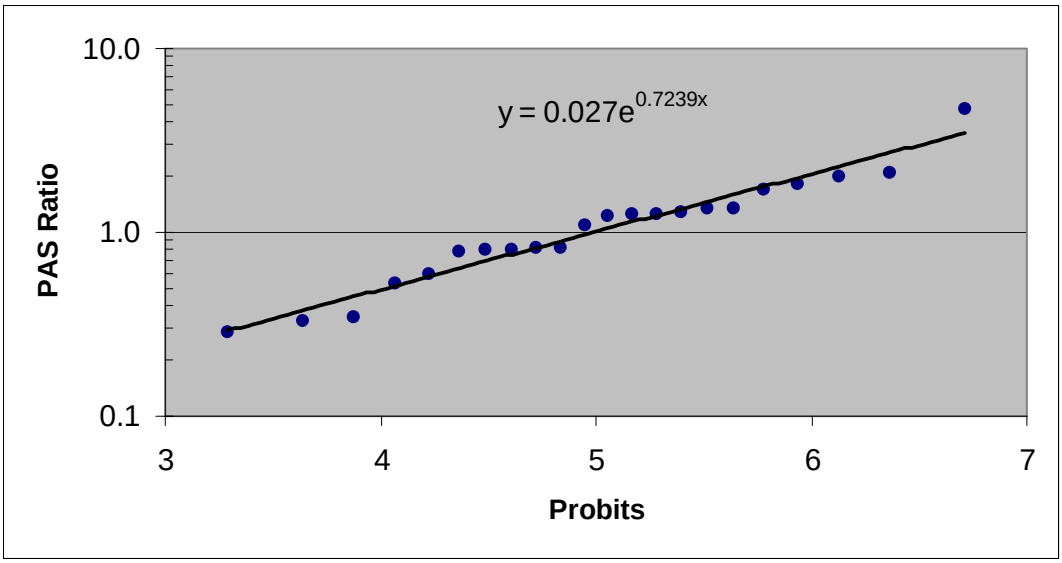
$$\text{Results}(q0) := \left| \begin{array}{l} k_{urine,urine} \leftarrow 0 \\ \text{for } i \in 1..urine \\ \quad \text{for } j \in 1..urine \\ \quad\quad k_{i,j} \leftarrow 0 \\ k \leftarrow \text{RateMatrix}(k) \\ \gamma \leftarrow \text{eigenvals}\left(k^{T}\right) \\ C \leftarrow \text{coeff}(k, q0) \\ q_{lung} \leftarrow \sum_{i=AI1}^{BBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} + \sum_{i=TAI1}^{TBBseq} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{bone} \leftarrow \sum_{i=CV}^{TM} q\left(T_d, i, C, \gamma\right) \cdot e^{-\lambda \cdot T_d} \\ q_{liv} \leftarrow \left(q\left(T_d, LIV1, C, \gamma\right) + q\left(T_d, LIV2, C, \gamma\right)\right) \cdot e^{-\lambda \cdot T_d} \\ q_{urine} \leftarrow q\left(T_d, urine, C, \gamma\right) \\ \text{for } j \in 1..\text{rows}(t) \\ \quad e_{exp_j} \leftarrow \left[q\left(t_j, urine, C, \gamma\right) - q\left[\left(t_j - 1\right), urine, C, \gamma\right]\right] \cdot e^{-\lambda \cdot t_j} \\ \begin{pmatrix} e_{exp} \\ q_{liv} \\ q_{bone} \\ q_{lung} \\ q_{urine} \end{pmatrix} \end{array} \right.$$

$$N := 1000$$

$$m := 1..N$$

PAS Uncertainty

S. C. Hall (*Comparison of Right and Left Side Label Sampling Results, Masters Thesis,UAB, 1991)* compared the results of PAS measurements performed simultaneously on the left and right lapel. A lognormal probability plot of the ratio of the left PAS measurement to the right PAS measurement is shown below.



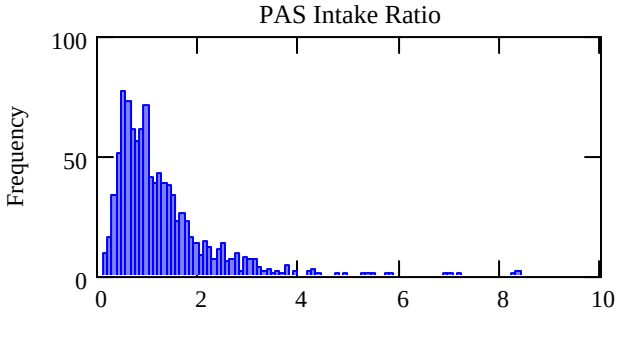
The median ratio (geometric mean) is 1.0 and the geometric standard deviation is 2.0 (the value at 6 probits). The ratio of the actual intake to the intake indicated by a PAS measurement is assumed to follow the same distribution. The *PAS* array defined below contains 1000 ratios drawn from this lognormal distribution.

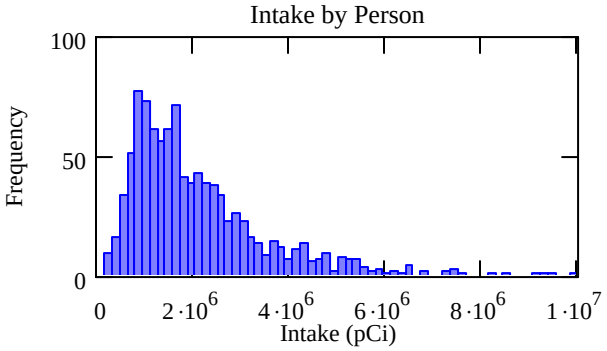
$PAS_m := rlnorm(1, ln(1), ln(2))_1$

$G := histogram(100, PAS)$

max(PAS) = 8.35

min(PAS) = 0.11





All of the functions defined above are executed below and the results assigned to the matrix A. Note that in Mathcad a function can return only one parameter, which may be a rather complex matrix as in this case.

$$A := \left| \begin{array}{l} \text{for } m \in 1..N \\ \quad A_m \leftarrow \text{Results}\left(\text{DepositionFractions}(m) \cdot PAS_m\right) \\ A \end{array} \right.$$

To make things clearer, the relevant parts of A are assigned to matrices with more meaningful names.

$\text{Intake} \equiv 1.731 \times 10^6$ The intake indicated by the PAS

$IRF_m := (A_m)_1$ The 24-hour incremental urinary excretion fractions for Pu-238.

$q_{urine_m} := \text{Intake} \cdot (A_m)_5$ The total amount of stable plutonium excreted to the urine compartment over 6532 days.

$q_{bone_m} := \text{Intake} \cdot (A_m)_3$ The skeletal burdens in pCi at 6532 days after intake.

$q_{liv_m} := \text{Intake} \cdot (A_m)_2$ The liver burdens in pCi at 6532 days after intake.

$q_{lung_m} := \text{Intake} \cdot (A_m)_4$ The lung burdens in pCi at 6532 days after intake.

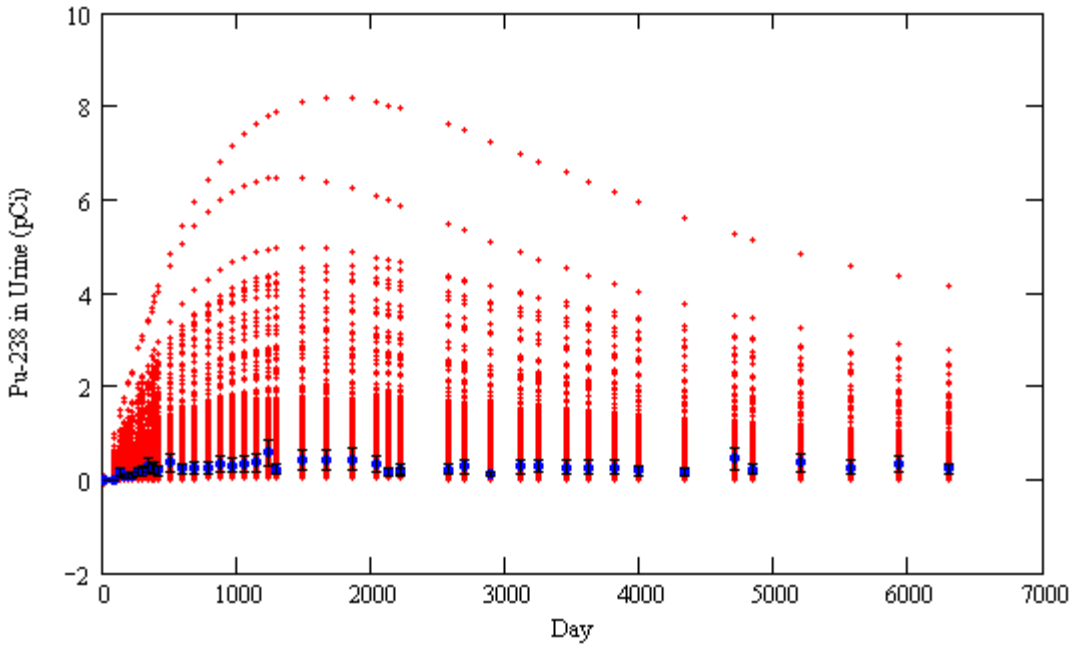
Urinary Excretion

$j := 1 .. N$

$i := 1 .. 48$

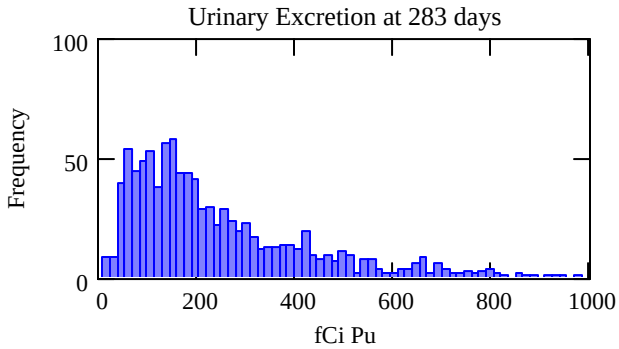
$e_{exp_{j,i}} := Intake \cdot \left(IRF_j\right)_i$

$\varepsilon_{high_i} := e_{obs_i} + 0.5 \cdot e_{obs_i}$ $\varepsilon_{low_i} := e_{obs_i} - 0.5 \cdot e_{obs_i}$



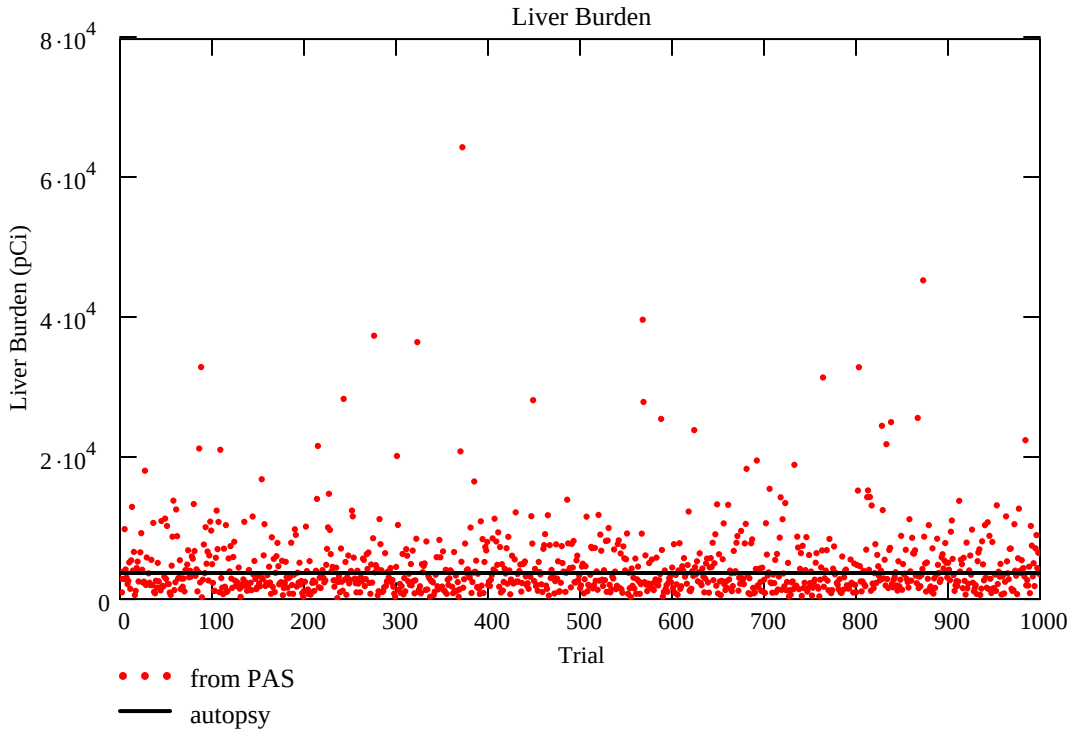
The uncertainties in the observed urinary excretion are arbitrarily set to +/-50% of the observed value.

$G := histogram\left(200, e_{exp}^{\langle 10 \rangle} \cdot 1000\right)$



Liver

The quantity q_{liv} is the liver burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Liver Autopsy Data

$137 \cdot Bq = 3.703 \times 10^3\ pCi$

+/-

$4 \cdot Bq = 1.081 \times 10^2\ pCi$

$\text{mean}(q_{liv}) = 4.704 \times 10^3$

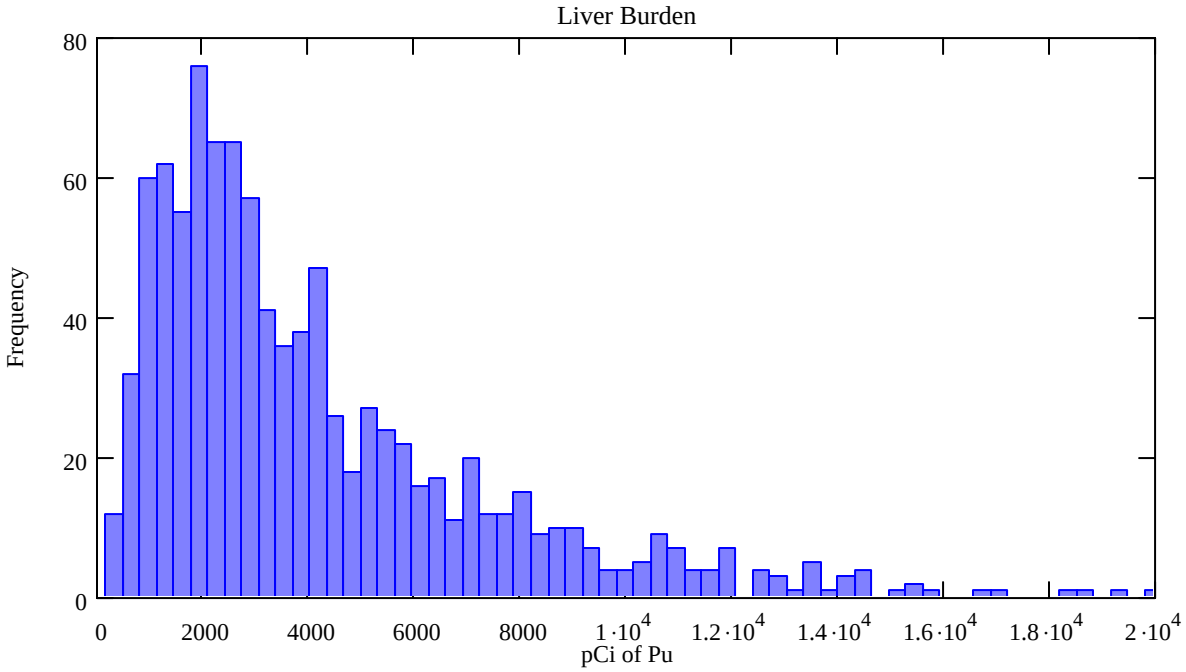
$\text{stdev}(q_{liv}) = 5.233 \times 10^3$

$\max(q_{liv}) = 6.453 \times 10^4$

$\min(q_{liv}) = 1.249 \times 10^2$

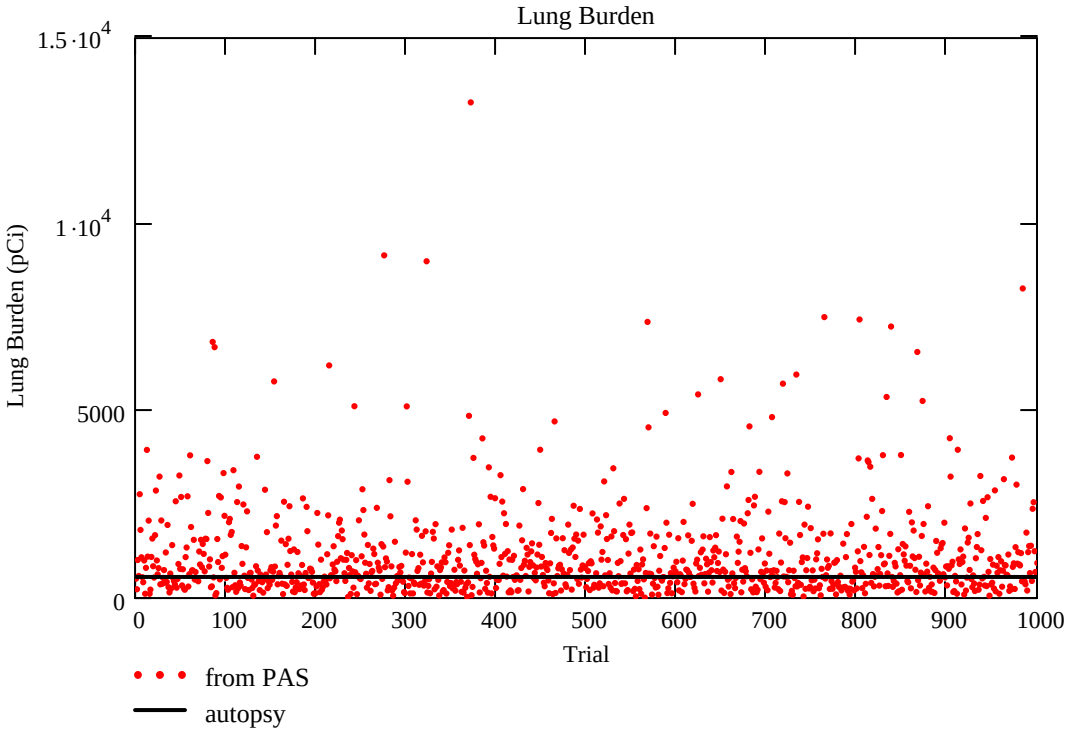
$\frac{\text{stdev}(q_{liv})}{\text{mean}(q_{liv})} = 1.112$

$G := \text{histogram}(200, q_{liv})$



Lung

The quantity q_{lung} is the lung burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Lung Autopsy Data

$20.9 \cdot Bq = 5.649 \times 10^{2}\ pCi$

$\text{mean}(q_{lung}) = 1.114 \times 10^{3}$

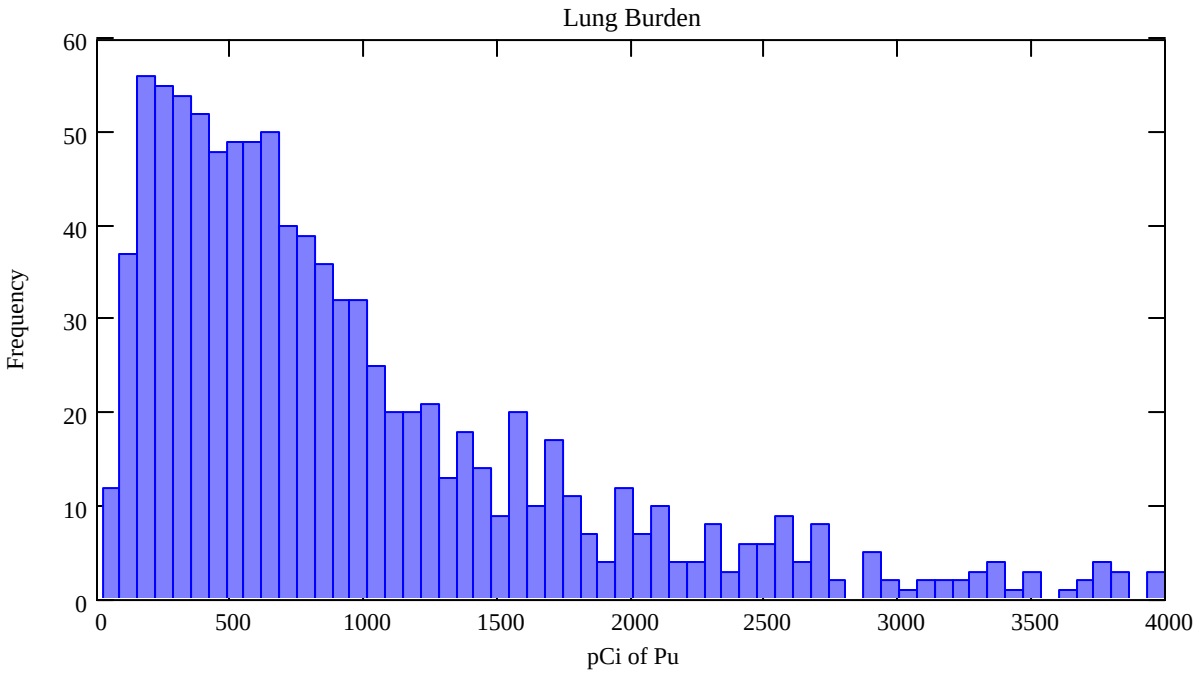
$\text{stdev}(q_{lung}) = 1.235 \times 10^{3}$

$\max(q_{lung}) = 1.328 \times 10^{4}$

$\min(q_{lung}) = 1.202 \times 10^{1}$

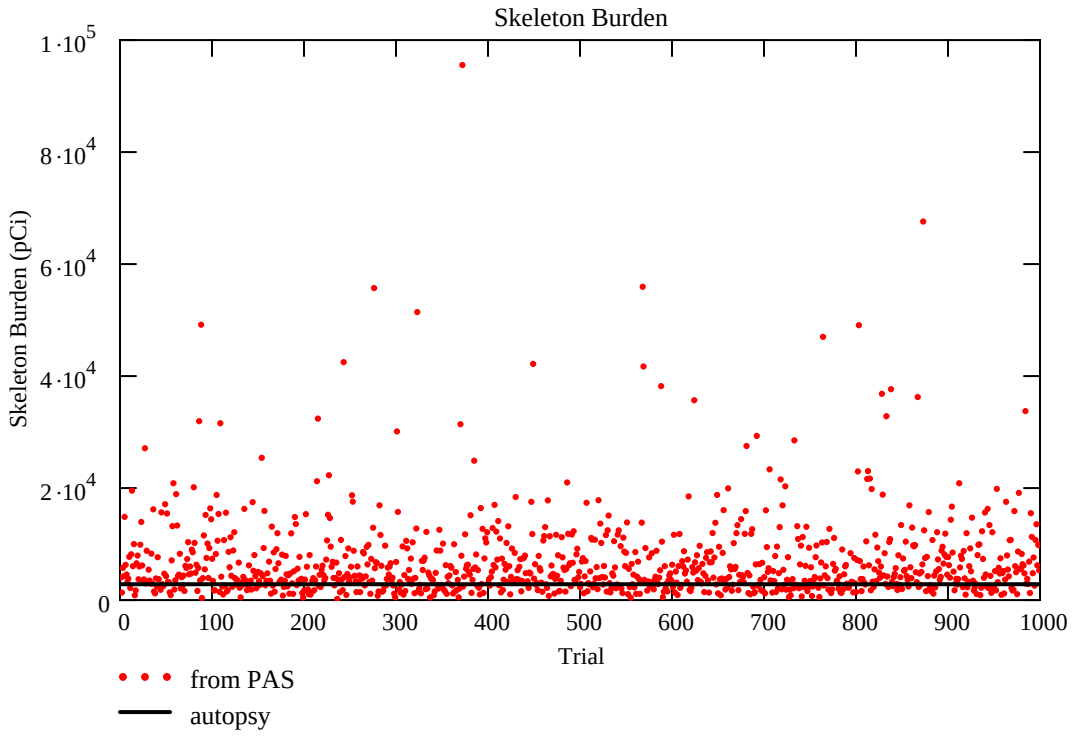
$$\frac{\text{stdev}(q_{lung})}{\text{mean}(q_{lung})} = 1.109$$

$G := \text{histogram}(200, q_{lung})$



Skeleton (including all marrow)

The quantity q_{bone} is the skeletal burden that would be calculated assuming that the intake was measured by a PAS and is equal to *Intake* every time.



Bone Autopsy Data

$104 \cdot Bq = 2.811 \times 10^{3}\ pCi$

+/-

$1 \cdot Bq = 2.703 \times 10^{1}\ pCi$

$\text{mean}(q_{bone}) = 6.952 \times 10^{3}$

$\text{stdev}(q_{bone}) = 7.708 \times 10^{3}$

$\max(q_{bone}) = 9.552 \times 10^{4}$

$\min(q_{bone}) = 1.851 \times 10^{2}$

$$\frac{\text{stdev}(q_{bone})}{\text{mean}(q_{bone})} = 1.109$$

$G := \text{histogram}(200, q_{bone})$