

Bioassays:

Assay Reproducibility versus Compound Precision using Bayesian Statistics

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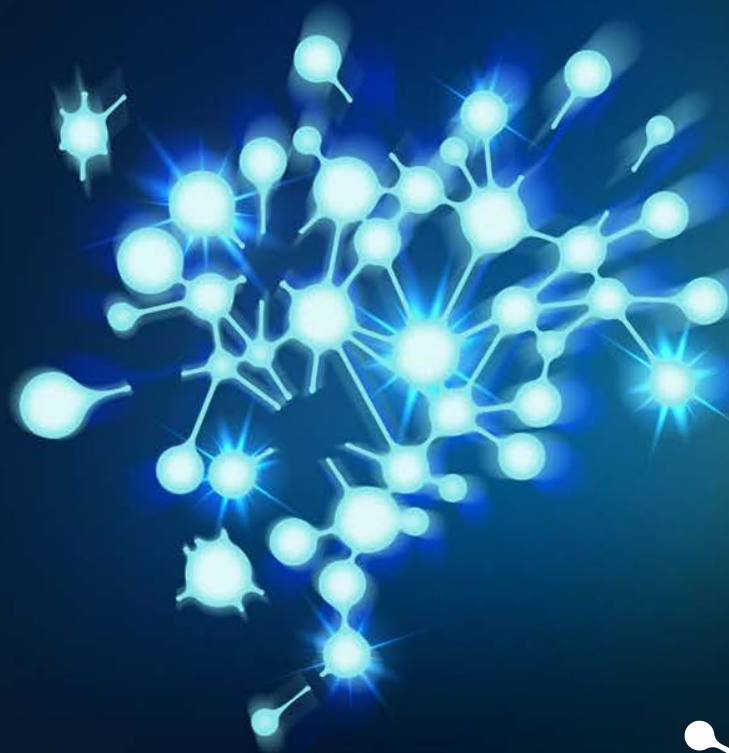
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Contents

- ▶ Introduction
- ▶ Bayesian methodology
- ▶ Application in Bioassays
- ▶ Conclusion



Introduction

What is the question?

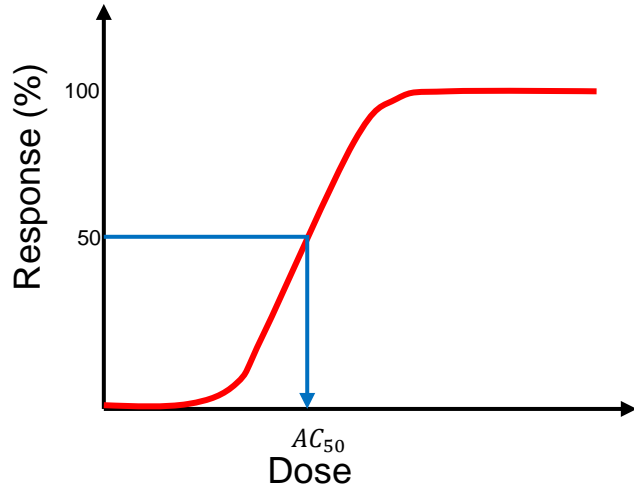
- ▶ In drug development, assays are developed for the screening of potent compounds. In the event of compound repeat, how do scientists discriminate between true differences in potency and random noise?



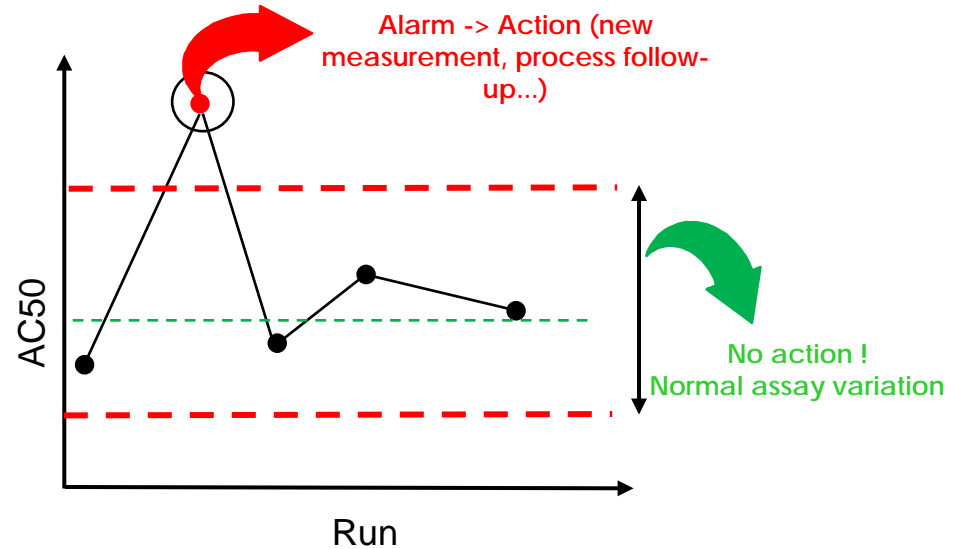
- ▶ How can we verify?



- ▶ Biological activity is often expressed as AC50



Time →



- ▶ Due to inherent process and assay variability, estimates between runs are bound to differ.



Why differences in compound potencies?

- ▶ Sources of variation include:
 - Reagent preparation
 - Pipetting errors
 - Location on plate
 - Reader uncertainty
 - Environmental conditions
 - Different operators
 - Time effect



● Methods implemented in practice

- ▶ **0.5log**: Expected threshold for within and between assay variability (EMA and ICH guidelines)
 - Difference in log potency < 0.05 (3-fold change in potency)
- ▶ Disadvantage: ignores true assay variability (fixed cut-off)



Methods implemented in practice

- ▶ **MSR:** The smallest ratio between two potencies that is considered to be statistical significance,
 - captures variability.

MSR	Requirement	Estimate	Implementation
Replicate Experiment MSR	<ul style="list-style-type: none"> • Two independent runs of 20 – 30 compounds • Potency should span the concentration range to be tested by assay 	$MSR = 10^{2 * S_d}$	<ul style="list-style-type: none"> • Captures within run variability • Assay validation for production • <3 for a good assay
Control compound MSR	<ul style="list-style-type: none"> • Log-potency (logAC50) estimates of control compound • Minimum of 6 runs is considered adequate to estimate between-run variability 	$MSR = 10^{2 * \sqrt{2} * s_d}$	<ul style="list-style-type: none"> • Captures between-run variation (within-run) • Monitor assay reproducibility over time
Database MSR	<ul style="list-style-type: none"> • logAC50 estimates of repeated compounds • Minimum of 6 runs 	$MSR = 10^{2 * \sqrt{2} * s_d}$	<ul style="list-style-type: none"> • Captures within and between-run variation • Monitor assay reproducibility over time

Haas, J. V et al.; 2017



Application of MSR and limitations

- ▶ MSR is recommended to check for overall reproducibility of an assay (prior and post-production monitoring): $MSR < \text{threshold}$ (dependent on practical experience).
- ▶ MSR as threshold for potency ratios, but literature is confusing...
 - Not recommended to evaluate potency precision of individual compounds (Haas et al. 2017): **With sufficient repeats**, current suggestion is to report geometric mean (backed transformed log potency) with 95% CI for the **mean**.
 - Compound specific MSR :
 - minimum of 6 repeats required
 - Significant difference between repeats when $Y_1/Y_2 > MSR_Y$
 - When more than two repeats $n > 2$, current estimate is compared to geometric mean
- ▶ Limitation:
 - Insufficient repeats in practice
 - For $n > 2$, variability between repeats are not considered (averaged out)



Proposal: Bayesian beta(β) – expectation tolerance interval

- ▶ Region within which β proportion of future observations are expected to lie given the variability observed in data.
 - Also known as prediction interval of a future observation with β probability
- ▶ Computed based on historical data



Use of information from reference compounds with multiple repeats

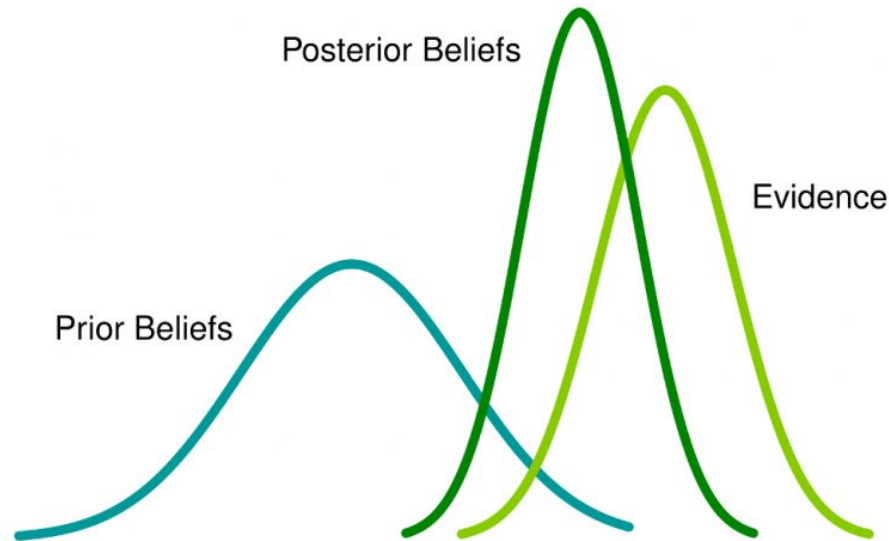
- Use of uncertainty in reference compounds estimates as prior
- Compute compound specific intervals upon first repeat
- Allows for assessment of compound repeat agreement



Bayesian methodology

Bayesian

- ▶ Bayesian statistics is a statistical approach that allow us to update our believes in the event of new data.
- ▶ Motivations for adopting Bayesian approach:
 - Natural and coherent way of thinking about science and learning

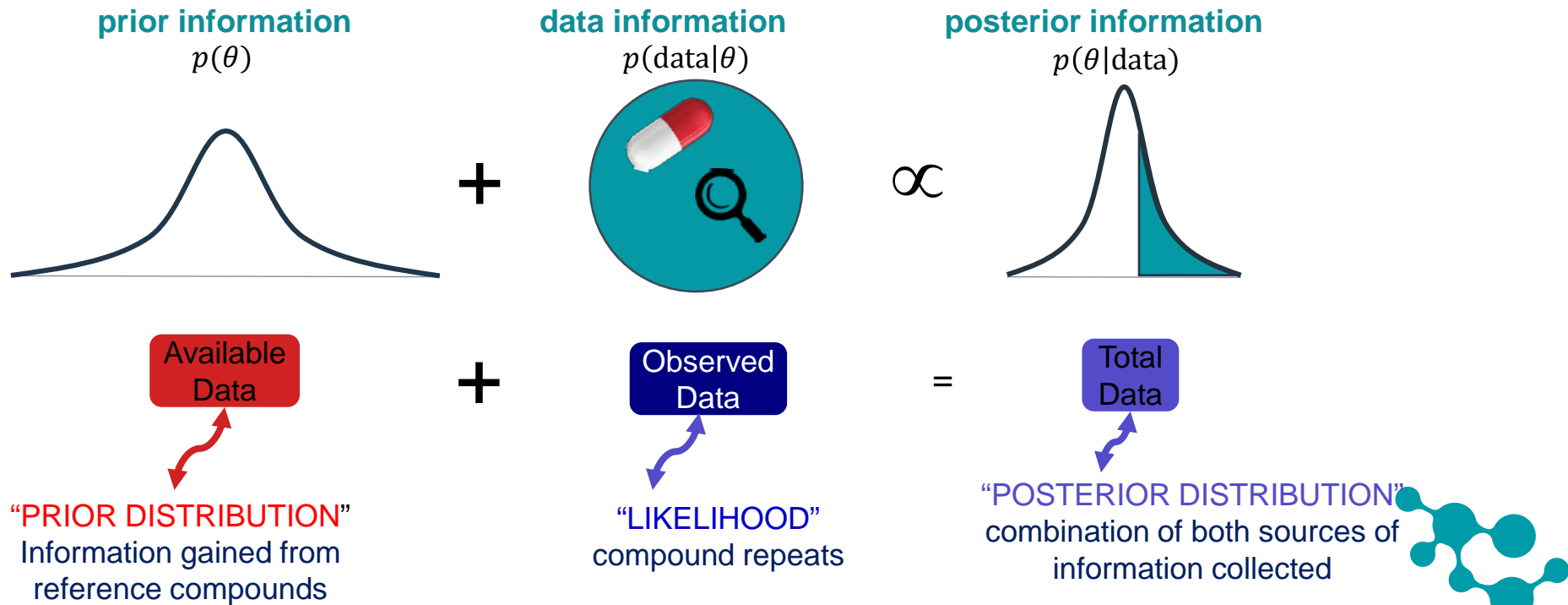


- ▶ Instead of point estimates (+/- standard deviation), we have a complete distribution for any parameter of interest



Bayesian principle

- ▶ Bayesian inference is the mechanism used to update the state of knowledge



Bayesian concepts

- ▶ Four major concepts:
 - Prior distribution
 - Likelihood
 - Posterior distribution
 - Predictive distribution



Prior belief

- ▶ Let's consider θ , the parameter of interest (ex: mean compound potency)

θ is treated as a random variable

- ▶ Prior distribution of parameter θ : $p(\theta)$
 - Distribution of θ before any data are observed
 - Reasonable opinion concerning the plausibility of different values of θ
 - Based on all available evidence/knowledge
 - Or non-informative prior
- ▶ Prior distribution → Specify the domain of plausible values
→ Specify the weights given to these values



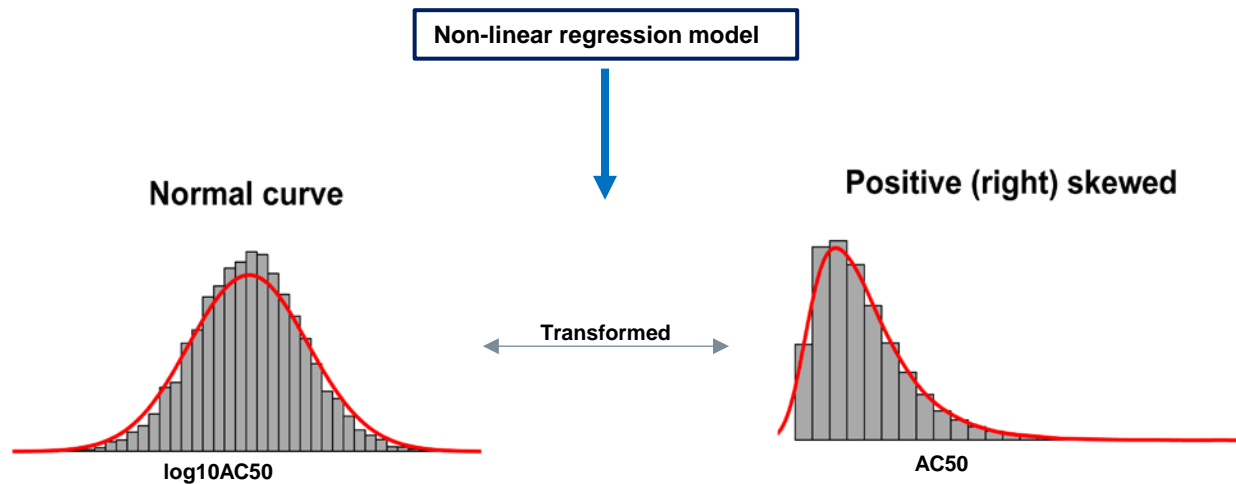
Evident and posterior belief

- ▶ Likelihood:
 - Conditional probability of the data given θ : $p(y|\theta)$
 - Based solely on data
- ▶ Posterior distribution:
 - Distribution of θ after observed data have been taken into account: $p(\theta|y)$
 - Final opinion about θ
- ▶ Predictive distribution:
 - Given the model and the posterior distribution of its parameters, what are the plausible values for a future observation y^* ?
 $p(y^*|\theta)$



Derivation of posterior distribution

- ▶ Let's assume that the log potency of a compound $y_i, i=1, \dots, N$, follow a normal distribution $N(\mu, \sigma^2)$ (= likelihood)



- ▶ Independent runs i.e fresh preparation of experimental materials



Derivation of posterior distribution

- ▶ Let's assume that the log potency of a compound y_i , $i=1, \dots, N$, follow a normal distribution

$N(\mu, \sigma^2)$ (= likelihood)

- ▶ We assume that the mean μ and variance σ^2 are unknown
- ▶ The objective is to estimate μ and σ^2 and predict a future measurement \tilde{y}
- ▶ We need to specify a **prior distributions** for the μ and σ^2 :
 - We select priors distributions that lead to same family of posterior distributions
 - Normal conjugate family approach

Prior mean: $\mu | \sigma^2 \sim N(\mu_0, \sigma^2 / \kappa_0)$

- We keep it non-informative

$$\mu_0 = \bar{y}_0$$

Prior variance: $\sigma^2 \sim Inv - \chi^2(v_0, \sigma_0^2)$

- Assay intermediate precision based reference compounds

$$\begin{aligned} \kappa_0 &= n_0 \\ \sigma_0^2 &= s_0^2 \end{aligned}$$

- \bar{y}_0 , n_0 , s_0^2 and v_0 are the prior sample mean, sample size for the mean, sample variance and degree of freedom of the variance respectively



► Likelihood: Data

$$L(\mu, \sigma^2 | \mathbf{y}) = \frac{1}{(2\pi\sigma^2)^{\frac{n}{2}}} \exp\left(-\frac{1}{2\sigma^2} [(n-1)s^2 + n(\bar{y} - \mu)^2]\right)$$

- s^2 and \bar{y} are sufficient statistics for μ and σ^2

► Posterior \propto Prior * Likelihood

$$\bar{\kappa}_n = \kappa_0 + n,$$

$$\bar{\mu}_n = \frac{\kappa_0\mu_0 + n\bar{y}}{\bar{\kappa}_n}$$

$$\bar{v}_n = v_0 + n$$

$$\bar{\sigma}_n^2 = \frac{1}{\bar{v}_n} \left(v_0\sigma_0^2 + \sum_i (y_i - \bar{y})^2 + \frac{n\kappa_0}{\kappa_0 + n} (\bar{y} - \mu_0)^2 \right).$$

- Posterior mean μ_n and variance σ_n^2 are a weighted averages of prior (μ_0, σ_0^2) and sample (s^2, \bar{y}) mean and variance
 - Weights depend on sample size



Marginal posterior distributions

- ▶ Mean: $p(\mu|\sigma^2, \mathbf{y}) = N(\mu|\bar{\mu}_n, \sigma_n^2/\bar{\kappa}_n)$
 $p(\mu|\mathbf{y}) = t_{v_n}(\mu|\bar{\mu}_n, \bar{\sigma}_n^2/\bar{\kappa}_n)$
- ▶ Variance: $p(\sigma^2|\mathbf{y}) = Inv - \chi^2(\sigma^2|\bar{v}_n, \bar{\sigma}_n^2)$
- ▶ The posterior distributions contains everything that can be said about μ and σ^2 .
- ▶ To summarize its information content:
 - Measures of location: posterior mode, posterior median, posterior mean
 - Measures of spread: Posterior variance
 - Bayesian credibility interval:
 - Get the quantiles of the distribution (2.5% and 97.5%)
 - An interval that contains 95% most plausible/credible values
 - Any probability on the values of the parameters



Posterior Predictive distribution

- ▶ Given the model and the posterior distribution of its parameters, what are the plausible values for a future observation \tilde{y} ?
- ▶ Compute plausible values of \tilde{y} conditionally on the available information:

$$p(\tilde{y}|data) = \int p(\tilde{y}|\theta) p(\theta|data) d\theta$$

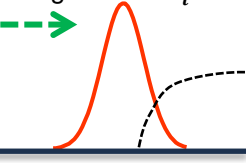
Model Posterior



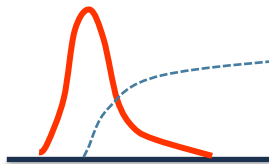
How to make predictions

1st, draw a mean and a variance from:

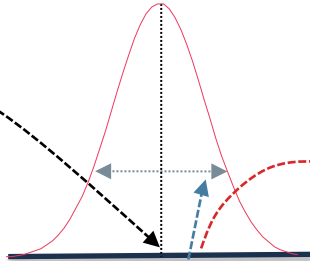
Posterior of mean μ_i
given the σ_i^2 drawn



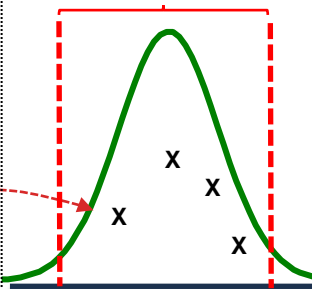
Posterior of Variance σ_i^2
given mean drawn



2nd, draw an observation from the resulting distribution
 $y_i \sim N(\mu_i, \sigma_i^2)$



3rd, repeat a large number of time to obtain the predictive distribution



β – expectation tolerance interval

► After mathematical development,

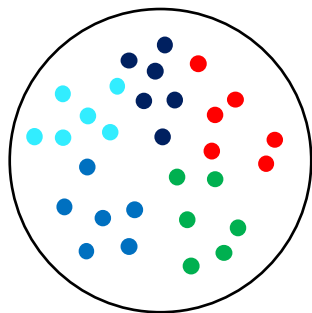
$$p(\tilde{y}|\mathbf{y}) = t_{\bar{v}_n} \left[\tilde{y} | \bar{\mu}_n, \frac{\bar{\sigma}_n^2 (1 + \bar{\kappa}_n)}{\bar{\kappa}_n} \right]$$



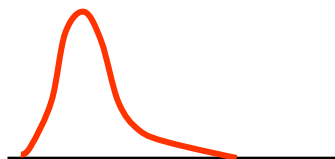
Application in Bioassays

Application in precision of compound repeats in assays

Potencies of 5 reference compounds

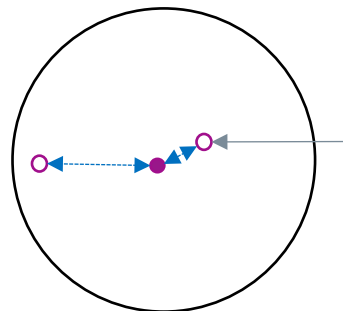


Intermediate precision

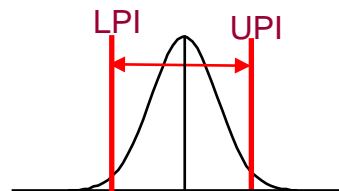


Prior information

Test compound



Compound repeat



Prediction



How to estimate assay variability: Intermediate precision (sd)

► Mixed- effect model:

- Fixed effect for ref. compounds and random effect for run.

$$y_{ij} = \mu_i + \gamma_j + \varepsilon_{ij}$$

$$\gamma_j \sim N(0, \sigma_\gamma^2)$$

$$\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$$

y_{ij} = log potency of compound i in run j

μ_j = mean log potency of compound i

γ_j = random effect of run j

ε_{ij} = measurement error for compound i in run j

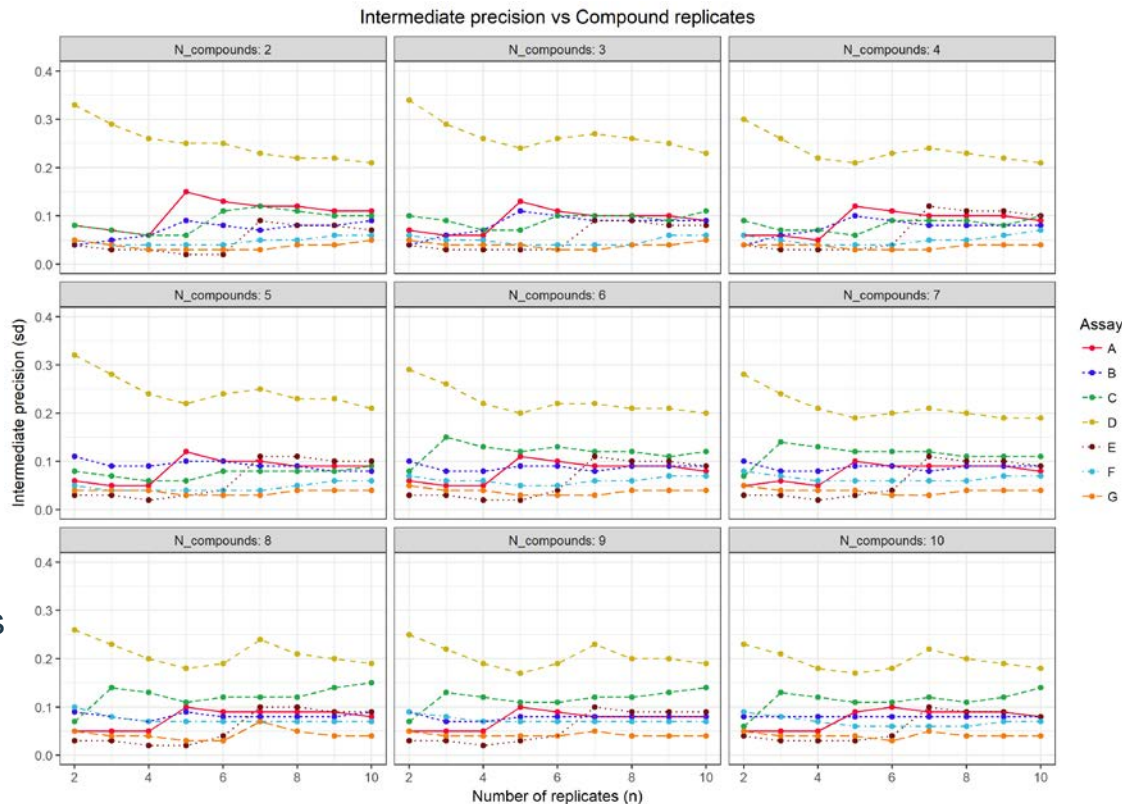
σ_γ^2 and σ_ε^2 are the run and measurement error variances respectively.

$$s_0 = sd = \sqrt{\sigma_\gamma^2 + \sigma_\varepsilon^2}$$



Sample size requirement

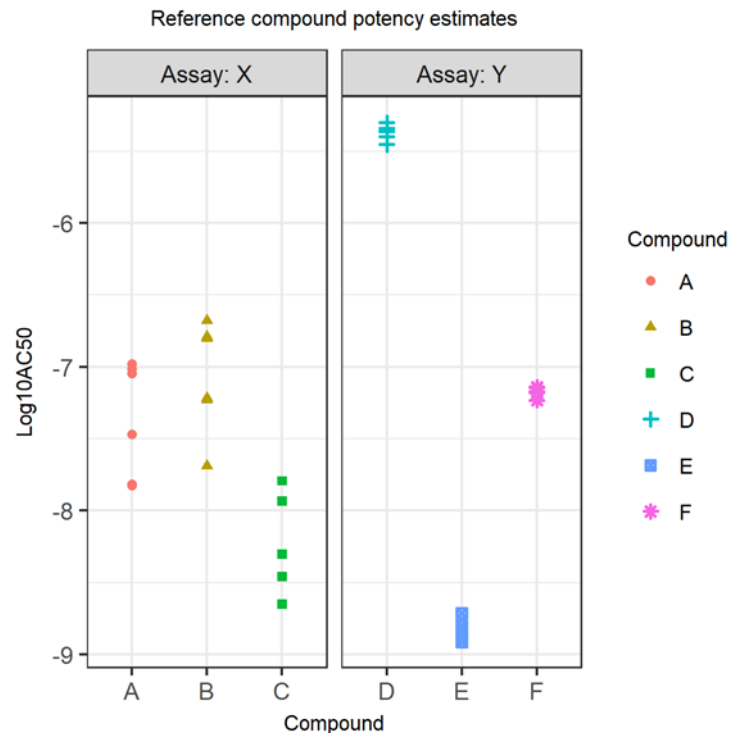
- ▶ Use of log potency of reference compound accrued over time
- ▶ A minimum of 6 repeat is proposed for Control compound and Database MSR.
- ▶ Is this a large enough sample?
 - This was assessed using real assay data
- ▶ Minimum recommendation:
 - 3 reference compounds with 6 repeat each ($n = 18$)
- ▶ This statistics does not depend on the actual log potencies of the compounds but if possible, compound selection may span the log potency range of assay



Example: Real assay data

- ▶ Compound **A** had a log potency estimates **-5.2** and a repeat of **-6.1**. Is the difference a true difference or noise from the assay?
- ▶ Consider two assays **X** and **Y**.

Run	Assay: X		Assay: Y	
	Ref. compound	Log10AC50	Ref. compound	Log10AC50
1	A	-6.98	D	-5.36
1	B	-6.79	E	-8.88
1	C	-7.93	F	-7.14
2	A	-7.82	D	-5.36
2	B	-7.69	E	-8.83
2	C	-8.65	F	-7.23
3	A	-7.04	D	-5.40
3	B	-6.68	E	-8.71
3	C	-7.79	F	-7.18
4	A	-7.82	D	-5.30
4	B	-7.23	E	-8.80
4	C	-8.30	F	-7.17
5	A	-7.01	D	-5.45
5	B	-6.80	E	-8.91
5	C	-7.93	F	-7.17
6	A	-7.47	D	-5.34
6	B	-7.22	E	-8.86
6	C	-8.46	F	-7.14



Example analysis

- ▶ Assay intermediate precision

Assay	Random effect	Variance	Intermediate precision (<i>sd</i>)
X	Run	0.1290	0.3755
	Residual	0.0119	
Y	Run	0.0002	0.0541
	Residual	0.0027	

- ▶ Prior:

$$\mu_0 = 0$$

$$\kappa_0 = 0.0001$$

$$\sigma_0^2 = 0.3755^2 = 0.1410$$

$$v_0 = 17$$

- ▶ Data : -5.2

$$s^2 = 0 \text{ and } \bar{y} = -5.2$$

- ▶ Posterior:

$$\bar{\kappa}_n = 1 + 0.0001 = 1.0001$$

$$\bar{\mu}_n = \frac{(0.0001 * 0) + (1 * -5.2)}{1.0001} = -5.2$$

$$\bar{v}_n = 17 + 1 = 18$$

$$\bar{\sigma}_n^2 = \frac{1}{18} (2.3970 + 0 + 0.0027) = 0.1333$$

- ▶ Posterior predictive distribution:

$$p(\tilde{y}|\mathbf{y}) = t_{18}[-5.2, 0.2666]$$

- ▶ $\beta(95\%)$ – expectation tolerance interval

$$[- 6.29, - 4.11]$$

- ▶ -6.1 is therefore within interval in assay X



Demo in R-Shiny

► Let's go shiny.....

Bioassay: Compute beta-expectation tolerance interval of a test compound

Prior Distributions

Mean parameters

Mean

N(Mean):

Variance Distribution

SD

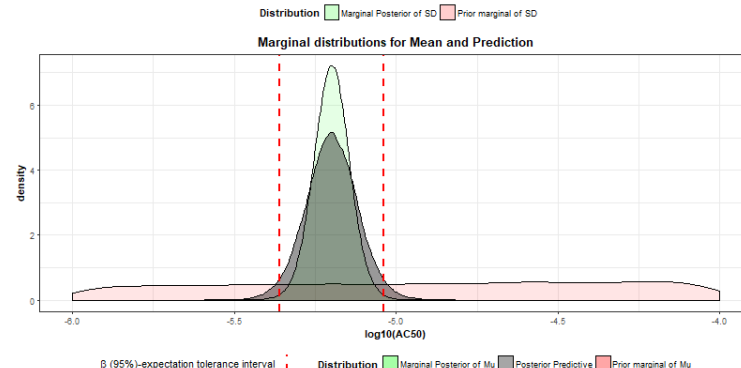
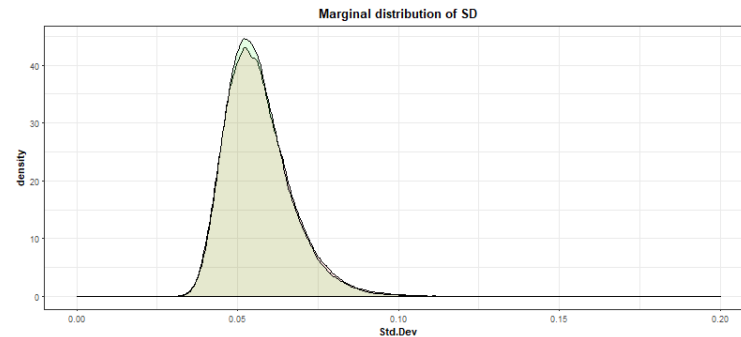
N(SD):

x-axis limits (min,max):

Data

Observations (comma delimited):

x-axis limits (min,max):



95% beta-expectation tolerance interval
Lower PI = -5.36
Upper PI = -5.04

Distribution ■ Marginal Posterior of Mu ■ Posterior Predictive ■ Prior marginal of Mu



With n=3 repeats

- ▶ Example where posterior shifts, due to more estimates (strength of bayesian)

Bioassay: Compute beta-expectation tolerance interval of a test compound

Prior Distributions

Mean parameters

Mean:

N(Mean):

Variance Distribution

SD:

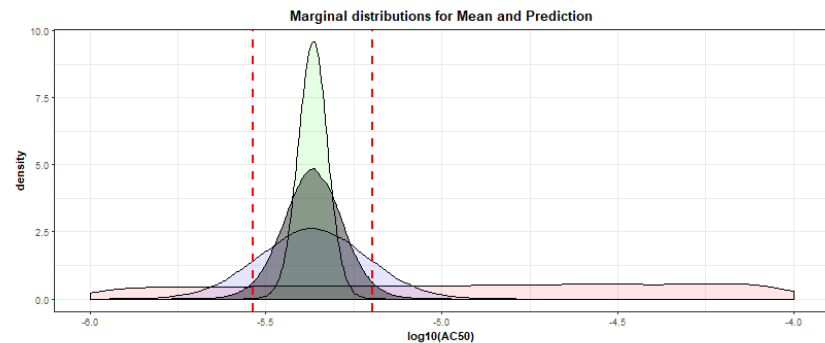
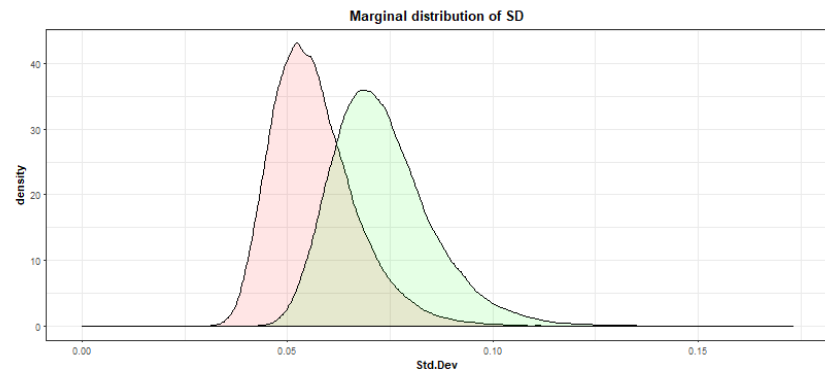
N(SD):

x-axis limits (min,max):

Data

Observations (comma delimited):

x-axis limits (min,max):



Conclusion

Summary

- ▶ Bayesian β – expectation tolerance interval approach:
 - An extension of Database MSR concept to capture Assay variability via reference compounds
 - Allows for compound specific prediction intervals to be computed upon the first repeat and updated as repeats are accrued.
 - Interval provides a save region within which differences in individual compound log potencies are considered to be within the normal assay variation limits.



Acknowledgement

- ▶ To Janssen Pharmaceuticals, Beerse, for the formidable collaboration and providing data for this exercise.



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Comparison

- ▶ Comparison Bayesian-Frequentist interval
 - Bayesian : Prediction interval : 95% most plausible/credible values of future observations.
 - Frequentist : Prediction interval : “If we repeat the same experiment a large number of times, the prediction interval will contain a future observation 95% of the cases.”

