

Comparing methods for averaging IC50s: can we forego complexity for a simpler approach?

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Agenda

1. Background & Motivation
2. Methods for Aggregating IC50s
3. Comparing Methods via Simulation
4. An Automated Solution
5. Conclusions & Next Steps

Background & Motivation

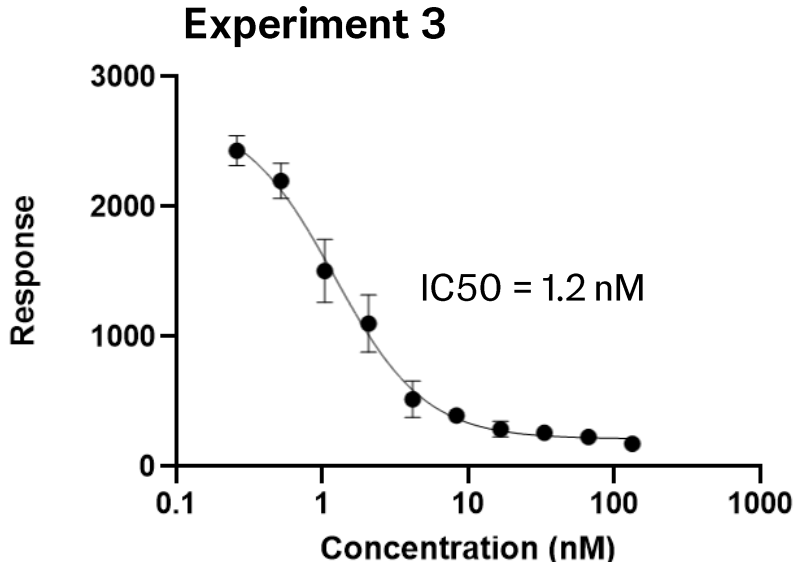
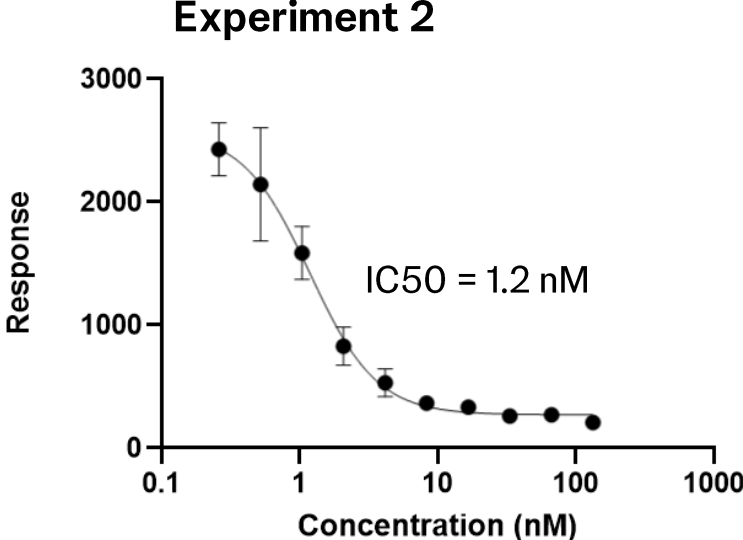
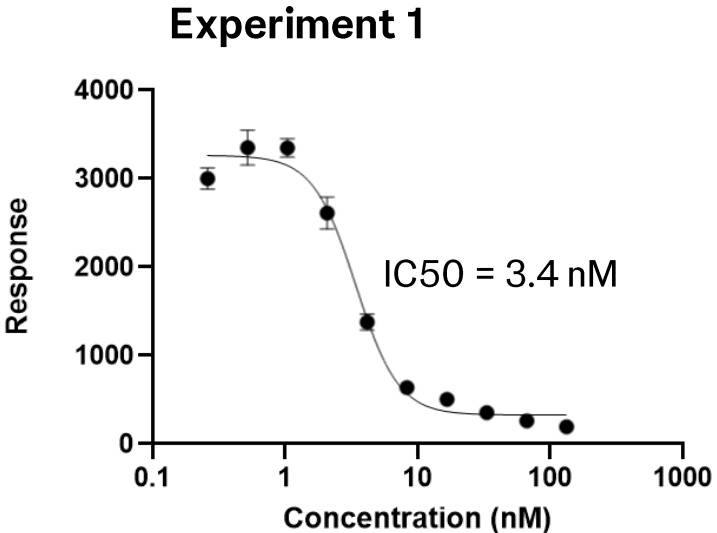
Motivation

- First in-human dose of a treatment is established in part by performing repeated concentration-response experiments and determining IC50 (concentration corresponding with half maximal response)
- Many scientists have contacted us regarding averaging IC50s for various discovery programs
- Need a sound way to aggregate IC50s across experiments or donors
 - Statistically accurate
 - Easy to understand

Motivation – A Practical Example

Example 1: Inhibition Data (Species 1) for Compound A

- Asked to average IC50s for small number of *in vitro* experiments for inhibitor of pro-inflammatory cytokine



Motivation – A Practical Example

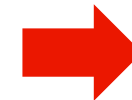
Example 1: Inhibition Data (Species 1) for Compound A

- Original Method: Calculate arithmetic average in excel
 - Over-predicts average since IC50 is log-normally distributed

Experiment	IC50 (nM)
Experiment 1	3.4
Experiment 2	1.2
Experiment 3	1.2



Measure	Estimate (nM)
Arithmetic Mean	1.9
Margin of Error	1.5

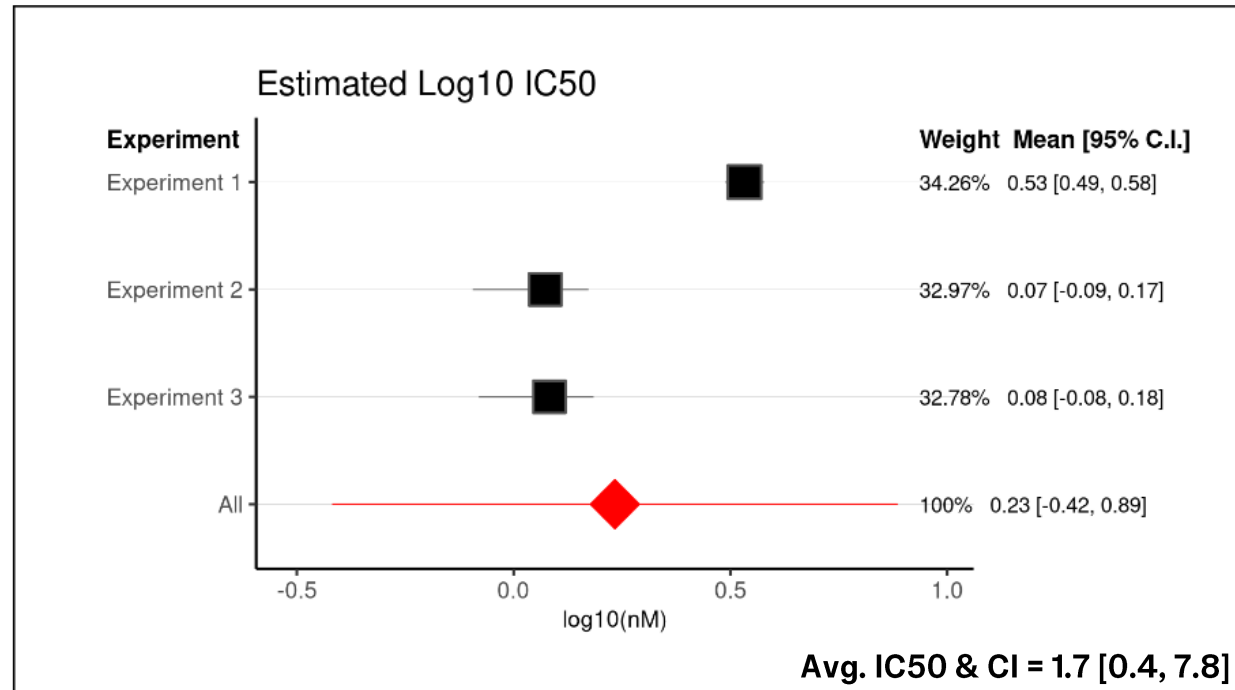


<i>Average IC50 & MoE</i>
1.9 nM +/- 1.5 nM

Motivation – A Practical Example

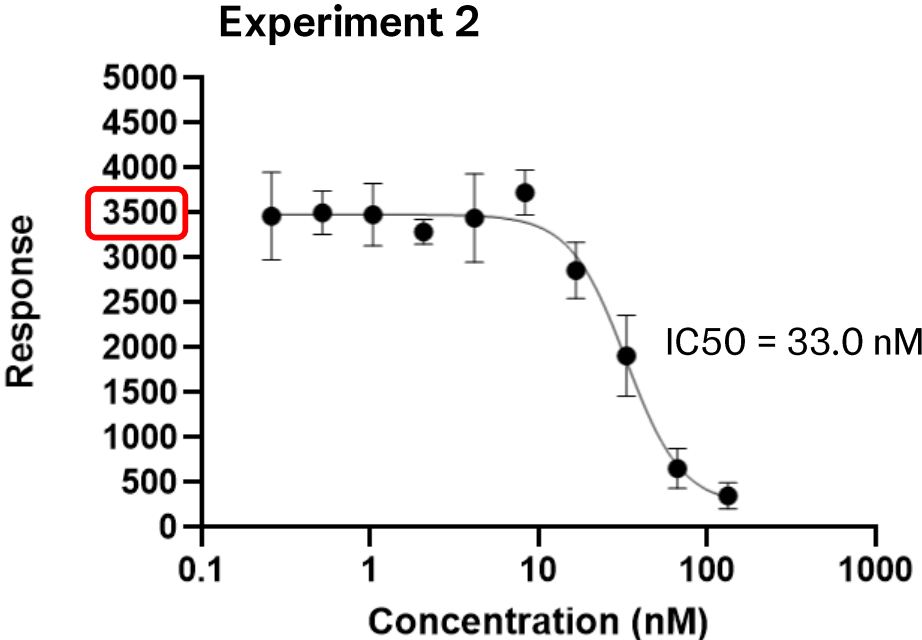
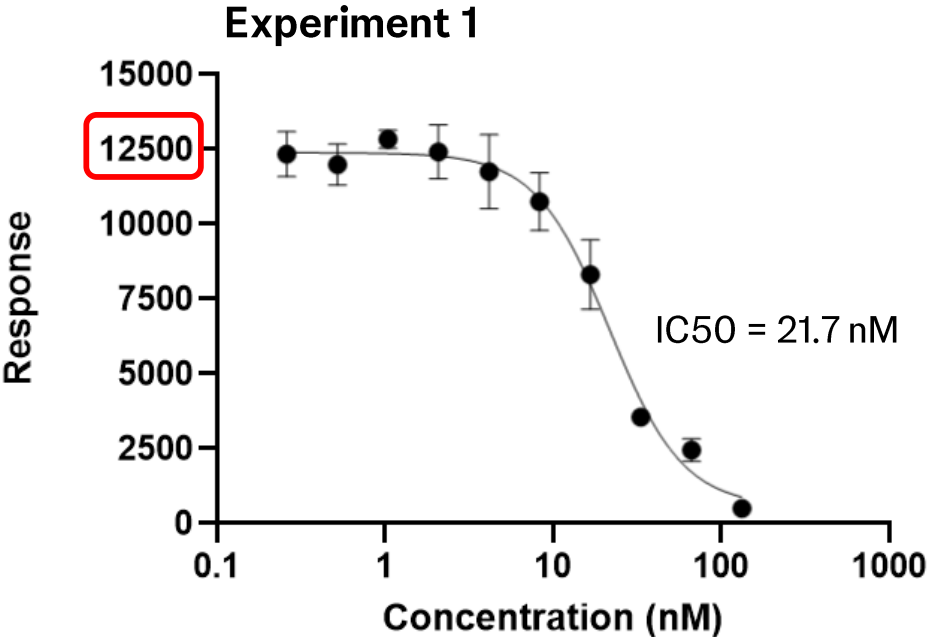
Example 1: Inhibition Data (Species 1) for Compound A

- Perform fixed-effect meta-analysis with Hedges' estimator and t-test confidence intervals by recommendation of Jiang et al. *
- Confidence intervals 'inflated' with t-test for small number of experiments due to low degrees of freedom



Motivation – A Practical Example

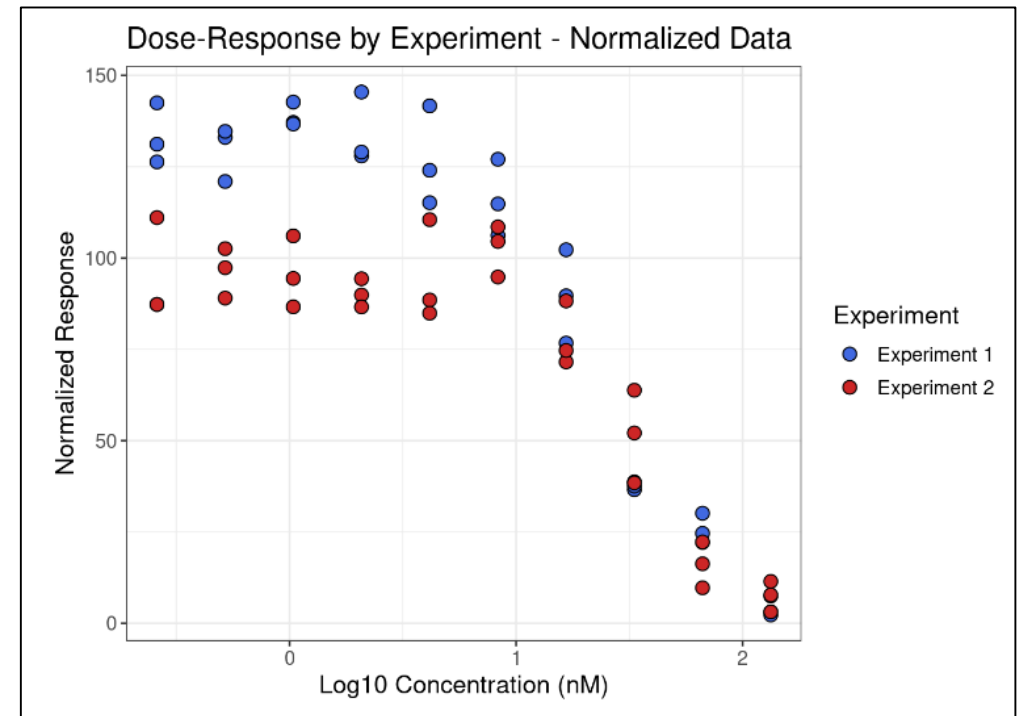
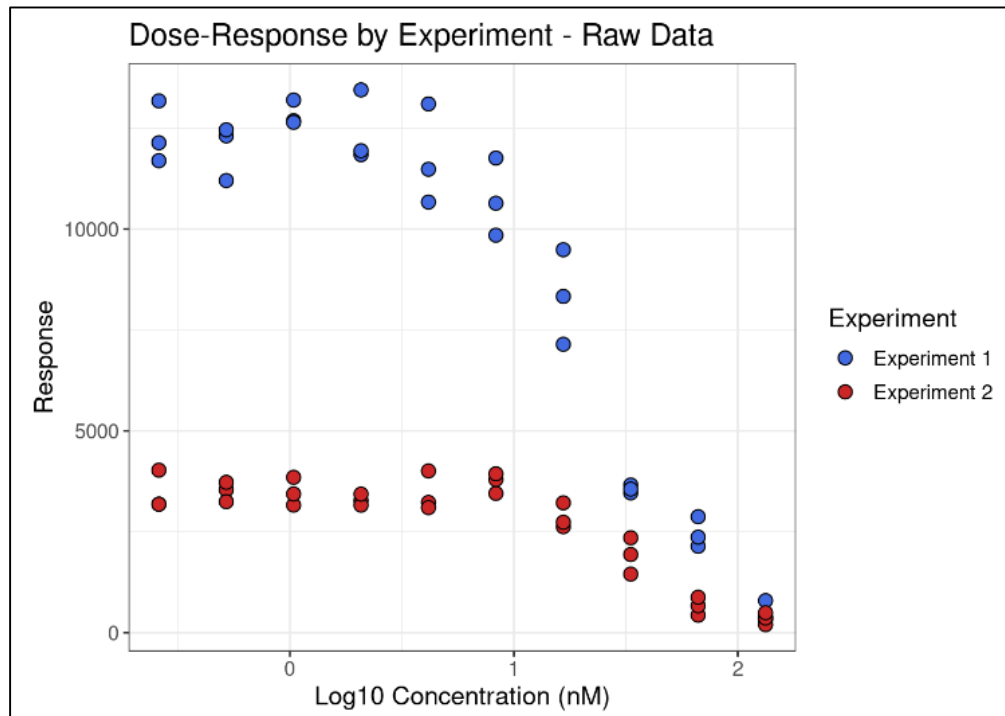
Example 2: Inhibition Data (Species 2) for Compound A – Different Scales



Motivation – A Practical Example

Example 2: Inhibition Data (Species 2) for Compound A – Different Scales

- Non-linear mixed effect (NLME) model recommended for $N = 2^*$
- When data is on very different scales, transformation may be required



Goals

- Find a method that is statistically accurate and simple
- Determine whether complex approaches (NLME) yield results similar enough to simple approaches (meta-analysis) to use a simplified approach moving forward
- Create an automated solution for scientists to calculate average IC50s

Methods for Aggregating IC50s

Geometric Mean

Report geometric mean across experiments as average IC50

Advantages

- Easy to understand
- More accurately predicts average IC50 than an arithmetic mean
- Can be calculated without help from statistician

Limitations

- Does not account for the variance associated with the estimated IC50s

Meta-analysis

Average IC50 calculated by weighting individual Log IC50 estimates by standard error

Advantages

- Easy to understand
- Fixed or random effects
- Can be implemented via Excel or Shiny Application
- Can use estimates from GraphPad Prism as input

Limitations

- Not recommended for less than three experiments*
- Common in Discovery due to cost
- Confidence intervals could be 'inflated' with small number of experiments
- Could lose information by weighting curves with high standard error to zero

Non-Linear Mixed Effect (NLME) Model

Model data for all experiments/donors together to calculate an aggregate IC50

Advantages

- Recommended method for calculating average IC50
- Works well when averaging small number of experiments

Limitations

- Convergence issues
- Results are misleading if curves do not have similar min and max parameters
 - May require transformation of data
- More complex – may require assistance of statistician

Examples Through Simulation - Methods

Methods for Comparison

1. NLME Models

- Performed on raw data and normalized data
- Explored with random effects on all parameters and random effect only on IC50

2. Meta-analysis

- Performed on individual experiment Log IC50 estimates, normalization not needed
- Explore random effects and fixed effects
 - DL Estimator (random effects)
 - Hedges' Estimator (fixed effects)
- Both methods explored with z-test and t-test confidence intervals

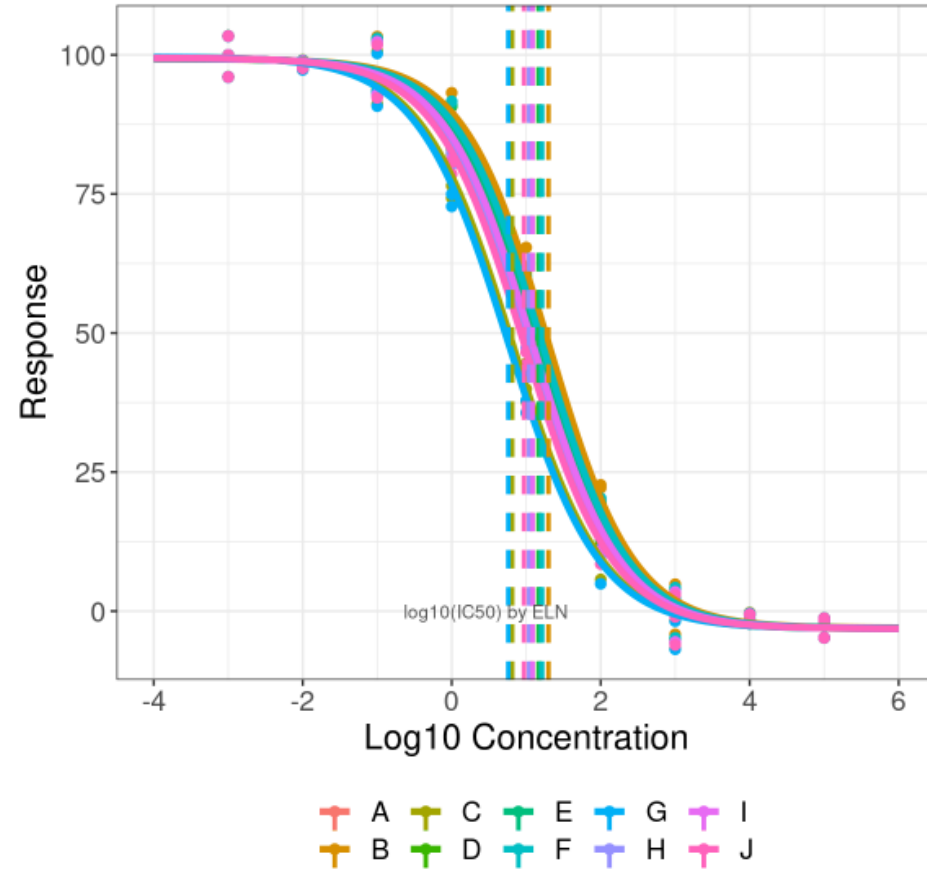
Simulation Process

- Simulate 10 dose-response curves to replicate experiments
- Compare average IC50s & confidence intervals across methods when averaging 2 experiments and 10 experiments under two scenarios:
 - Stable case (e.g., cell lines)
 - Very similar dose-response curves between experiments
 - Curves with more variation and on different scales (e.g., animal data)
 - Different top parameters

Examples Through Simulation – Low Variation

Simulation Setup – Low Variation Between Curves

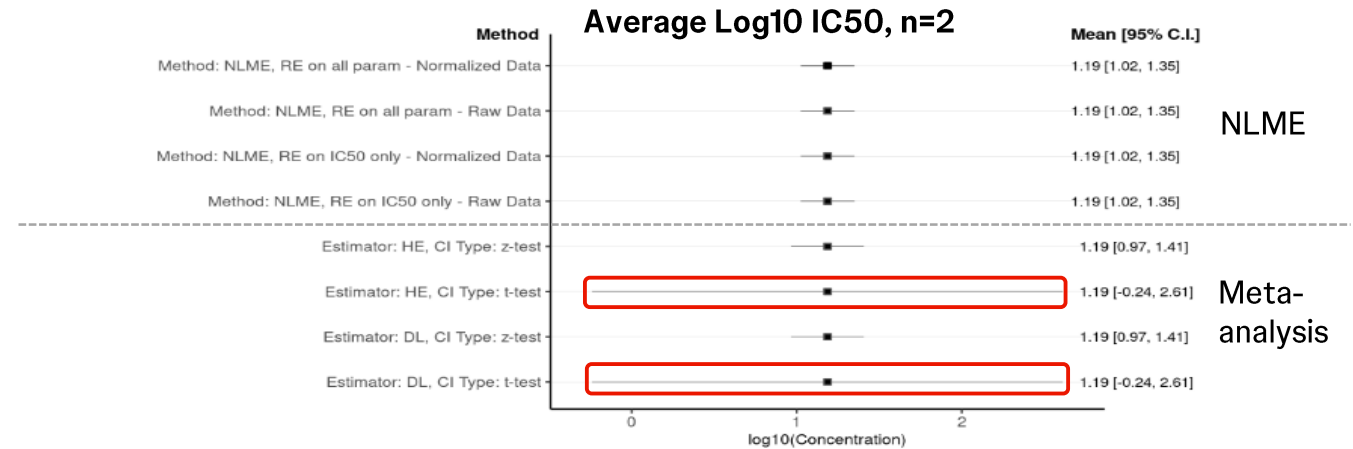
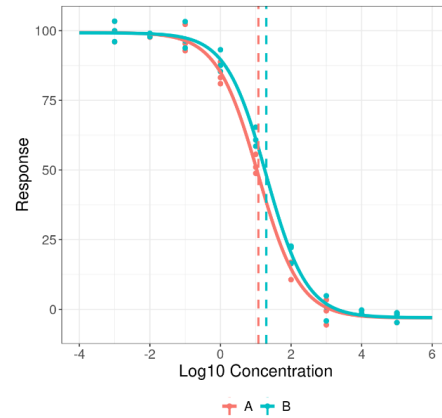
- Simulated dose-response curves for 10 experiments
- Low within-experiment variation for all experiments
- Little variation between IC50 estimates
- Nearly identical top and bottom parameters



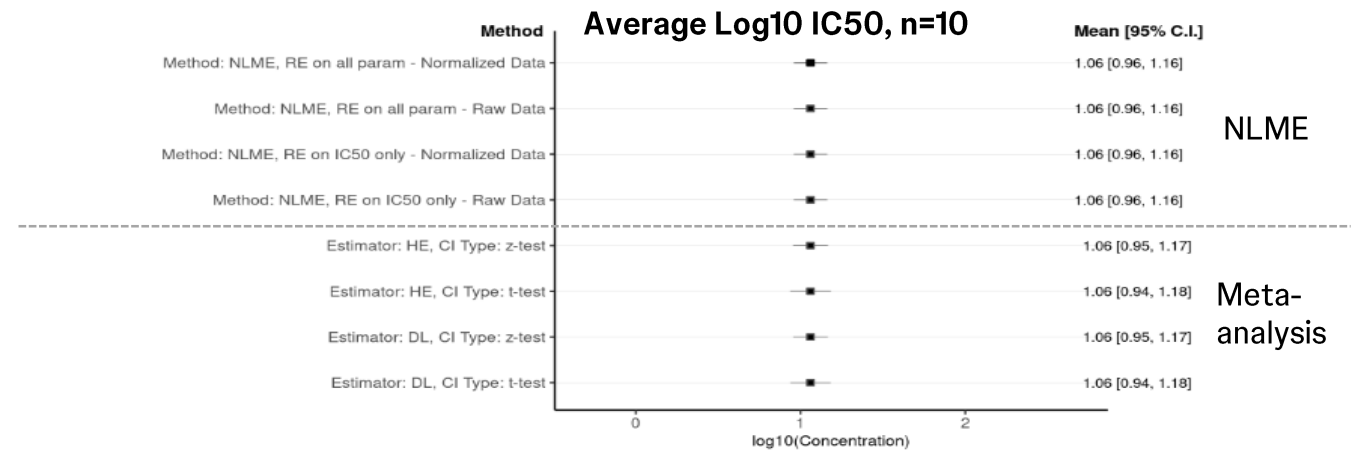
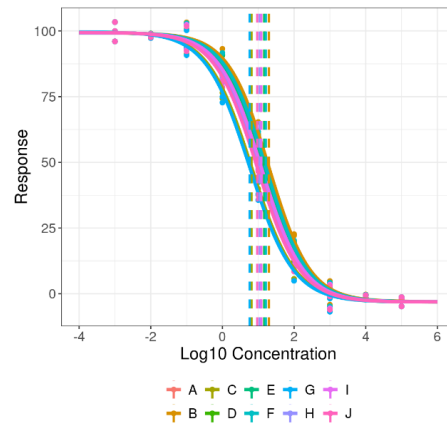
Simulation Results – Low Variation Between Curves

- Average IC50s nearly identical across methods for n=2 and n=10 experiments
- CIs similar for all methods except meta-analysis with t-test CIs for n=2

N=2 Experiments



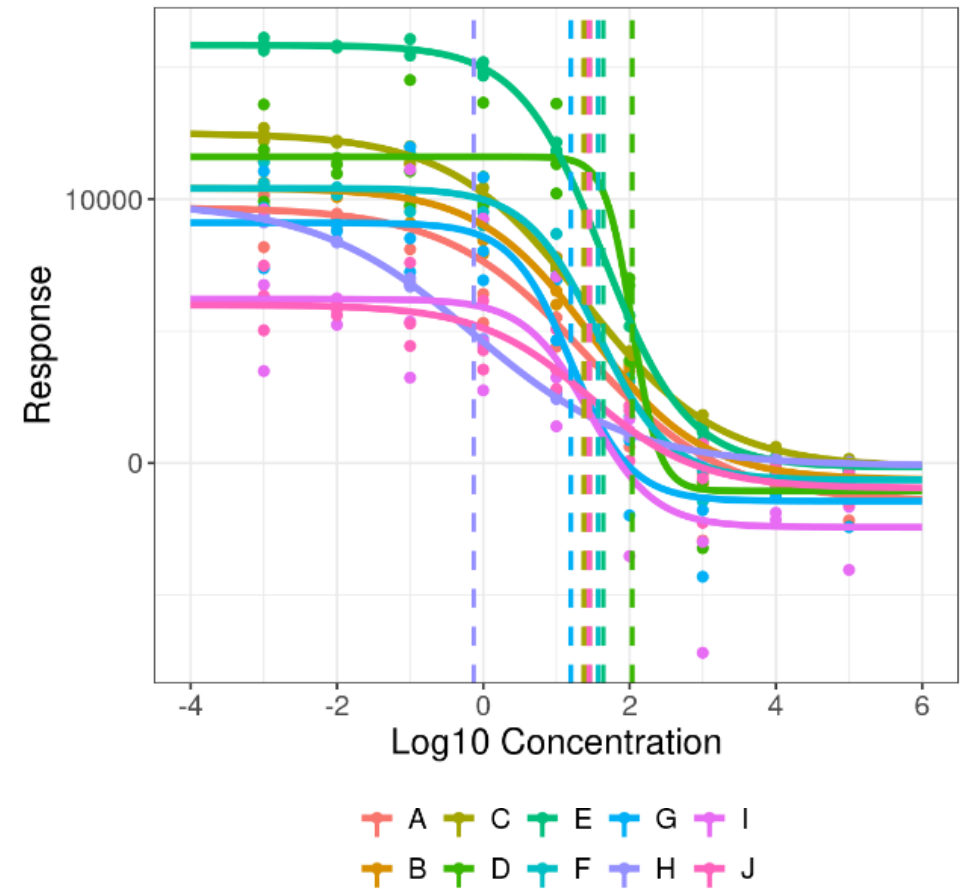
N=10 Experiments



Examples Through Simulation – Different Scales

Simulation Setup – Curves on Different Scales

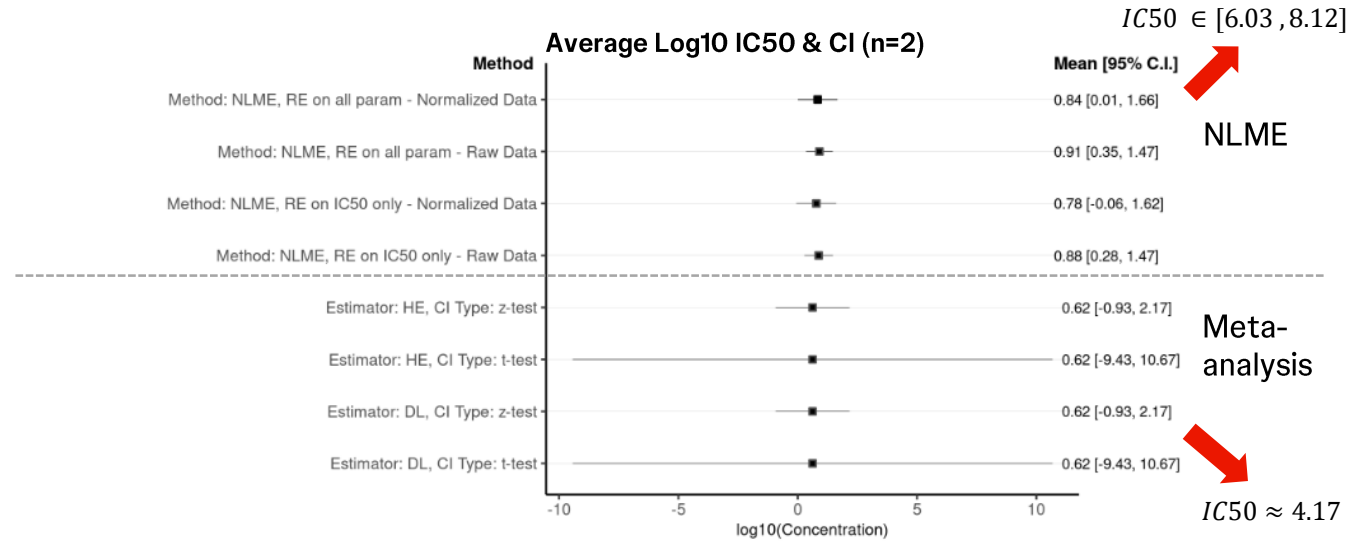
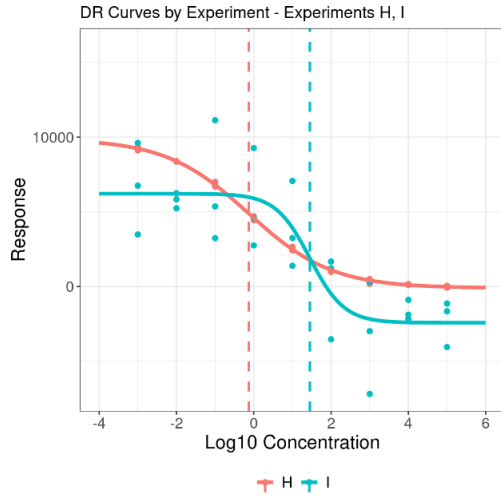
- Simulated dose-response curves for 10 experiments
- Higher variation between top parameters of curves
- Different within-experiment variation



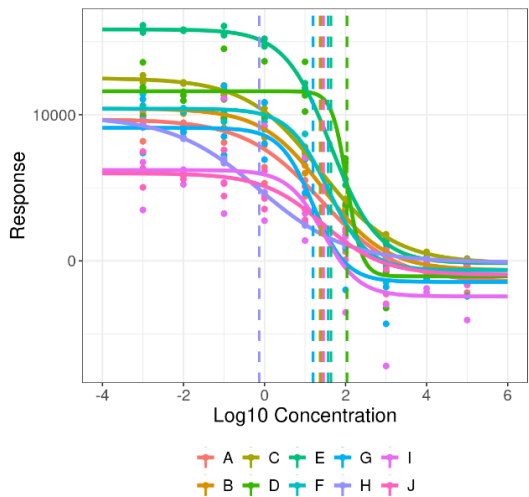
Simulation Results – Curves on Different Scales

- NLME on raw data w/o random effect on all parameters can produce very different average IC50 than other methods

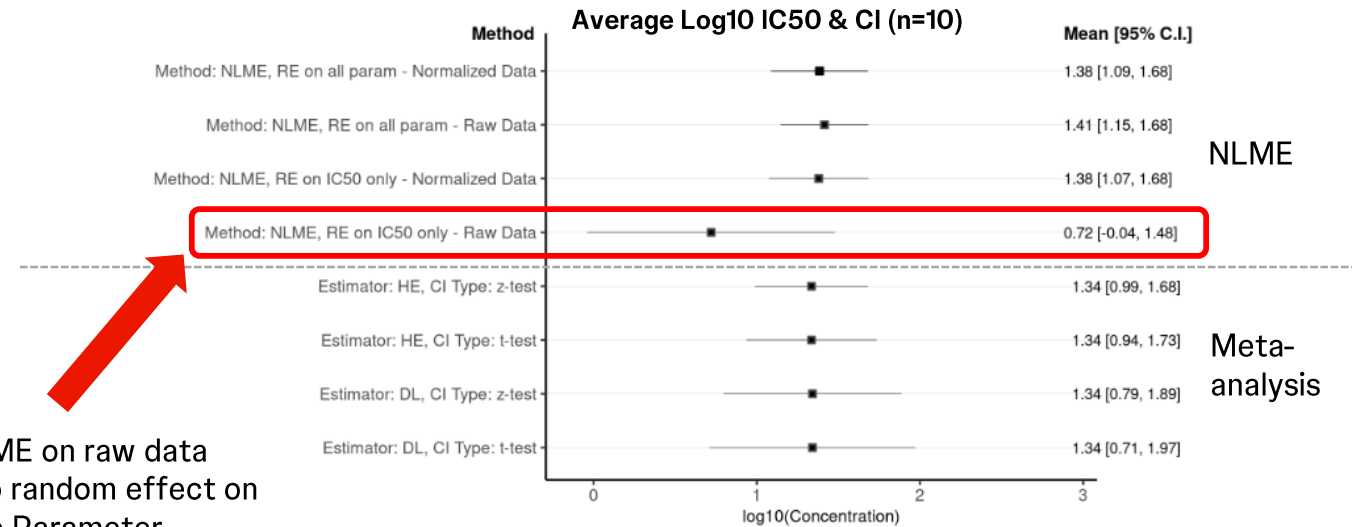
N=2 Experiments



N=10 Experiments



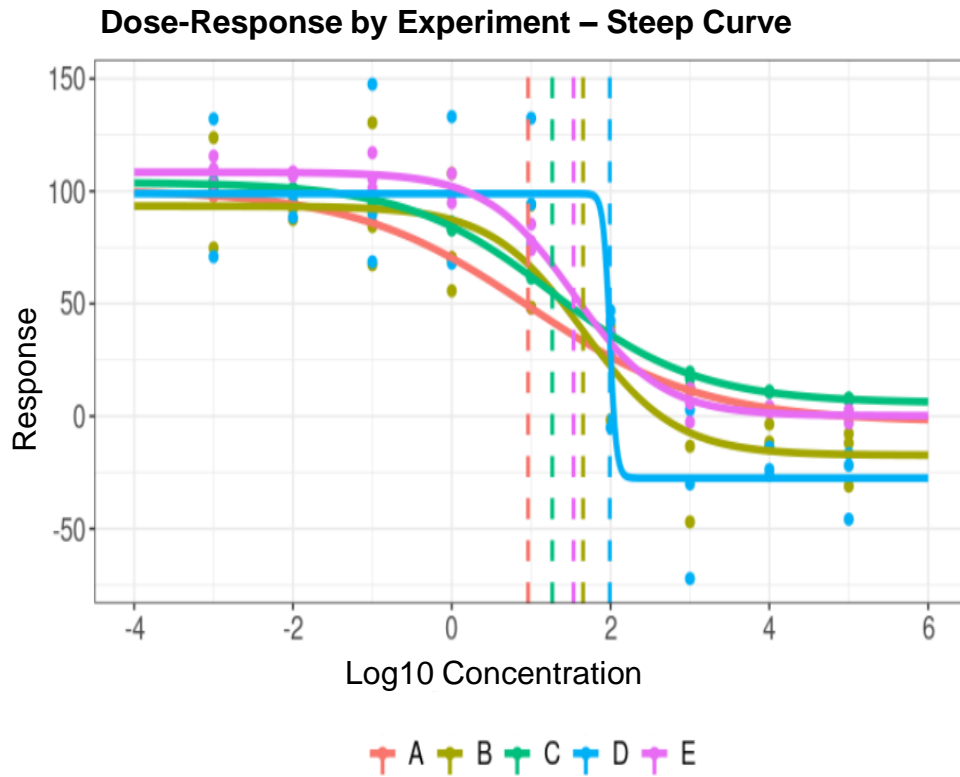
NLME on raw data w/o random effect on Top Parameter



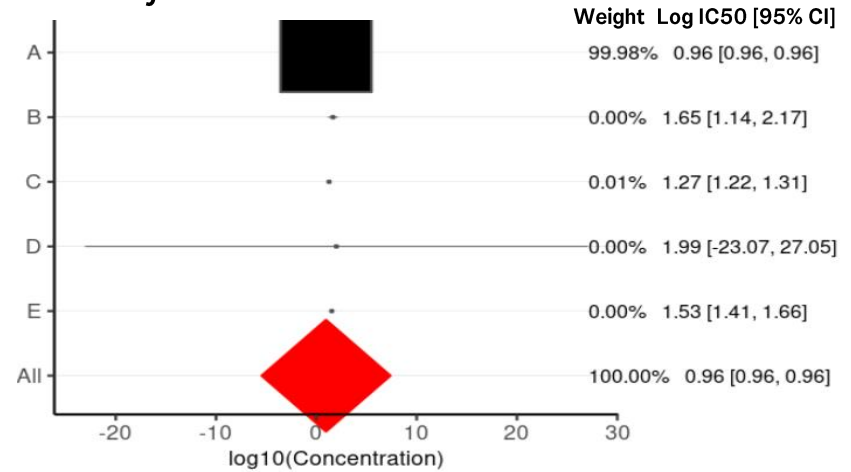
Examples Through Simulation – Steep Curves

Simulation Setup – Steep Curves

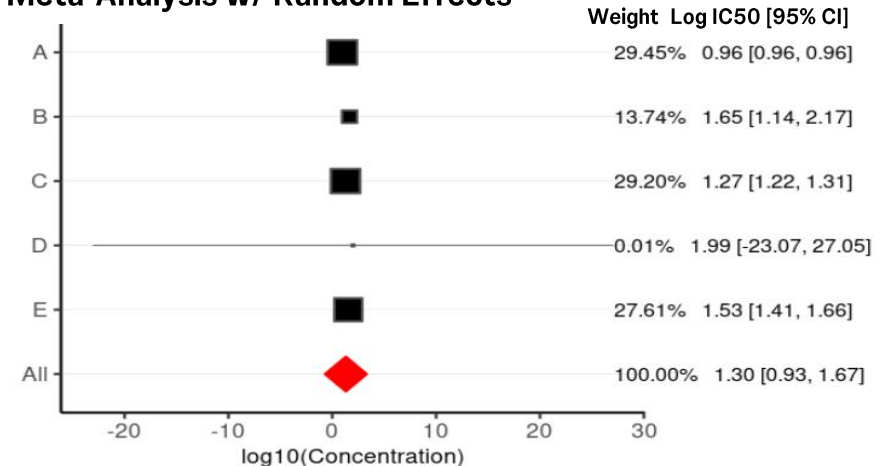
- Steep curves wreck the weighting scheme in meta-analysis with fixed-effects
- Meta-analysis will remove experiments with steep curves, resulting in loss of information
- If many steep curves present, convergence issues may occur with NLME



Meta-Analysis w/ Fixed Effects



Meta-Analysis w/ Random Effects



Summary

Summary

- There is no 'one size fits all' approach
 - Discovery often has limited sample size and variable data
- Most of the methods produce similar average IC50 estimates
 - Except NLME on raw data without random effects on all parameters when curves are on different scales
 - Except for steep curves
- Meta-analysis with random effects is a reasonable approach under most circumstances

An Automated Solution

An Automated Solution

- Ultimately, we want an option to aggregate IC50s that is easy to understand and more statistically accurate
- Scientists may want to explore data on their own to get an approximate average IC50 across their experiments
- Creating application that will calculate IC50s by donor and average across donors using meta-analysis with random effects and z-test confidence intervals

Application Demo – Upload Data

- Upload csv file for each experiment

DISCOVERY IMMUNOLOGY Average IC50 Generation - UNDER CONSTRUCTION (v2)

Steps:

1. Convert Prism table for one experiment/donor to a csv file. Concentration should be in the left-hand column and should not be transformed. Zero concentrations should be excluded for this version of the application.
2. Upload one csv file for every experiment/donor that you would like to average. There should be one column per replicate.
3. Check data has been imported correctly and review results.

Authors: Kristen Kohler & Jocelyn Sendeck
Please email kkohler2@its.jnj.com or jsendeck@its.jnj.com for support.

How do you want to handle zero concentrations?
Set Zero to 2 Log fold change difference from smallest concentration

Upload... No file selected

Transformed Data

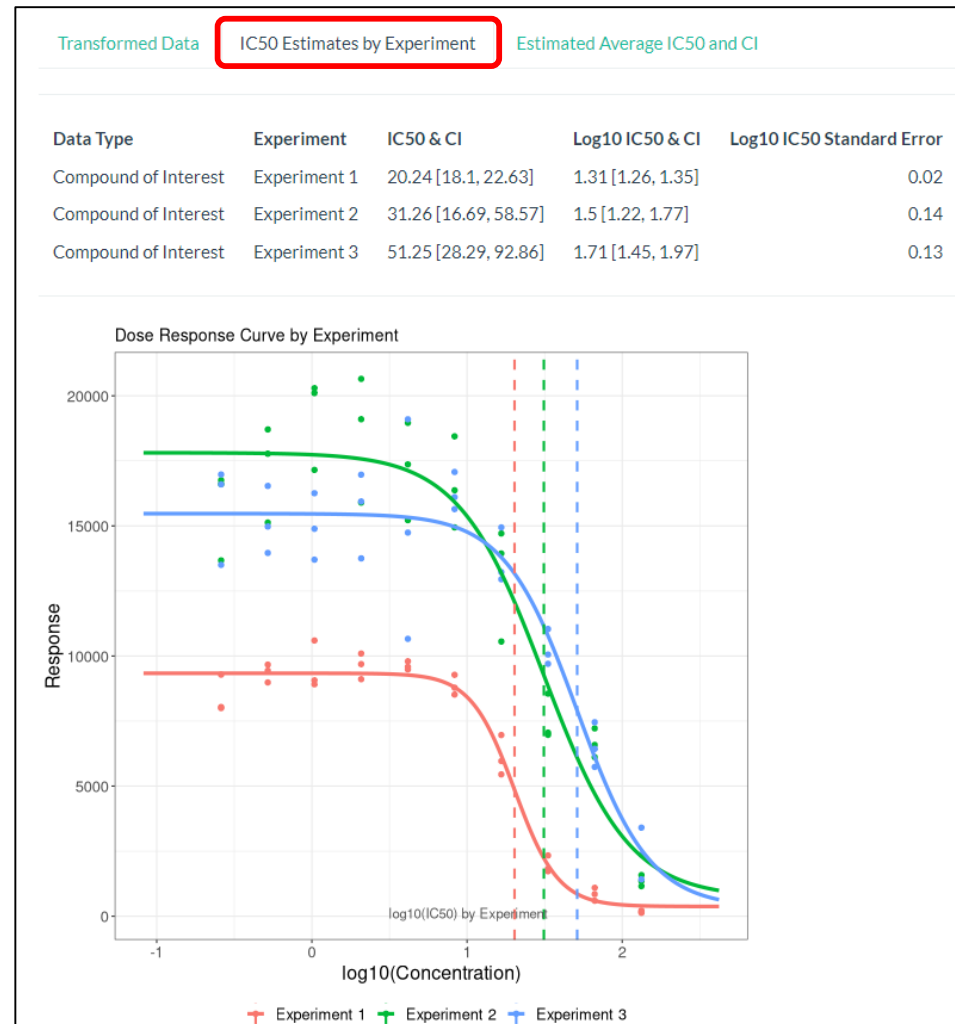
Choose all experiments

Average IC50 Application Files

Name	Status	Date modified
Experiment 1.csv	🔄	1/18/2024 5:44 PM
Experiment 2.csv	🔄	1/25/2024 12:47 PM
Experiment 3.csv	🔄	1/18/2024 5:45 PM
IC50 Data Experiment 1.pzfx	✅	1/19/2024 7:54 AM
IC50 Data Experiment 2.pzfx	✅	1/19/2024 7:54 AM
IC50 Data Experiment 3.pzfx	✅	1/19/2024 7:54 AM

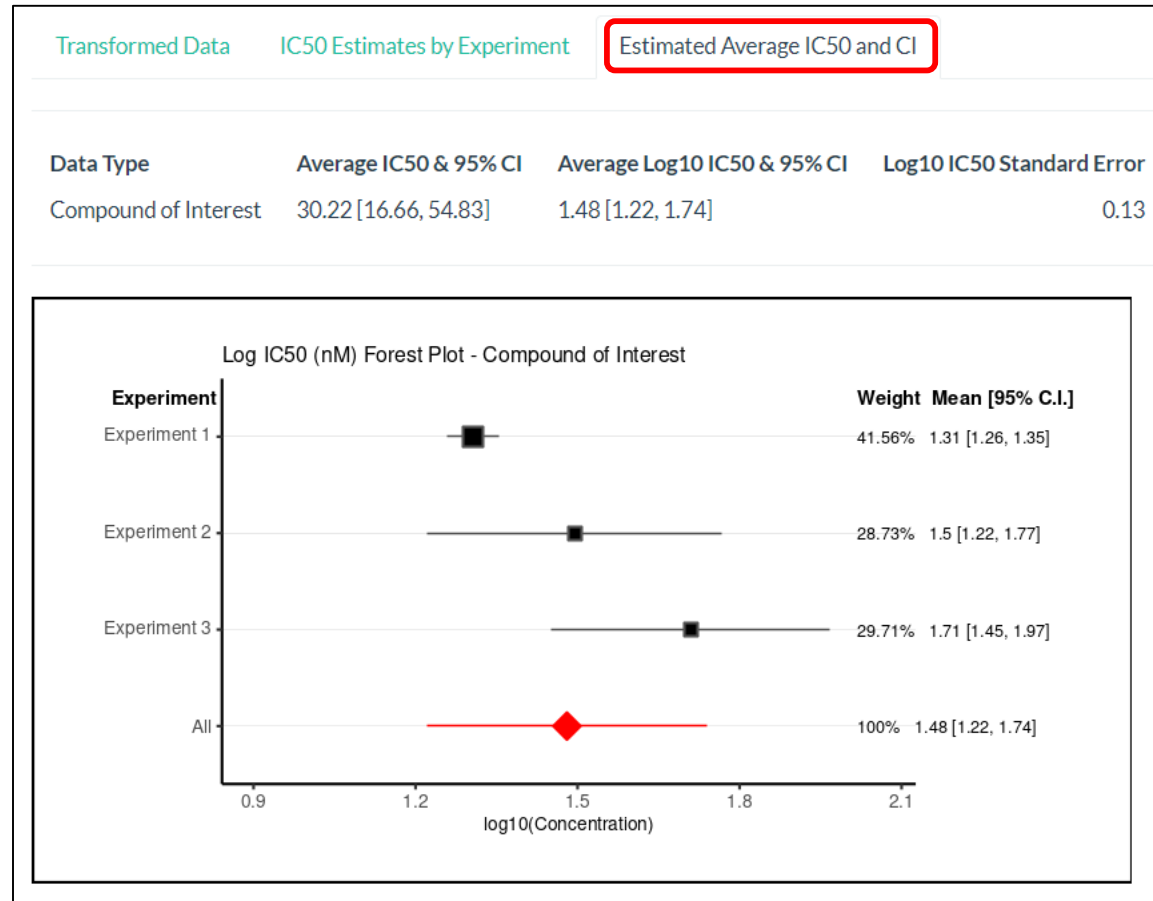
Application Demo – View IC50 by Experiment

- View IC50s and dose-response curves by experiment/donor



Application Demo – View Average IC50 & Forest Plot

- View weighted average IC50 calculated via meta-analysis and forest plot with results by experiment & overall



Future Application Add-ons

- Ability to compare IC50s of different treatments/compounds
- Ability to apply acceptance criteria
- Downloadable pdf report that could be uploaded to Electronic Lab Notebook (ELN)

Conclusion & Next Steps

Conclusion

- There is no 'one size fits all' approach
 - Discovery often has limited sample size and variable data
- Meta-analysis with random effects is a reasonable approach under most circumstances
 - Except for steep curves
- Shiny application can be used to help scientists get a more statistically accurate average IC50 estimate quickly

Next Steps

- Continue to explore methods and additional scenarios
 - Working group established in J&J Discovery Statistics to compare methods for special cases such as steep curves & non-responders
- Continue collaborating with scientists to build out application and deploy internally for use

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- Indra Sarabia
- Astrid Clarke
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Thank you

If you have any questions, please contact:

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References

- *‘Summarizing EC50 Estimates from multiple dose-response experiments: A comparison of a meta-analysis strategy to a mixed-effects model approach’*, Jiang X. , Kopp-Schneider A.

Back-Up Slides

Code Snippets – Curve Simulation Example

```
experiment_num = 10

var.vec <- c(1500, 700, 200, 1500, 200, 700, 1500, 100, 2500, 1000)
data_sim_diff_var = NULL

for (k in 1:experiment_num){

  set.seed(k*100)

  x_vec = -3:5
  A_sim1 = 15 + rnorm(1,0,5)
  B_sim1 = 10000 + rnorm(1,0,3000)
  lic50_sim1 = 1 + rnorm(1,0,.7)
  slope_sim1 = -.75 + rnorm(1,0,.4)

  rep_num = 3

  y_sim1 = NULL

  for (i in 1:rep_num){

    set.seed(experiment_num*i)

    var.tmp <- var.vec[k]

    y_sim1 =
      c(y_sim1,
        A_sim1 + (B_sim1-A_sim1)/(1+10^(slope_sim1*(lic50_sim1 - x_vec))) +
          rnorm(length(x_vec),
              0,
              var.tmp))

  }

}
```

Code Snippets – NLME Example

```
#set convergence criteria
control = nlmeControl(maxIter = 100,    msMaxIter = 1000,    tolerance = 0.1,    abs.tol = 1e-20)
```

```
eval(parse(text=paste0("analysis.data <- data.modeling %>% filter(Experiment.num <= ", i+1 , ")") )))

TOLVAL = 0.0001
YVAR = "Response"
XVAR = "Log10.Concentration"

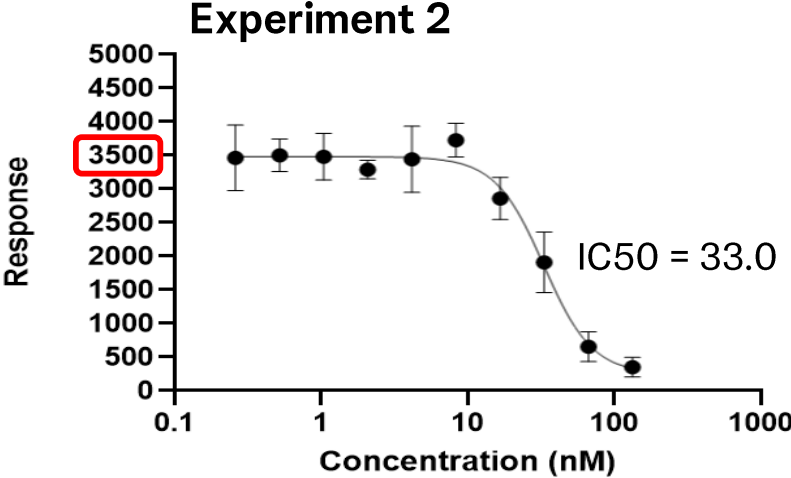
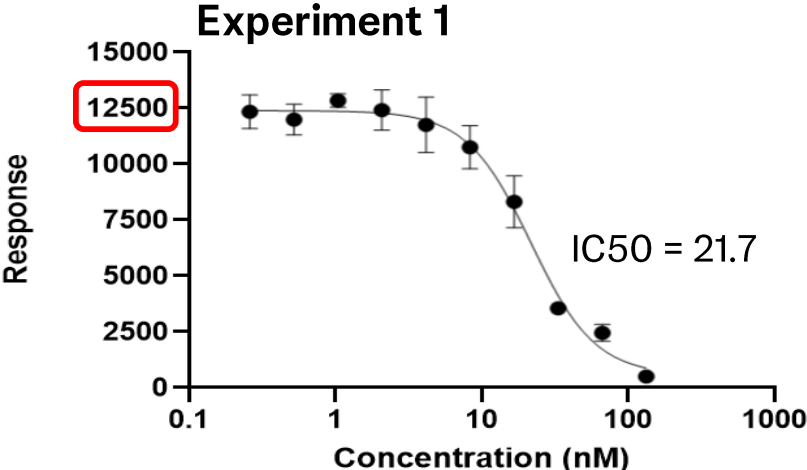
currentFormula <- as.formula(paste(YVAR,"~ SSfpl(",XVAR,",", A, B, xmid, scal)"))

forAnalysis <- analysis.data

currentNls <- try(nls(currentFormula, data = forAnalysis),silent=TRUE) # this gets your nlme starting values
startVals <- coef(currentNls)
currentModel <- try(nlme(currentFormula,
                        data = forAnalysis,
                        groups = ~Experiment,
                        fixed = A + B + xmid + scal ~ 1,
                        control = control,
                        random = pdDiag(xmid ~ 1),
                        # random = pdDiag(A + B + xmid + scal ~ 1),
                        start = list(fixed = startVals)),
                    silent = TRUE)
```

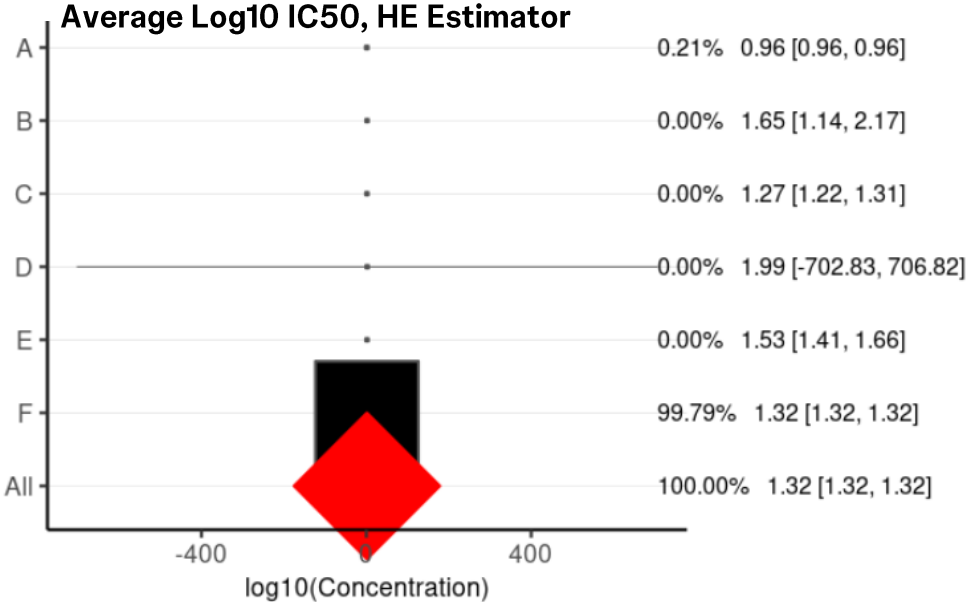
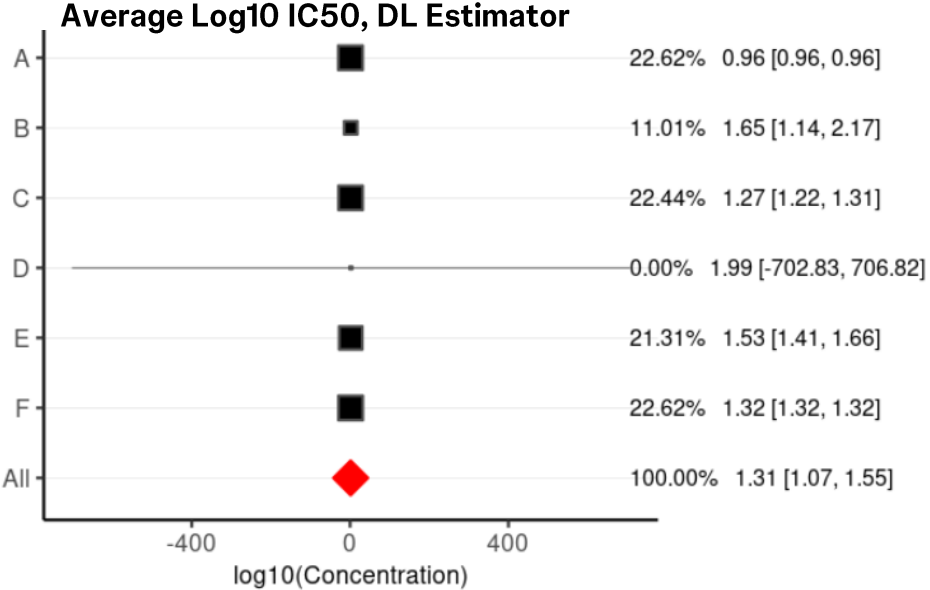
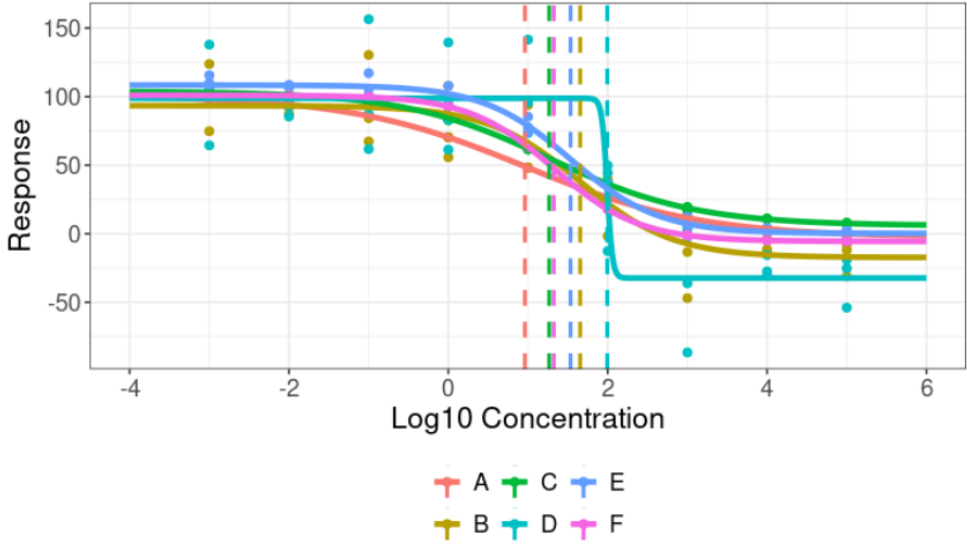
Practical Example with Method Comparison

Example 2: Inhibition Data for Compound A (Species 2) – Different Scales



Method	Avg Log IC50 & CI
Meta-analysis w/ random effect (RE) & t-test CI	1.42 [.26, 2.59]
Meta-analysis w/ random effect (RE) & z-test CI	1.42 [1.24, 1.60]
Meta-analysis w/ fixed effects & t-test CI	1.42 [0.26, 2.59]
Meta-analysis w/ fixed effects & z-test CI	1.42 [1.25, 1.60]
NLME on raw data, RE on IC50 only	0.19 [-1.32, 1.71]
NLME on raw , data RE on all parameters	1.35 [1.30, 1.34]
NLME on normalized data, RE on IC50 only	1.42 [1.31, 1.53]
NLME on normalized data, RE on all parameters	1.42 [1.29, 1.55]

Curves with Convergence Issues



Method	Avg Log IC50 & CI
Meta-analysis w/ random effect (RE)	1.31 [1.07, 1.55]
Meta-analysis w/ fixed effects	1.32 [1.32, 1.32]
NLME on raw data, RE on IC50 only	1.56 [1.35, 1.77]
NLME on raw, data RE on all parameters	Does Not Converge
NLME on normalized data, RE on IC50 only	1.48 [1.27, 1.70]
NLME on normalized data, RE on all parameters	1.52 [1.29, 1.74]

Meta-analysis Equations

Weighted Average

$$\hat{\mu} = \frac{\sum_{i=1}^k \hat{w}_i \phi_i^{(e)}}{\sum_{i=1}^k \hat{w}_i}$$

Weights

$$w_i = 1/(\tau^2 + \sigma_i^2)$$

Estimators

$$\hat{\tau}_{HE}^2 = \max \left\{ 0, \frac{1}{k-1} \sum_{i=1}^k \left(\phi_i^{(e)} - \frac{1}{k} \sum_{i=1}^k \phi_i^{(e)} \right)^2 - \frac{1}{k} \sum_{i=1}^k \hat{\sigma}_i^2 \right\}$$

Hedges' Estimator (fixed effects)

$$\hat{\tau}_{DL}^2 = \max \left\{ 0, \frac{\sum_{i=1}^k m_i (\phi_i^{(e)} - \overline{\phi^{(e)}}_m)^2 - (k-1)}{\sum_{i=1}^k m_i - \frac{\sum_{i=1}^k m_i^2}{\sum_{i=1}^k m_i}} \right\}$$

DerSimonian-Laird (DL) Estimator (random effects)