

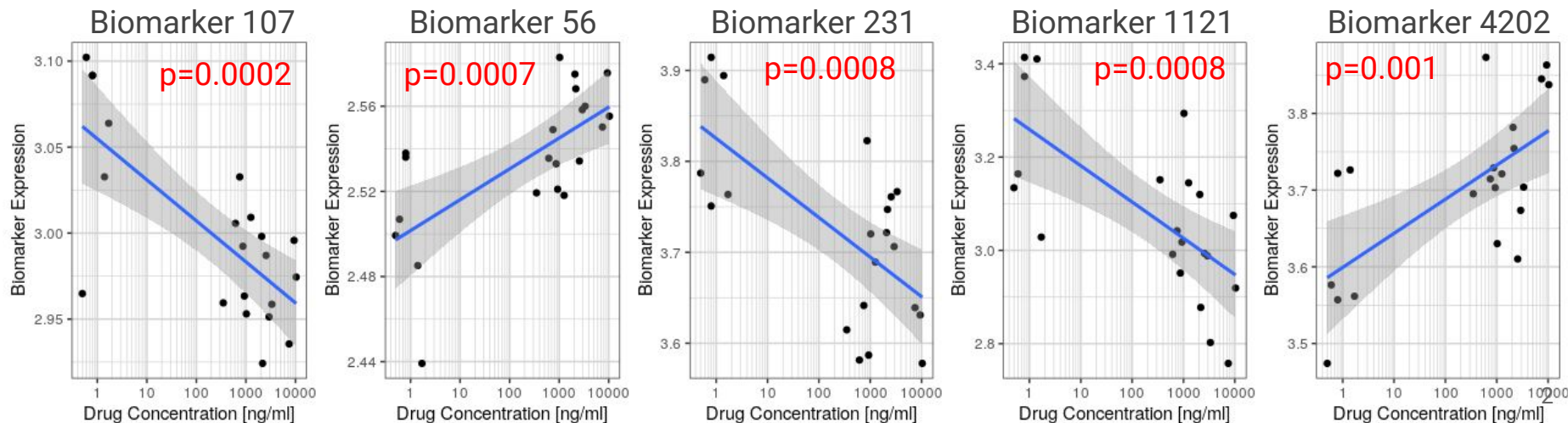
The “See” – Value App: Visual Decision Making for Drug Development

H. Diehl¹, A. M. Stein², N. Roy Chowdhury², T. Broderick¹

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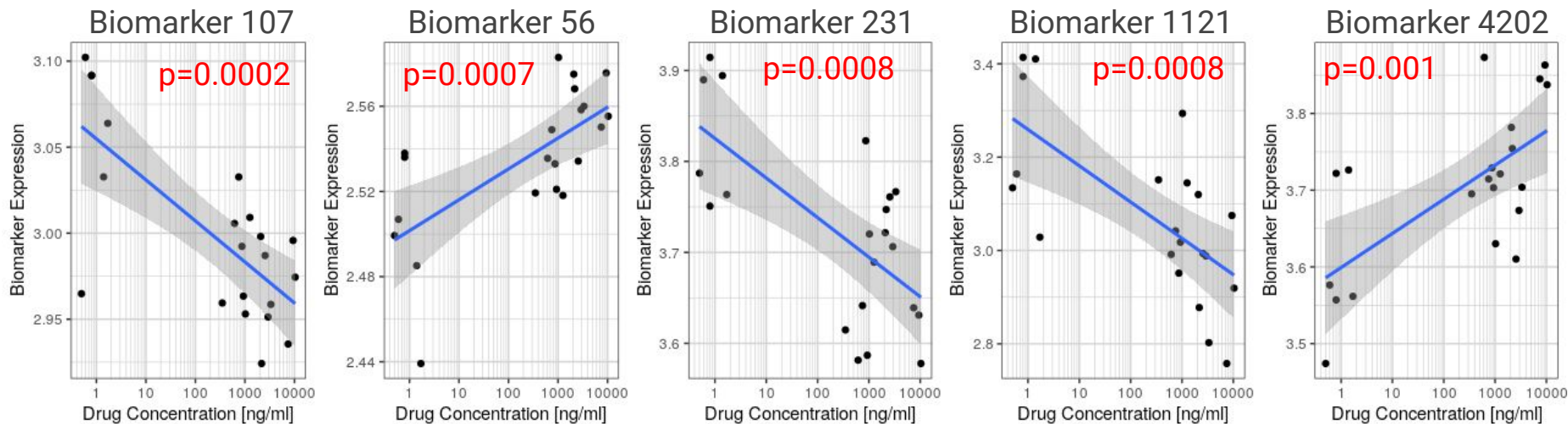
Scenario: Biomarker Exploration

Looking for “proof of action” you look at how over 5000 biomarkers respond to a drug at different concentrations. You pick the top 5 biomarkers with the strongest response, and think it looks pretty good:



Scenario: Biomarker Exploration

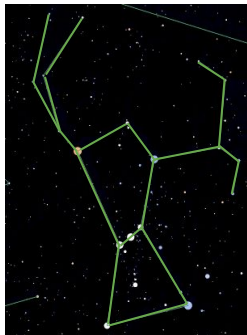
Further exploration would reveal no real effect - in fact this is synthetic data with exposure and concentration independently generated.



What went wrong?

Problem

Signals seen in exploratory data analysis inform trial design.



But humans are great at seeing signals even when they aren't there.

Solution

A visual check for significance that is...

- **Fast, easy, and intuitive**
- **Convincing even when users are incentivized to see a signal**



Contribution: “See”–Value App

www.see-value.org

We provide a Shiny app that..

- Facilitates visual permutation tests as described by Buja, Majumder, Roy Chowdhury and others.
- Supports common inference tasks used in drug development.
- Enables team-based voting and significance calculations.

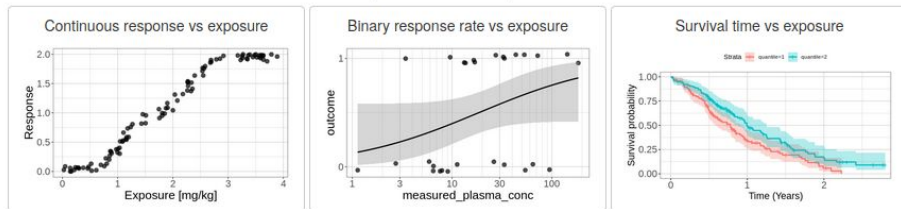
VizInf Menu Analyze Walkthrough Calculate

'See'-Value App: Facilitating Visual Inference in Pharmacology

This tool is intended to help you intuitively evaluate the presence of trends in your data. Rather than relying on standard measures of statistical significance, this tool is meant to help you gain visual intuition for the information contained in the data by asking the user whether they can pick the true data out of a **lineup** plot.

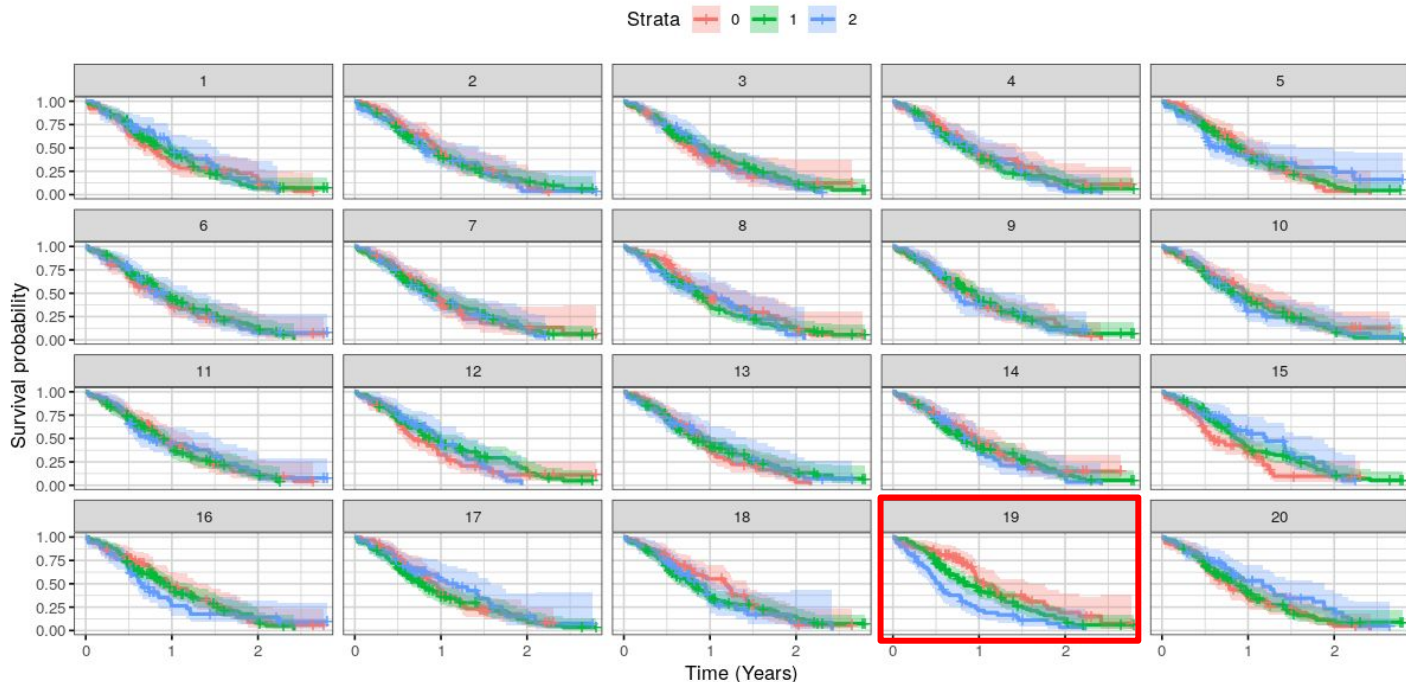
Start by uploading an analysis shared with you or selecting your analysis type below. You will be able to create a lineup plot from your own uploaded data or view lineups from preloaded example data.

Exposure-Response



A Lineup Protocol

Protocol described by Buja et al (2009), Majumder et al (2015), Roy Chowdhury, et al (2015), and others.



Which plot looks most different from the others?

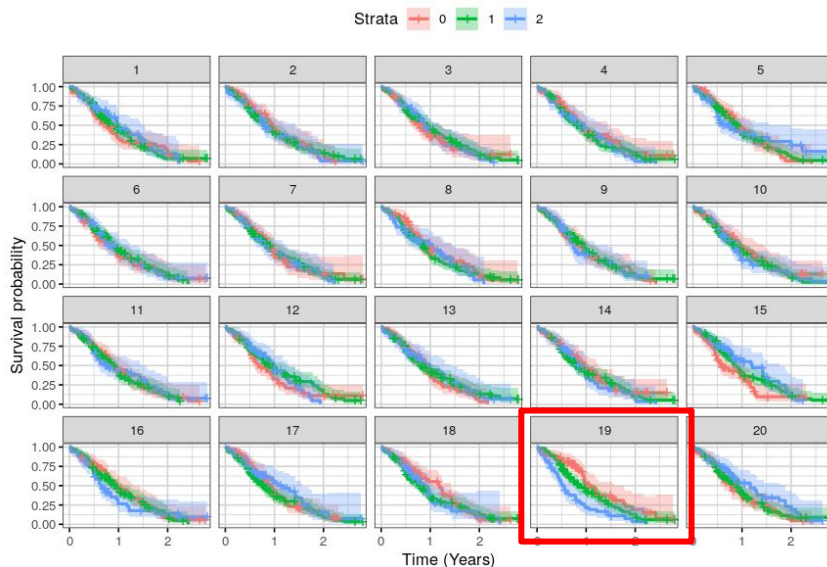
A Lineup Protocol

Hypothesis:

Strata influences survival

Permutation:

If strata has no influence, then scrambling the label won't change plot appearance.

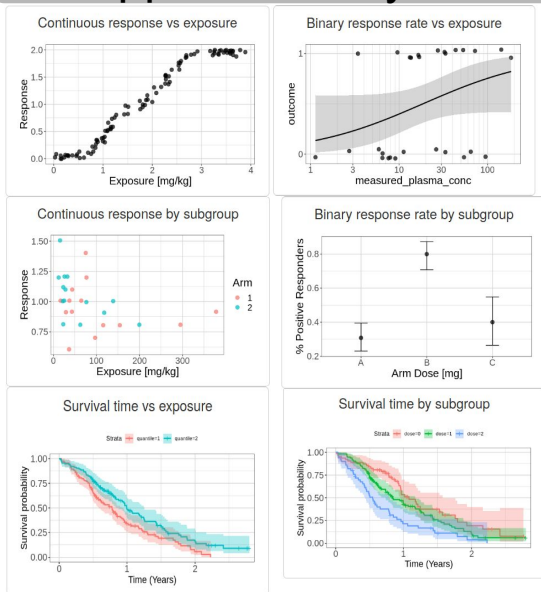


Lineup Test:

1. Plot the real data along with the scrambled data.
2. Pick the “most unusual” plot.
3. If it is your real data, it may be significant.

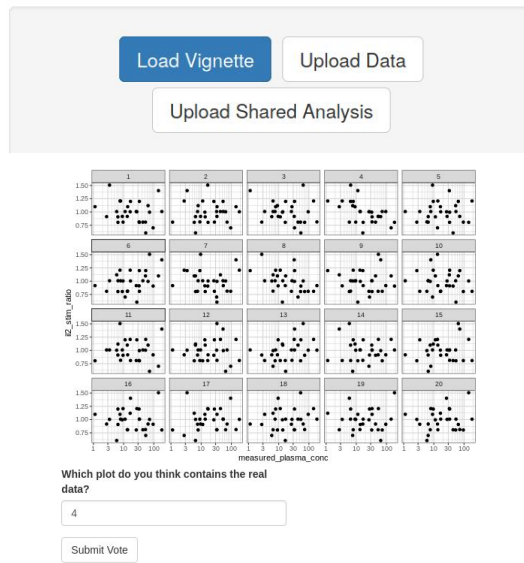
App workflow: Team Based Voting

Step 1: Select a supported analysis.



With options growing

Step 2: Explore pre-loaded vignette



Learn and practice with lineups

Step 3: Upload and configure your data

Load Vignette

Upload Data

Upload Shared Analysis

Upload Data

Browse... fake_continuous_exposure_binary_response.csv

Upload complete.

Exposure

measured_plasma_conc

Outcome

il2_stim_ratio

Plot Settings

☒ Log X

☒ Log Y

☒ Logistic Overlay

Generate Lineup

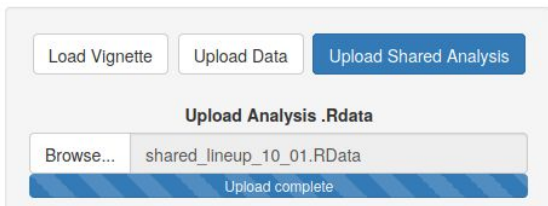
Save your analysis setup to share with team members (file includes your uploaded data).

Download Analysis Setup

Download sharable configuration

App workflow: Team Based Voting

Step 4: Teammates vote and report



...

Which plot do you think contains the real data?

You selected plot 1, but the true data was in plot 14.

Analysis leader tallies
correct/incorrect votes

Step 5: 'See'-Value calculated in-app

Total Participants Performing Lineup Test

of Participants Correctly Identifying Data

'See'-Value: $2e-11$

Interpretation similar to
traditional p-value

Conclusion

Avoid tricking yourself into thinking you have significant results!

Try out the app at:
www.see-value.org

Feedback to:
hdiehl <at> mit.edu

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References

Buja, Cook, Hofmann, Lawrence, Lee, Swayne, and Wickham. 2009 [Statistical inference for exploratory data analysis and model diagnostics](#)

Majumder, Hofmann and Cook. 2013 [Validation of Visual Statistical Inference. Applied to Linear Models](#)

Roy Chowdhury, Cook, Hofmann, Majumder, Lee, and Toth. 2015 [Using visual statistical inference to better understand random class separations in high dimension, low sample size data](#)

DSAIRM by [Handel Group at UGA](#) for app template

[nullabor](#) package by Cook et al. for lineup generation