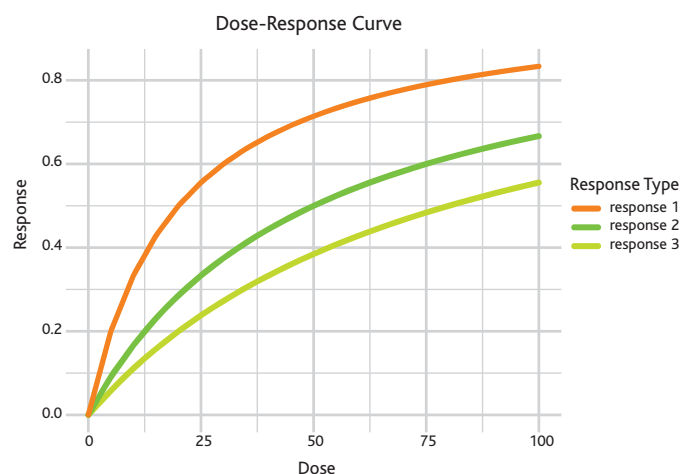# Rancho biosciences

# Using Bioinformatics and Computational Toxicology to Better Understand Toxicity Endpoints

Rancho Biosciences has skilled teams of data curators, data scientists, and bioinformaticians who together can not only provide highly curated and harmonized toxicology datasets, but can then use those datasets to identify critical signatures. Integrating clinical data, adverse events, toxicity measurements, and -omics data provides valuable insight into the mechanisms underlying toxicity endpoints.

Rancho bioinformaticians can identify biomarkers from a number of possible data types (including bulk RNAseq, single cell/nuclei RNAseq, variant calls, and protein expression) and correlate those data with clinical/tox endpoints. Identification of genes/pathways that show a dose-response trend with a particular drug's adverse effect can help elucidate the transcriptional response underlying the effect.

Furthermore, basic trend analysis can be applied in attempts to predict toxicity and adverse effects of new compounds without initially testing the compound itself. Rancho Biosciences has had a hand in massive undertakings of curating, harmonizing, and understanding toxicology related data (e.g. NCATS Inxight Drugs web portal). With such knowledge and resources at hand, a list of appropriate molecules for relevant predictive trend analysis can be identified when possible. Various potential models (linear, binary, logarithmic etc...), adapted to currently available data for similar compounds, can help better understand potential effects as well as identify potential treatment regimes. Rancho bioinformaticians, data curators and data scientists will work together with our clients to identify meaningful, actionable trends in data to accelerate research and gain novel insights.

Dose-Response Curve
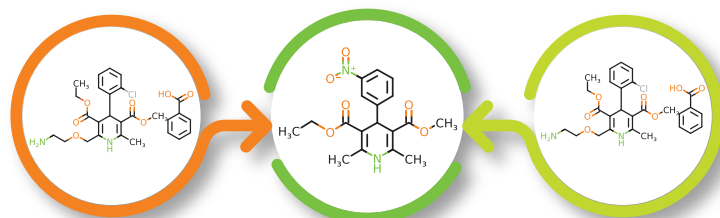
Use known tax endpoints of similar molecules to predict new ones