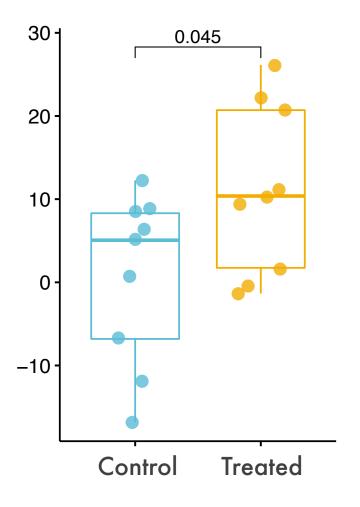
Effects of publication bias and hidden multiplicity on reproducibility in biomedical discovery research





What is a good sample size for replicating a study?



Published study:

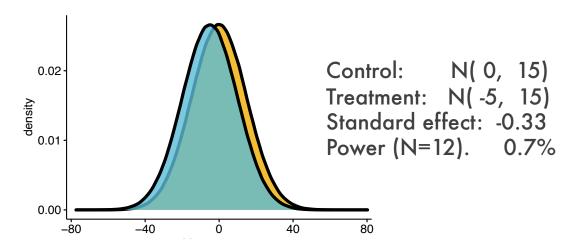
- Compare 9 treated and 9 control mice
- · Observed difference between means: 10 units
- Observed mean standard deviation: 10 units
- P-value: 0.049

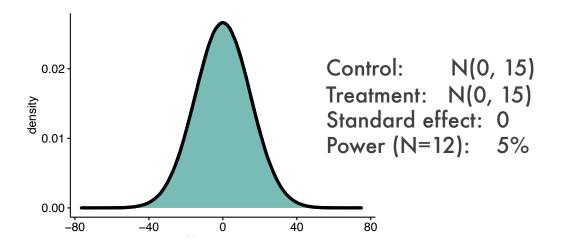
Problem:

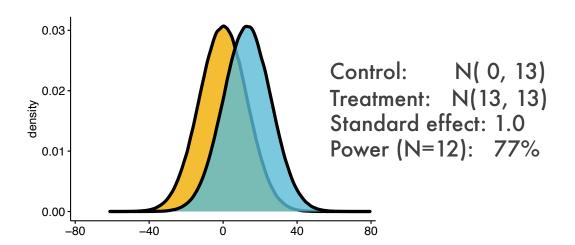
How many animals should we use to achieve 80% power to detect a potential positive difference as statistically significant?

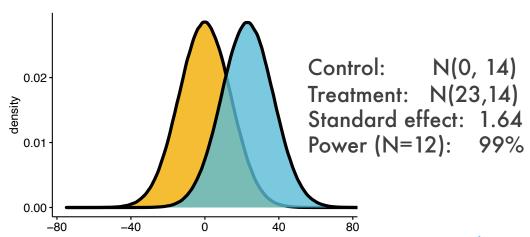


The observed results can arise from a variety of models



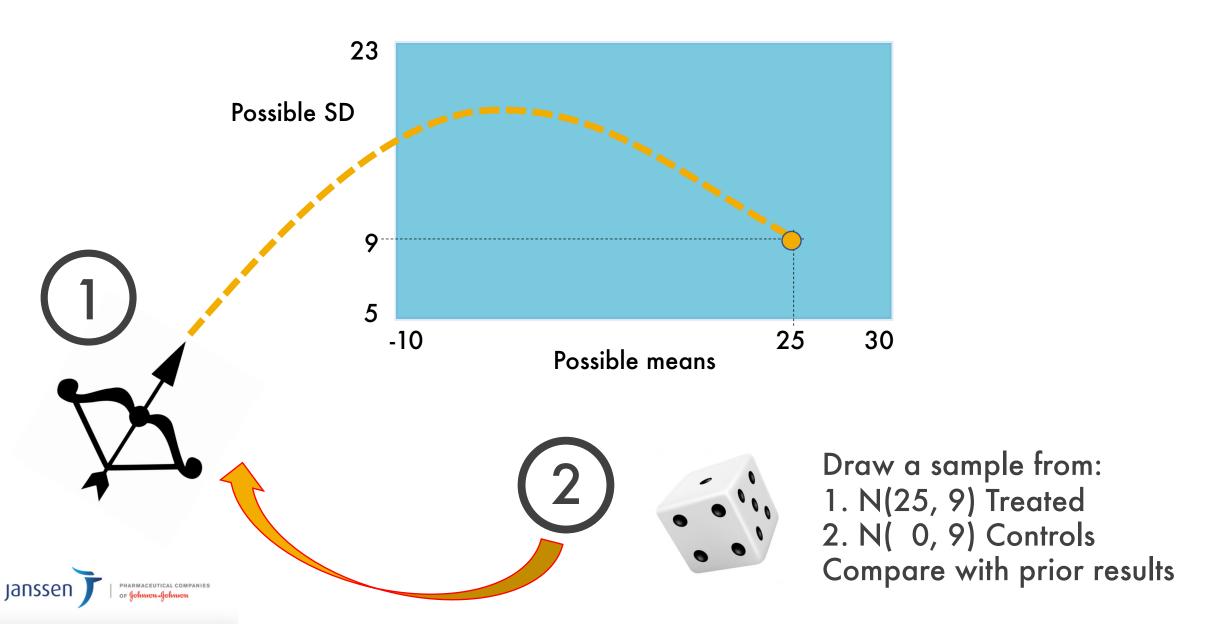




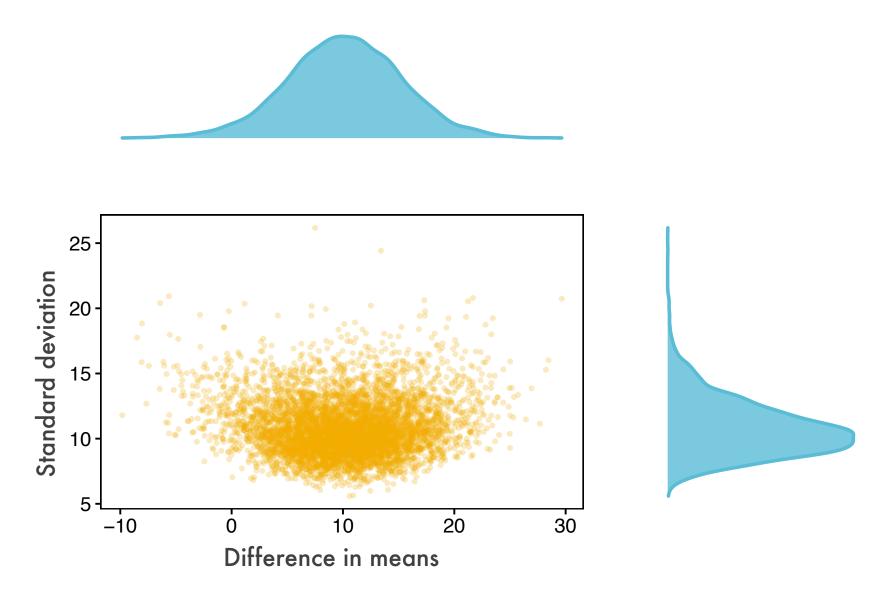




We used simulations to explore all possible model parameters

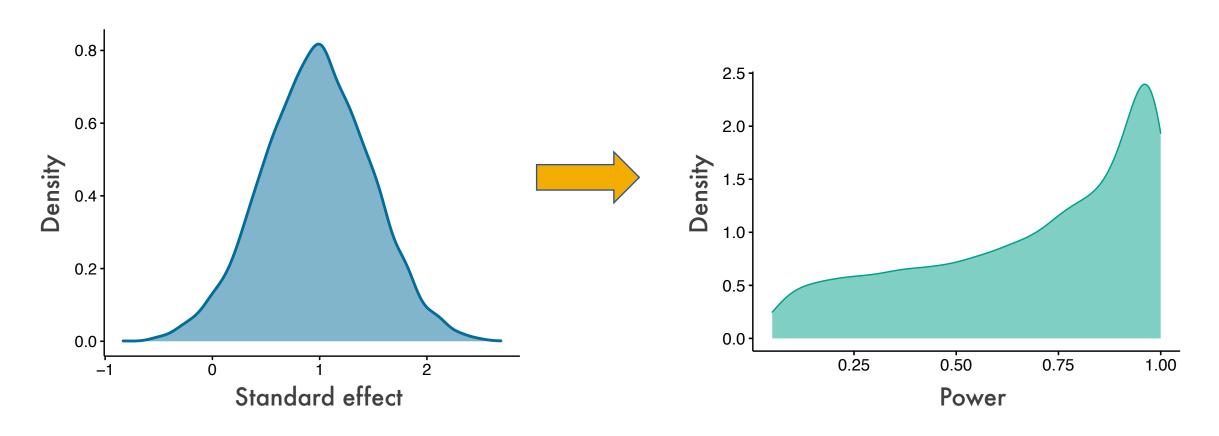


Different sets of model parameters can yield observed results



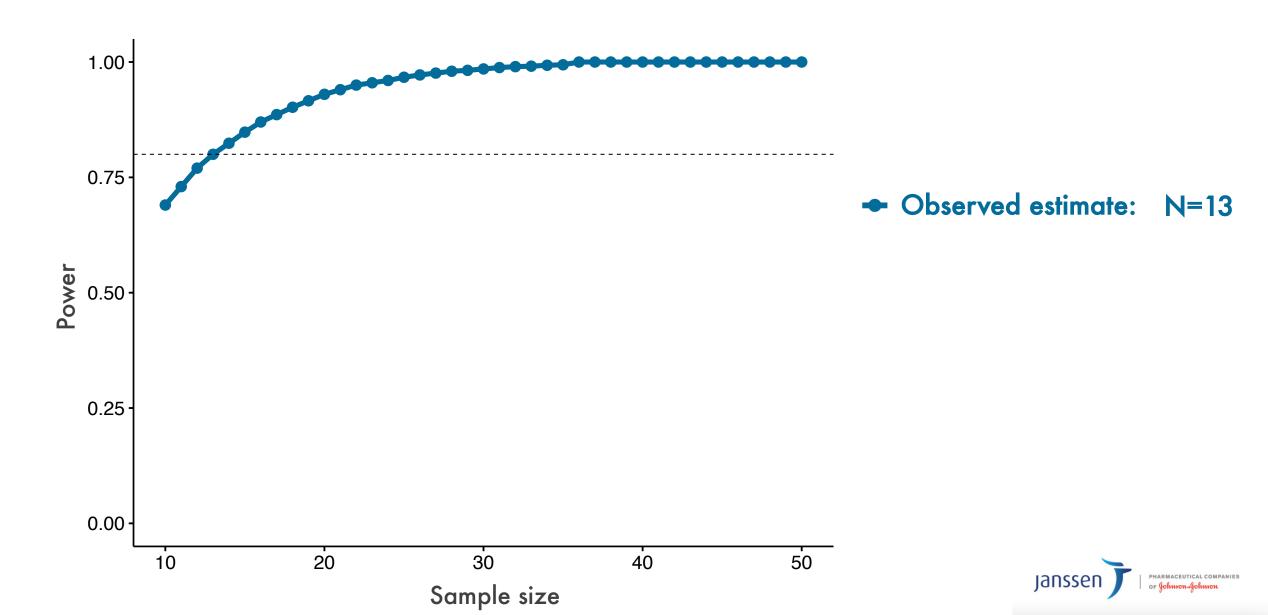


Treatment effects and power vary for each model

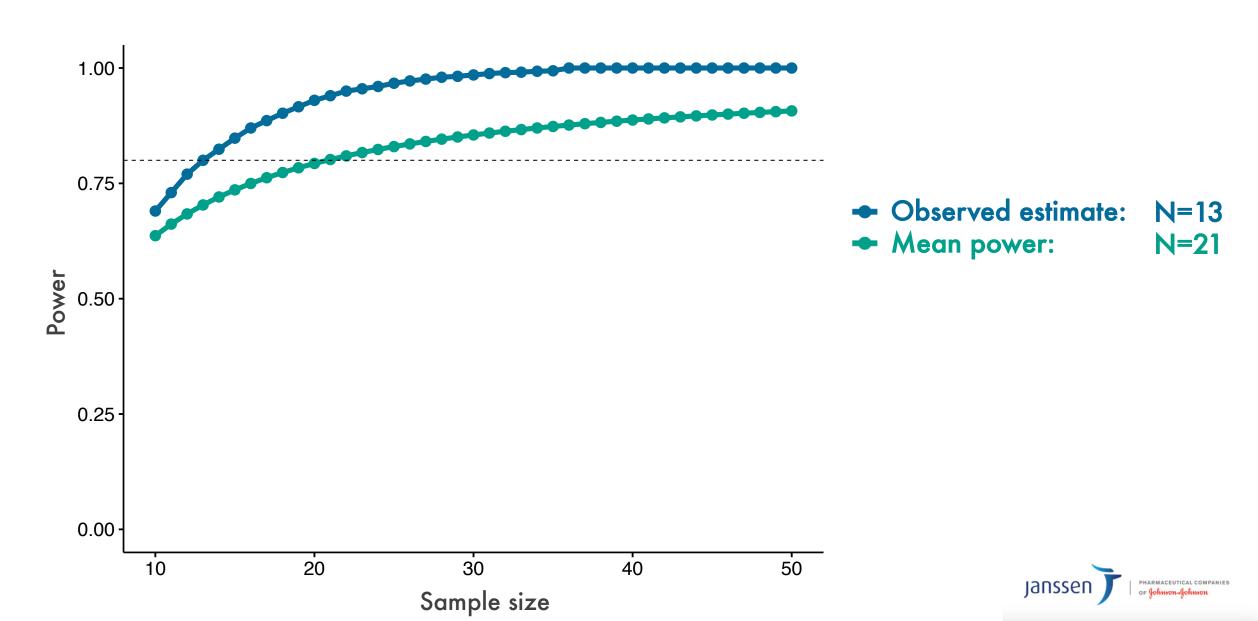




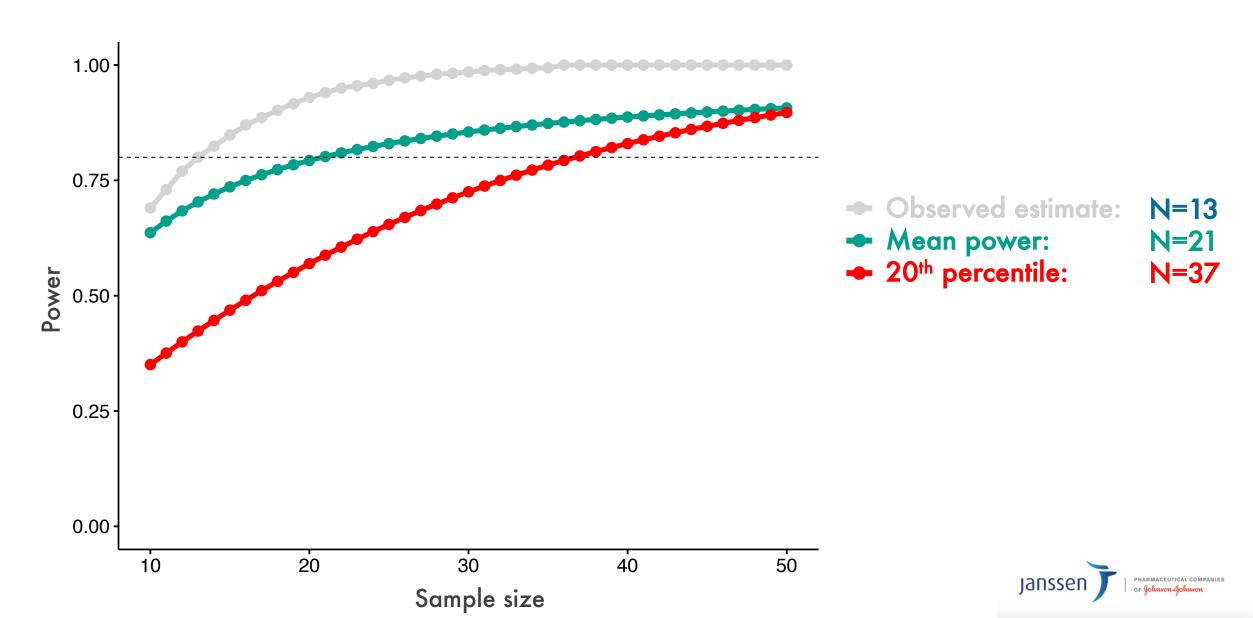
Most calculations assume observed effect is 'true' effect



Considering all possible models makes a difference

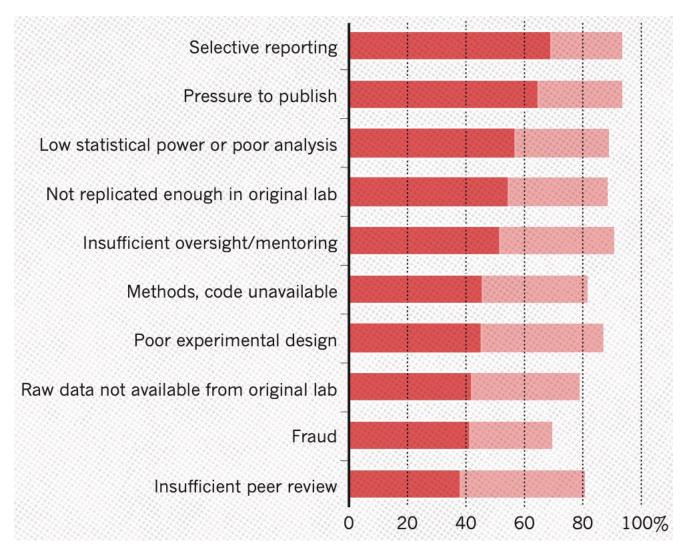


We can quantify the uncertainty of power calculations



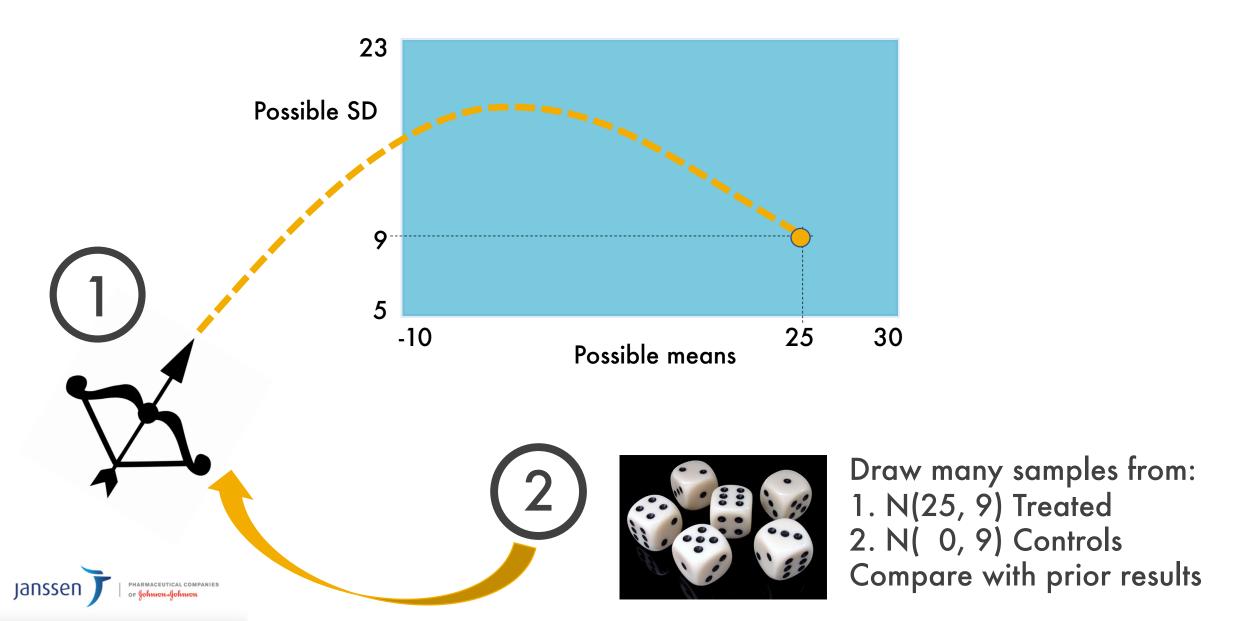
Publication bias and hidden multiplicity skew results

- 1M biomedical research papers published each year (2/minute)
- 7,600 medical research organizations in US alone
- Employ >100,000 people in US;
 >400,000 in Europe

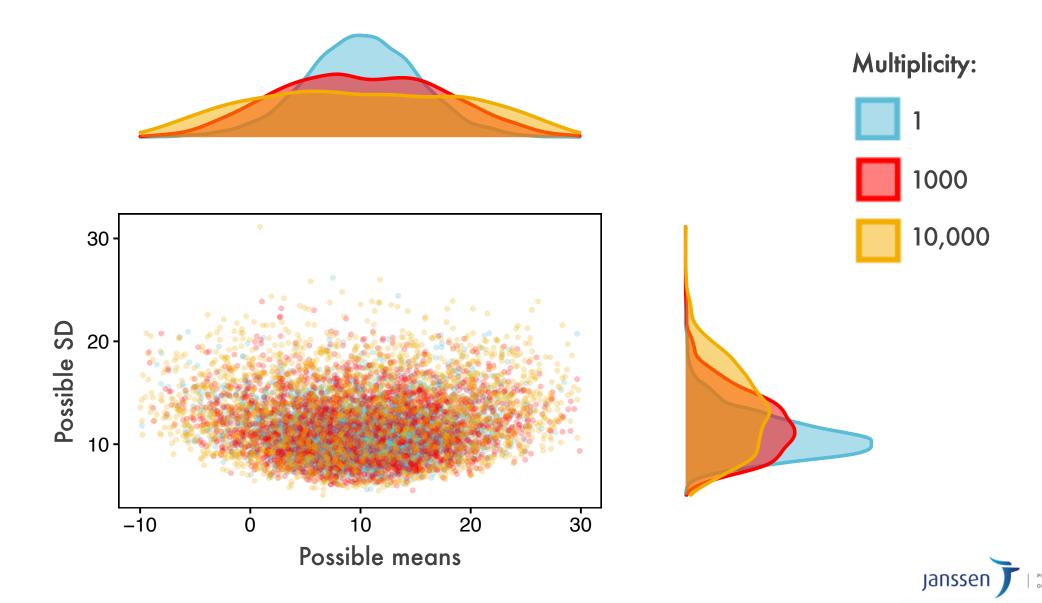




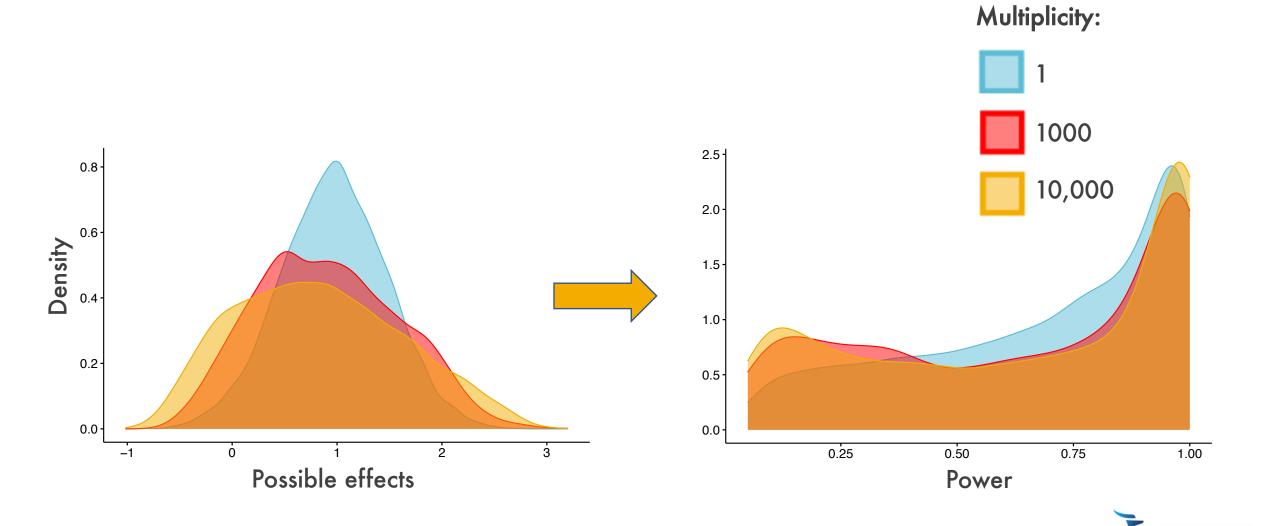
We modified our simulations to explore the effect of bias

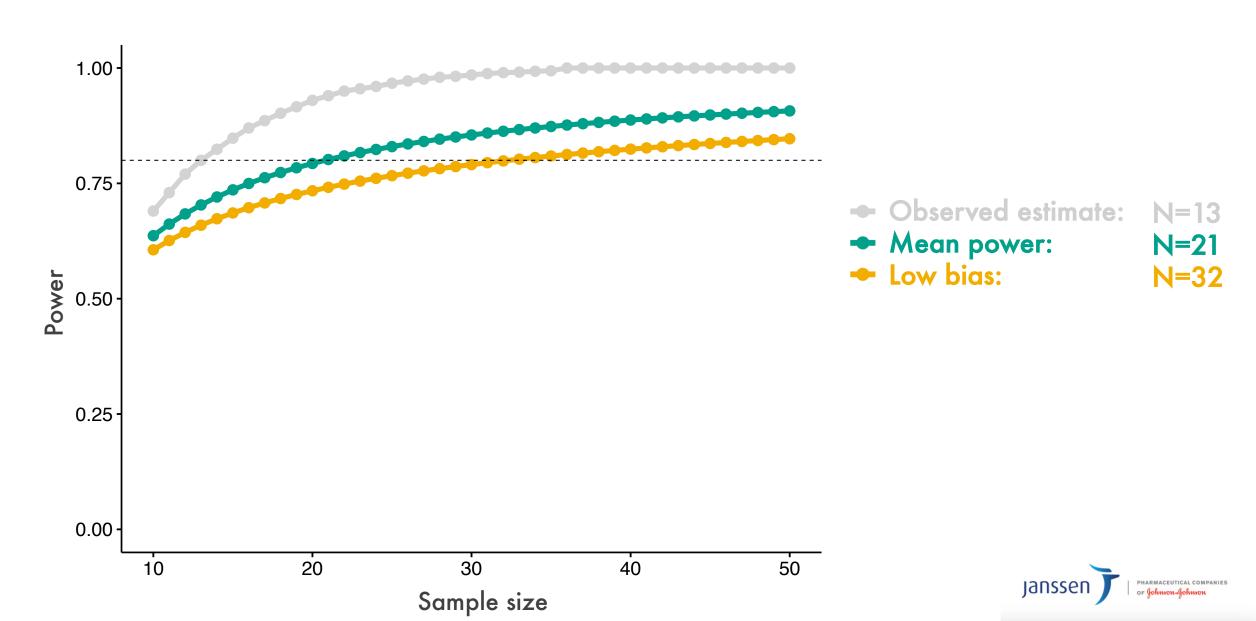


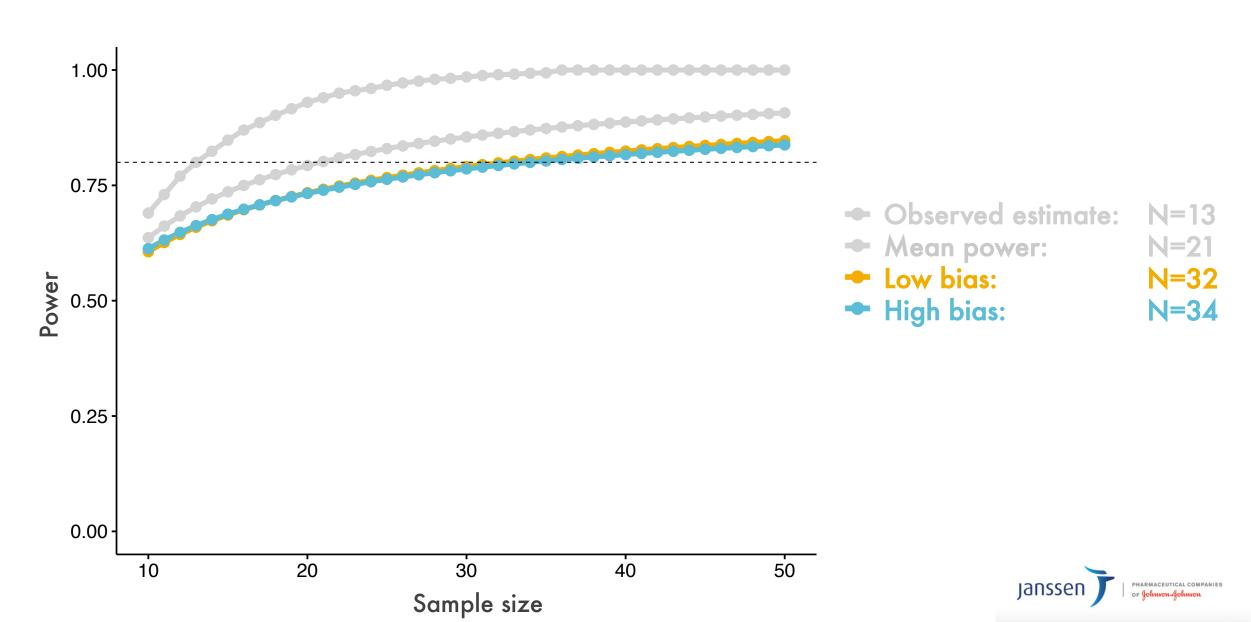
Bias changes the distribution of possible parameters

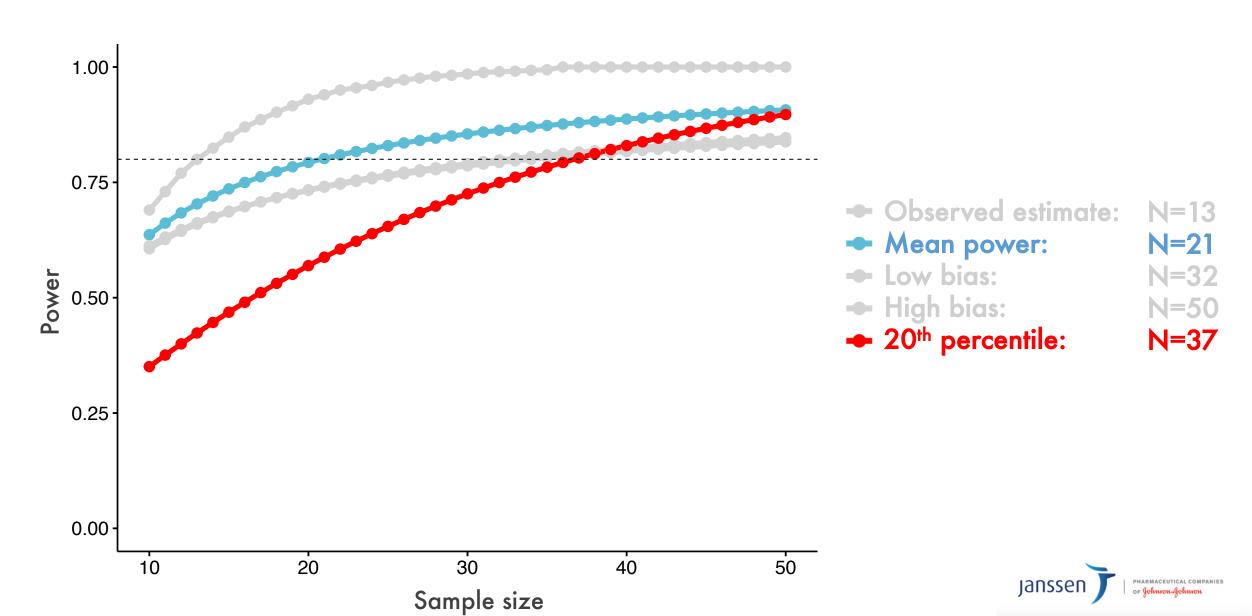


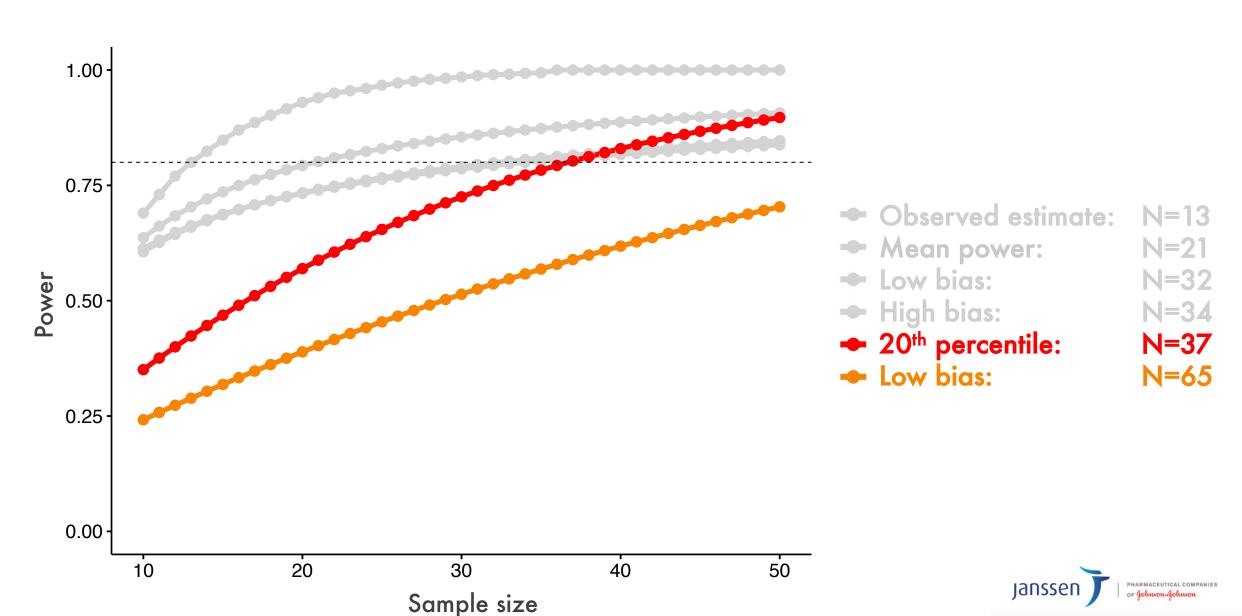
Bias changes the distribution of possible effects and power

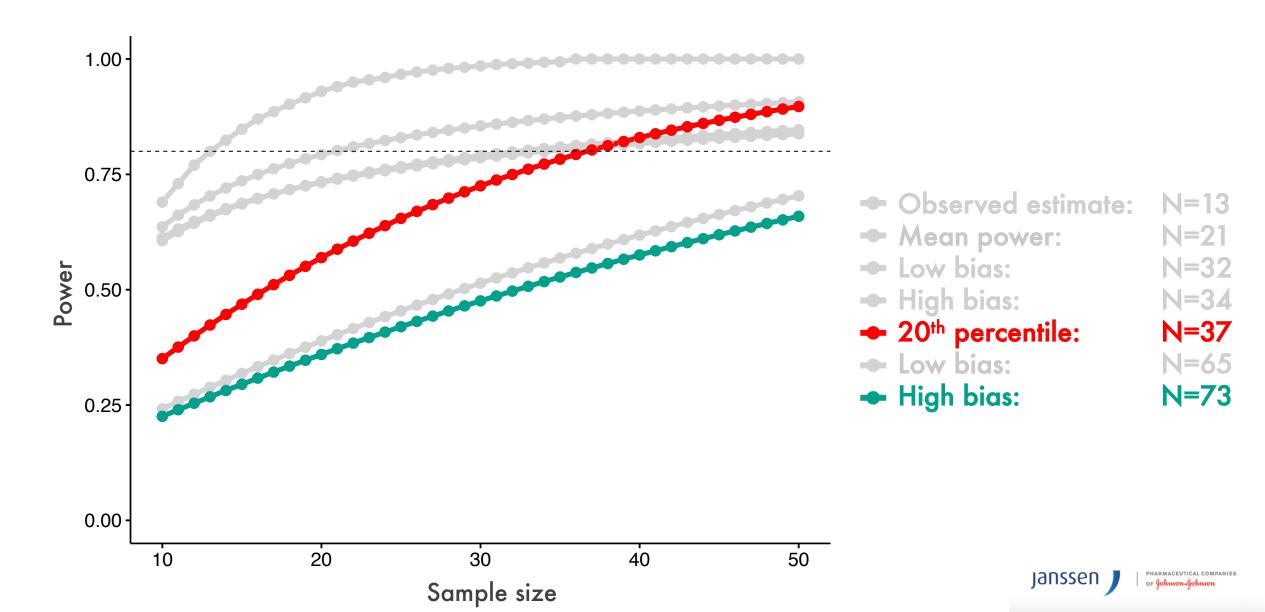












Replications require large sample sizes

- Assuming observed parameters reflect reality leads to underpowered studies
- P-values are not the only problem; estimates can vary in magnitude, direction
- The proposed method can be tailored to a given replication study
 - Uses all available information, can extend to unequal variance
 - Quantifies uncertainty in power calculation
 - Accommodates publication bias and hidden multiplicity
 - Can be computationally intensive

