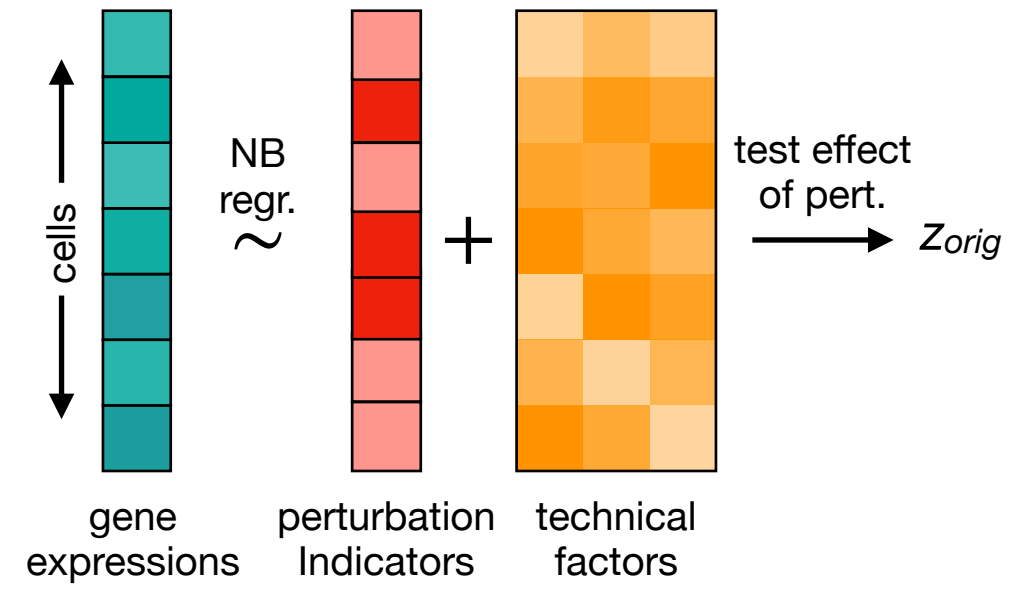
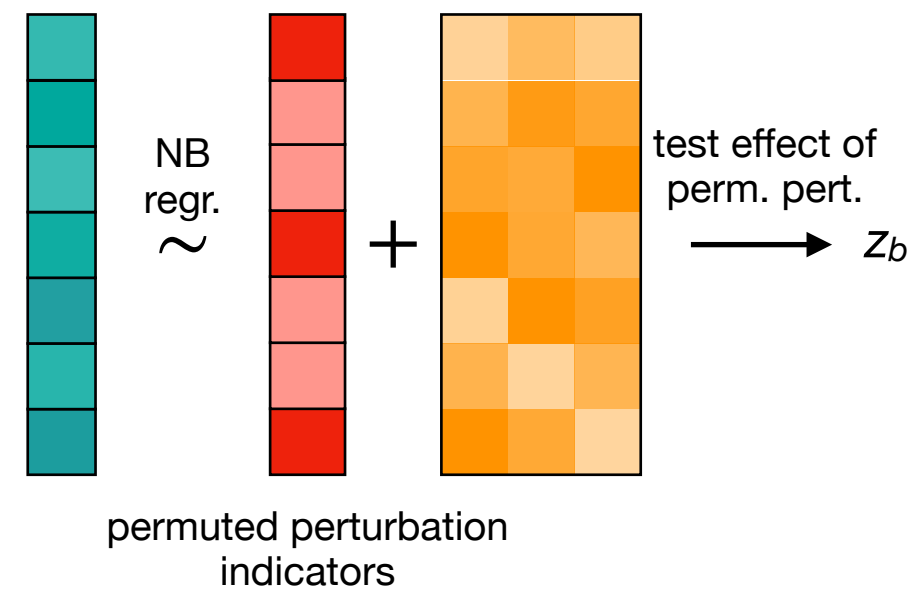


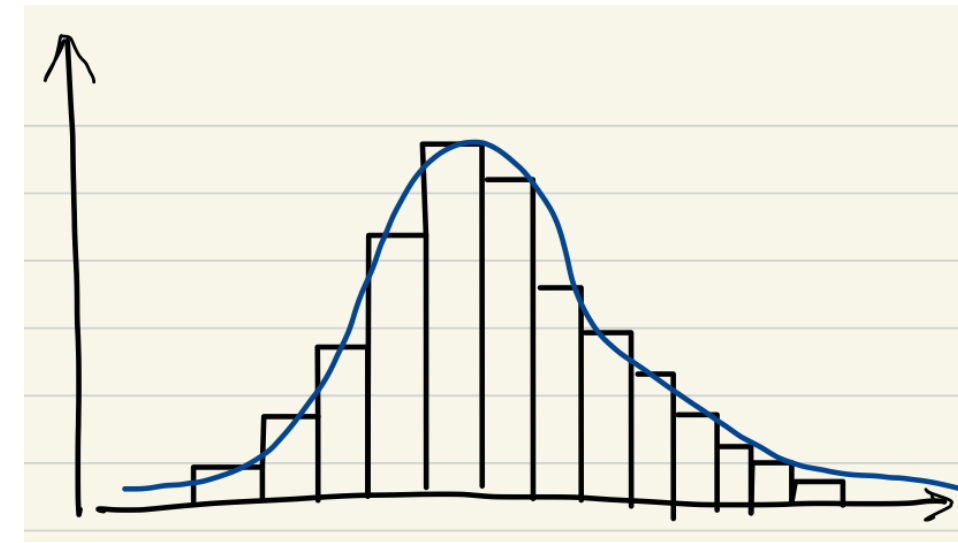
- ① Obtain z-score from NB regression of gene expression on perturbation indicator and technical factors



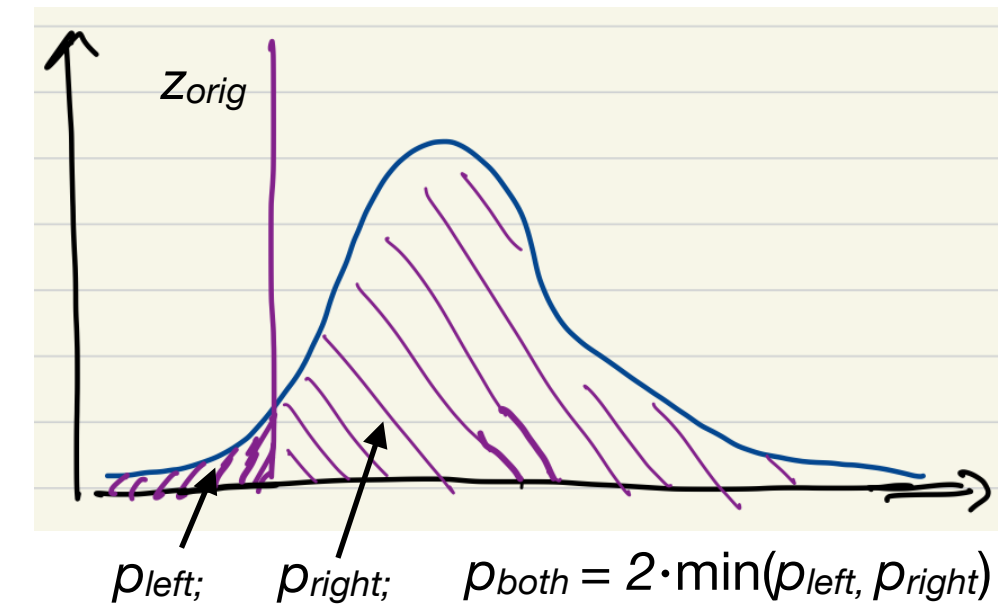
- ② For $b = 1, \dots, B$:
Permute perturbation indicator and rerun NB regression to obtain null z-score z_b



- ③ Fit smooth curve to null z-scores z_b

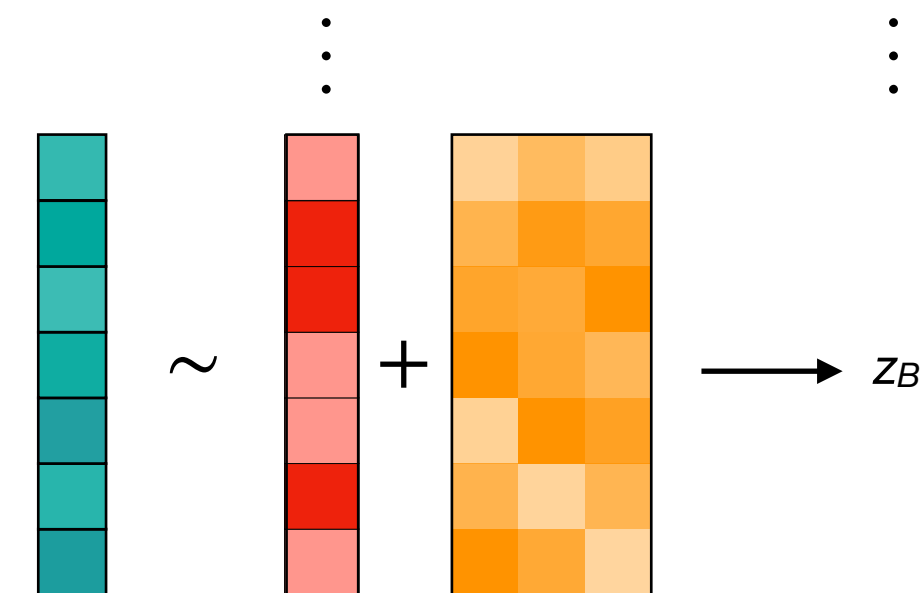
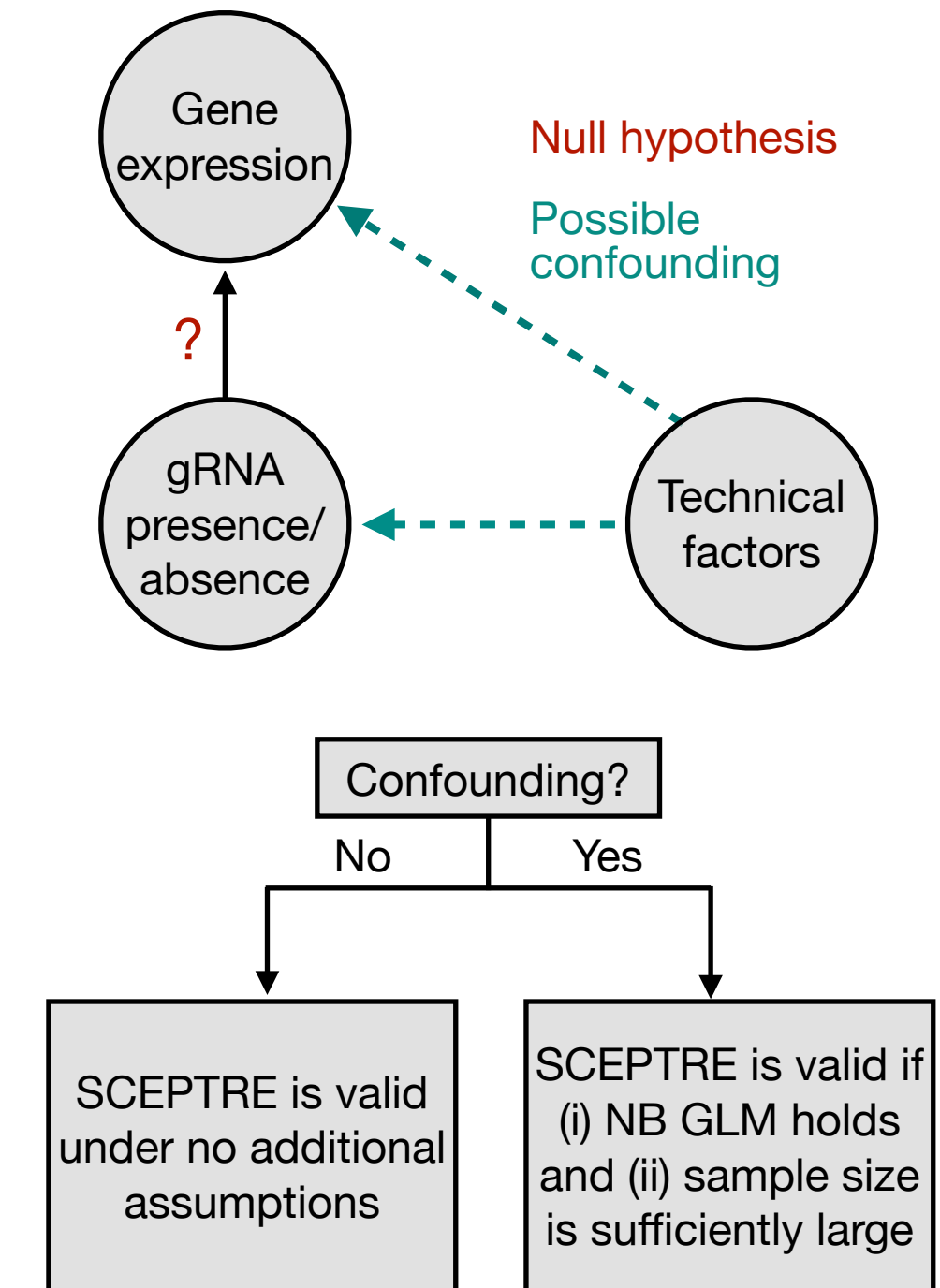


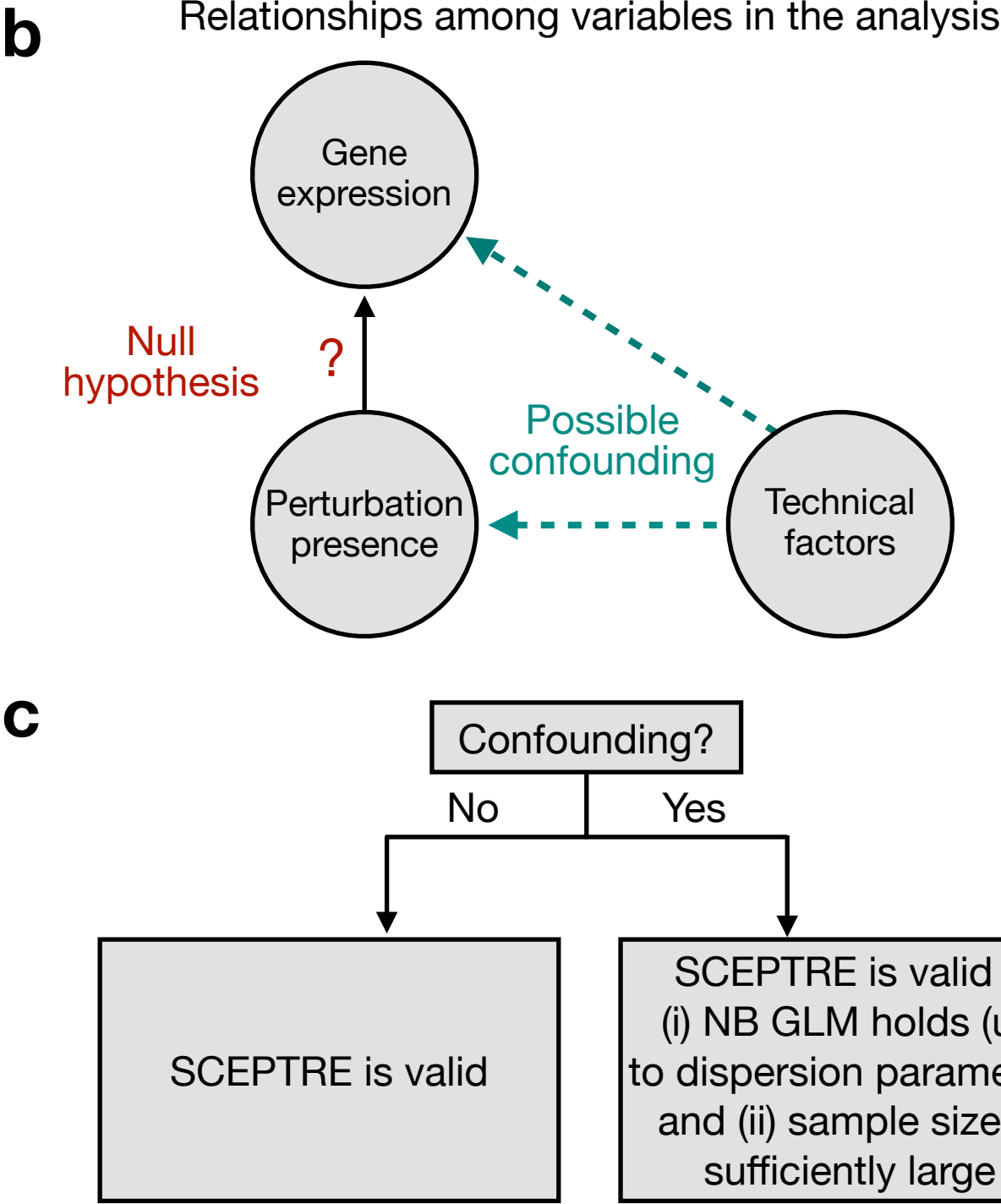
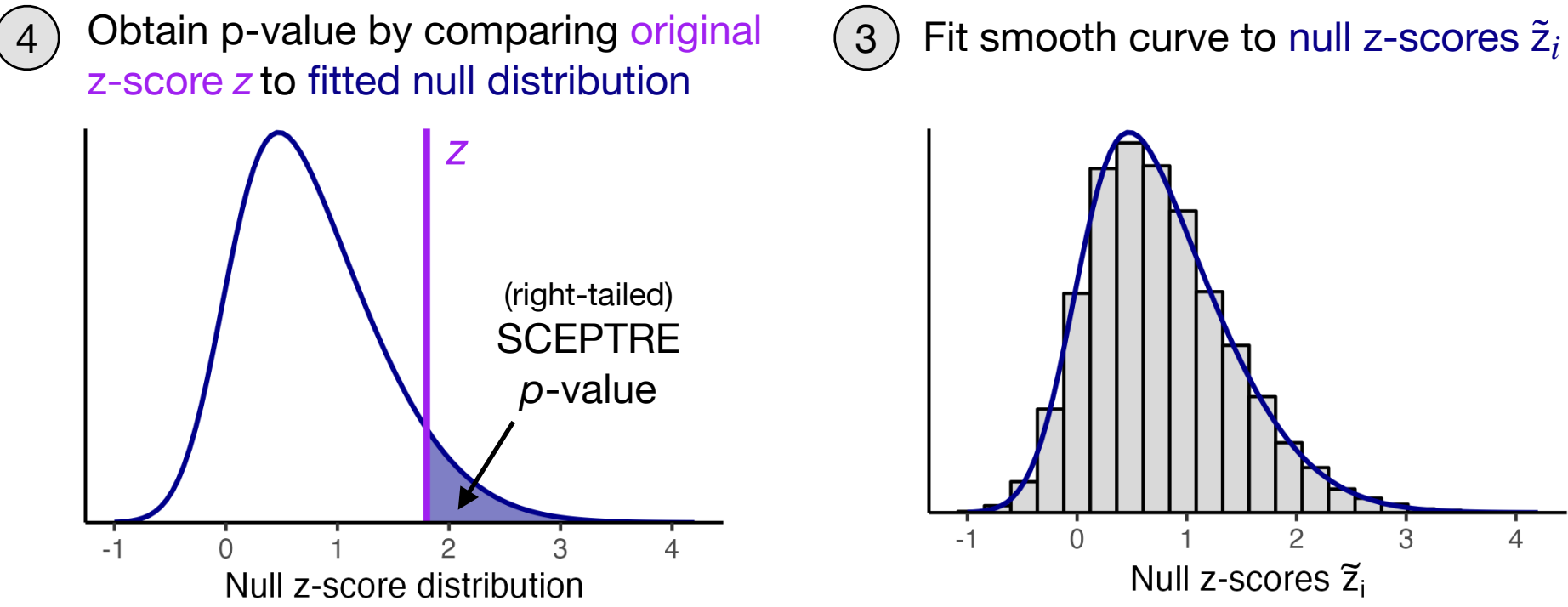
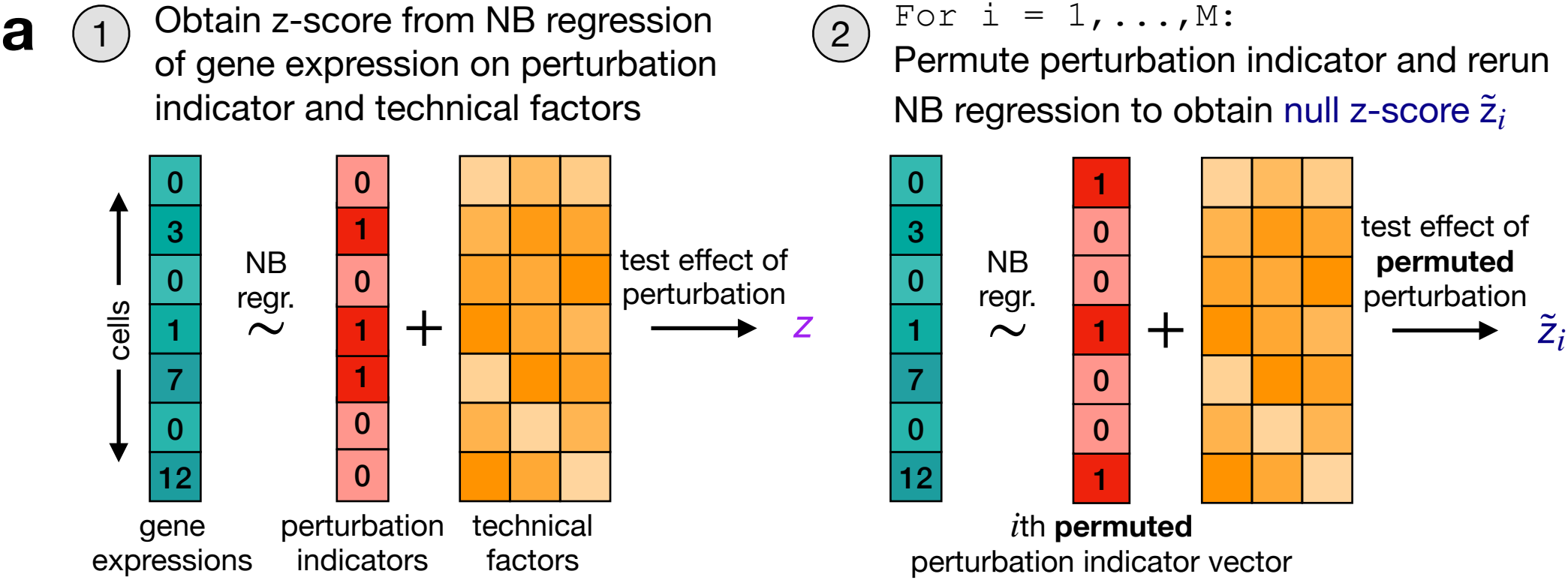
- ④ Obtain p-value by comparing original z-score Z_{orig} to fitted null distribution



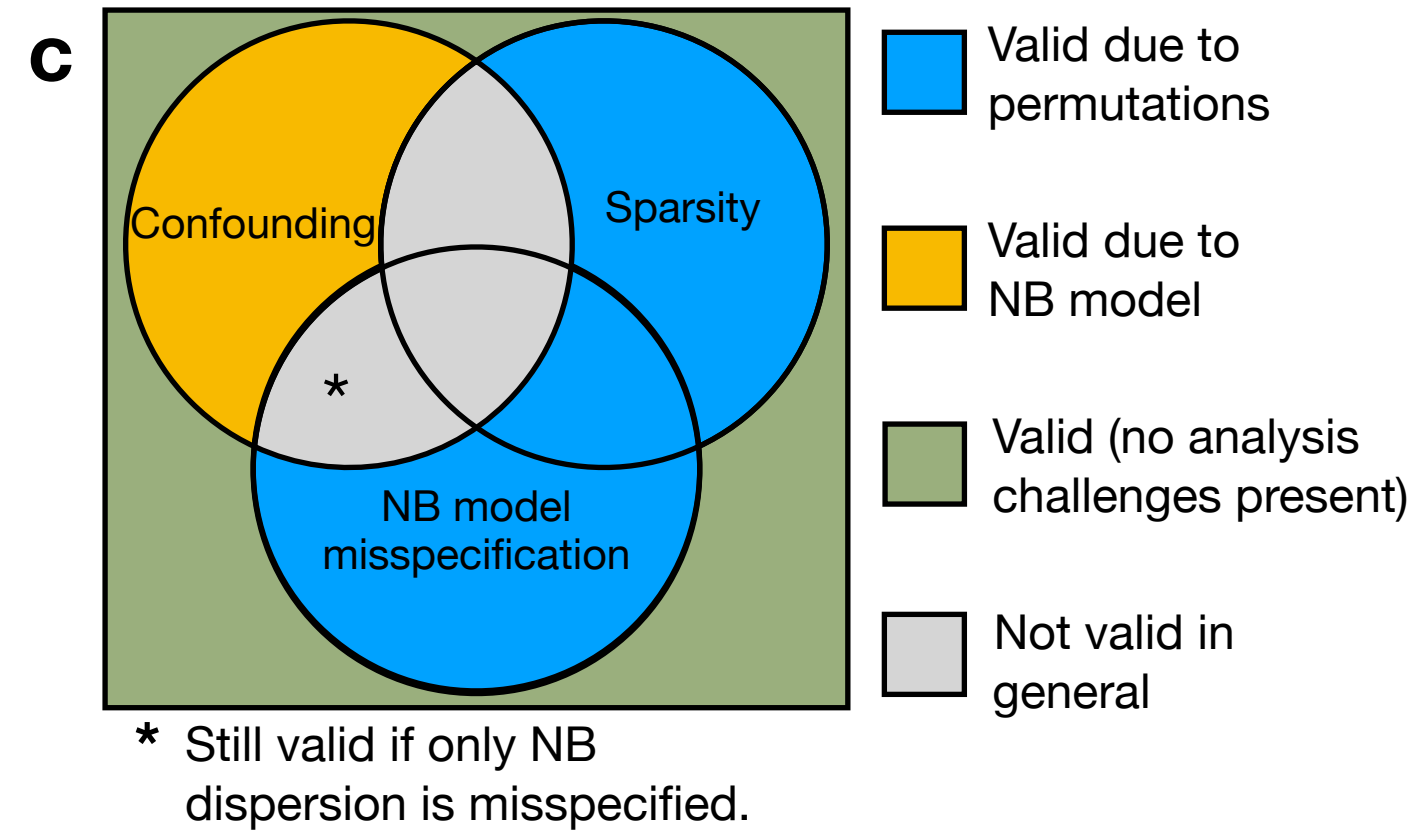
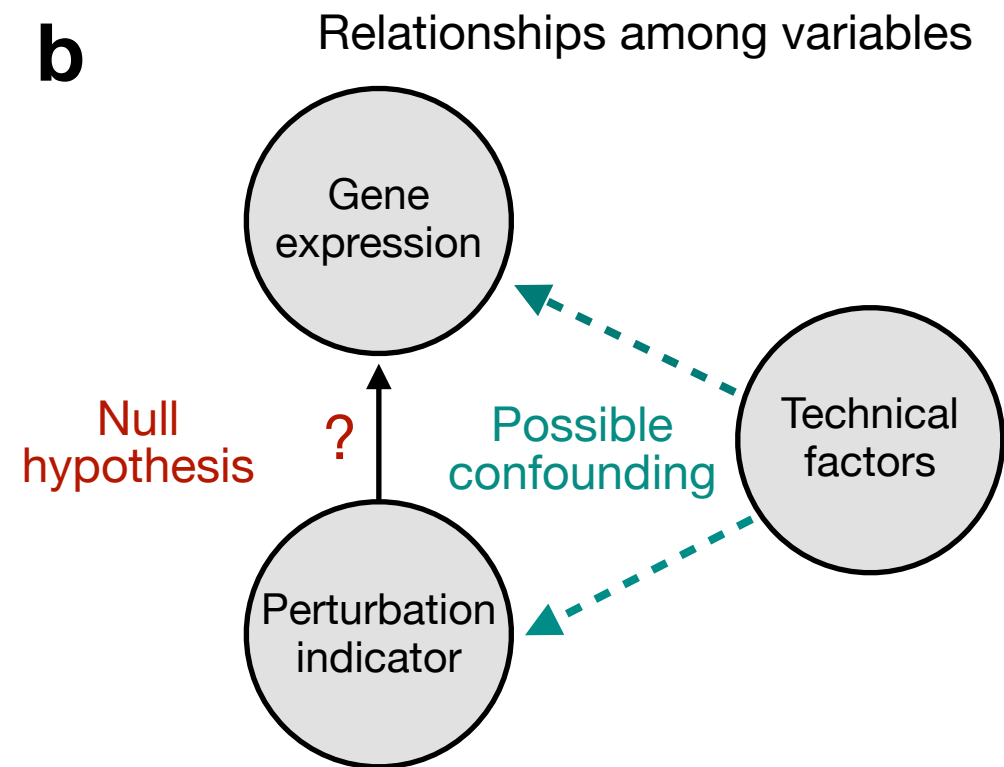
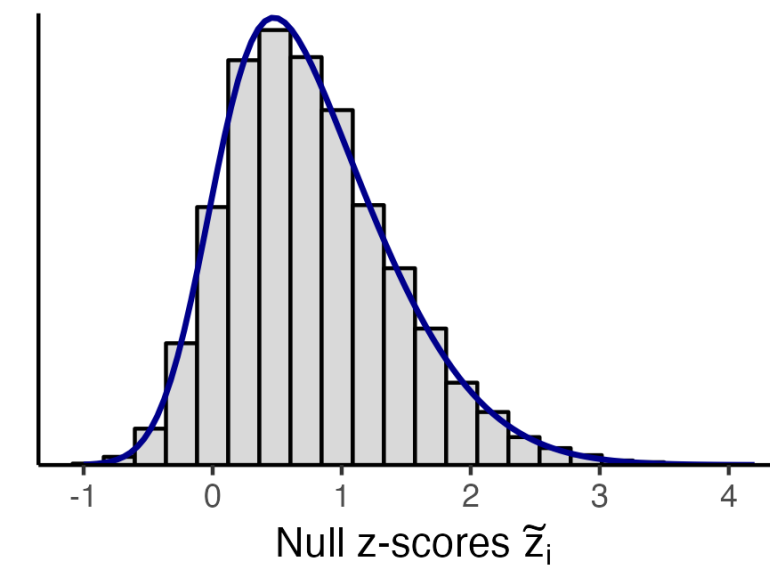
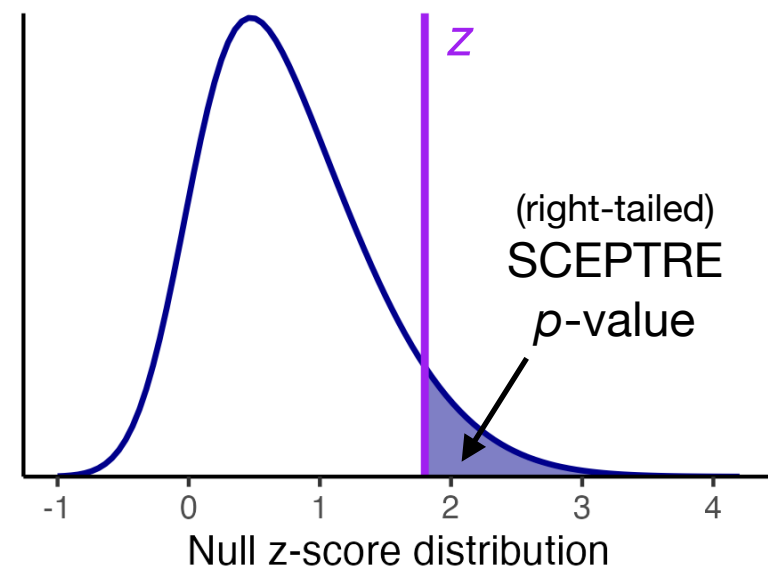
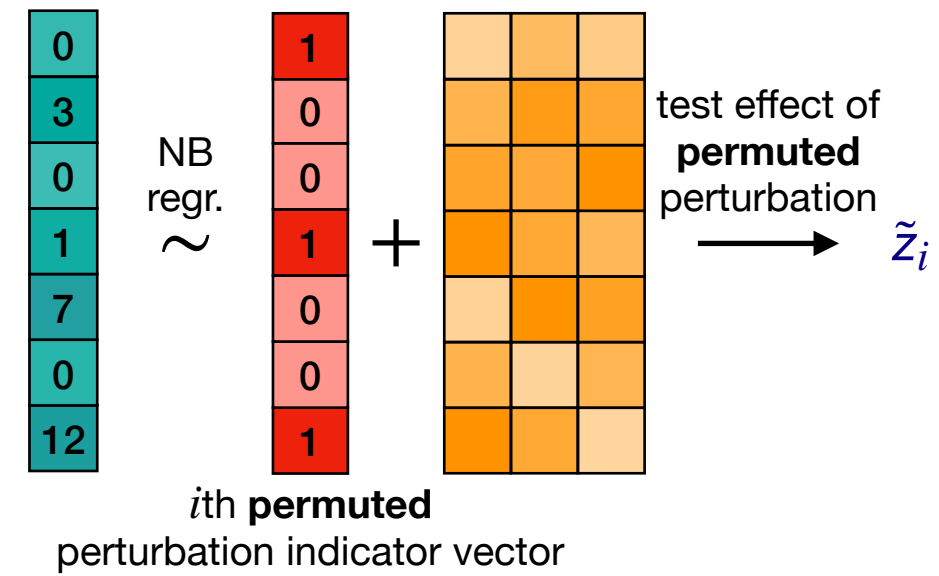
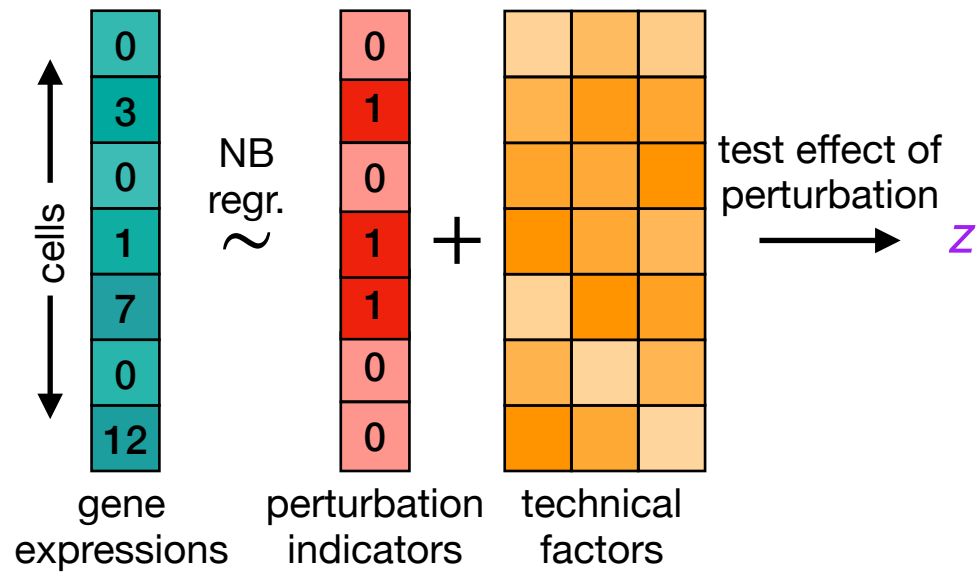
Z_{orig}

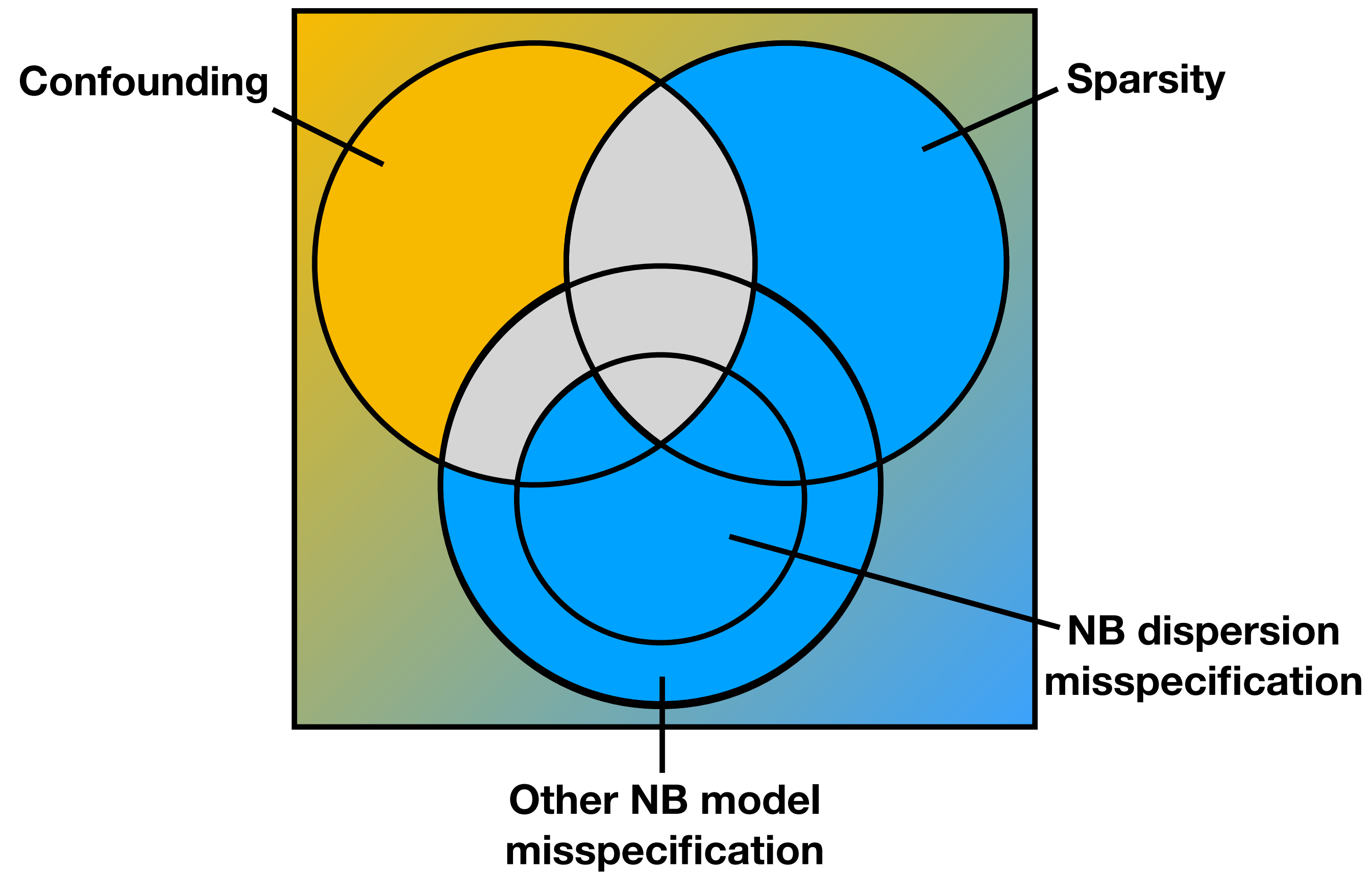
Relationship between variables in analysis



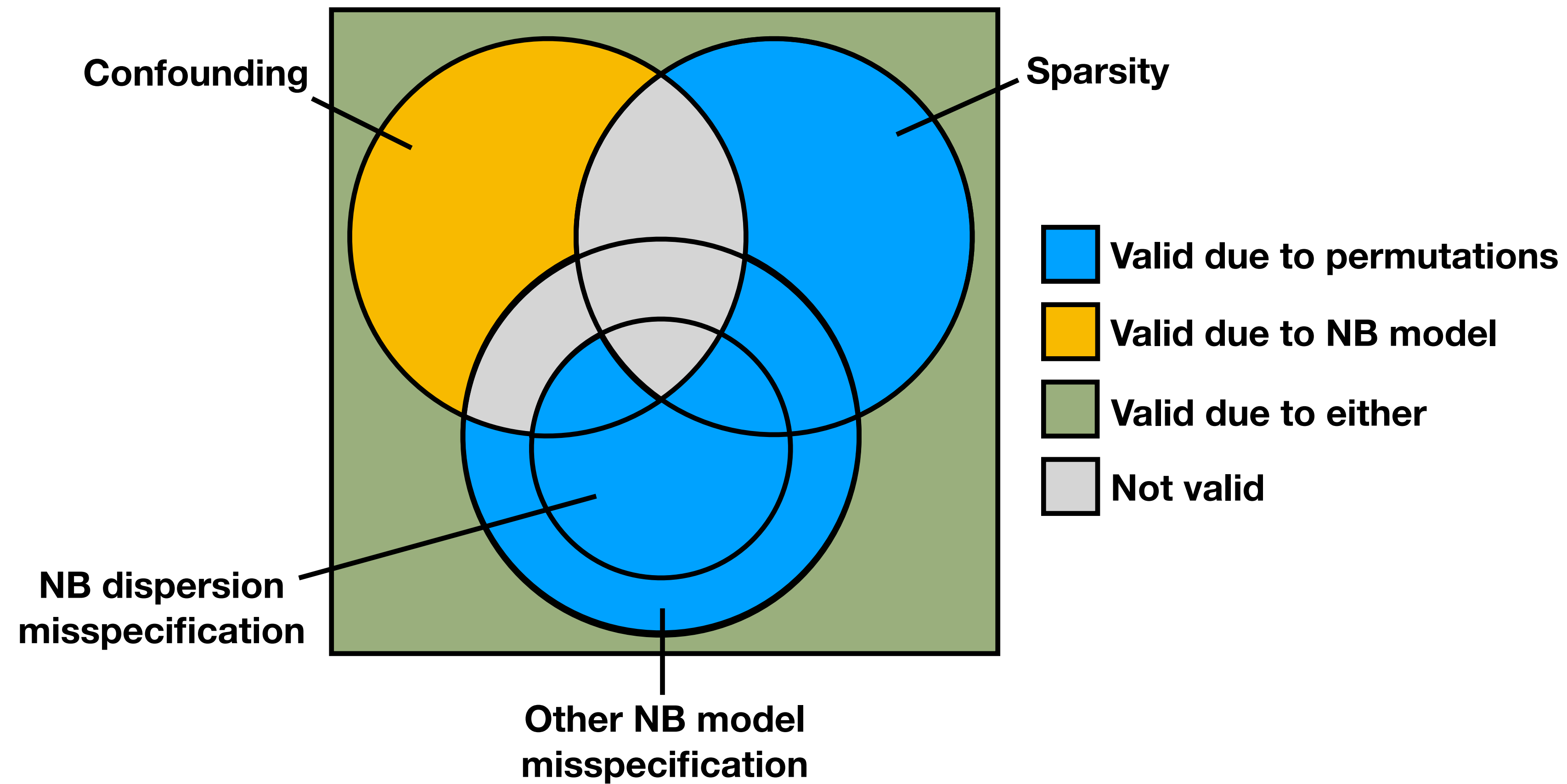


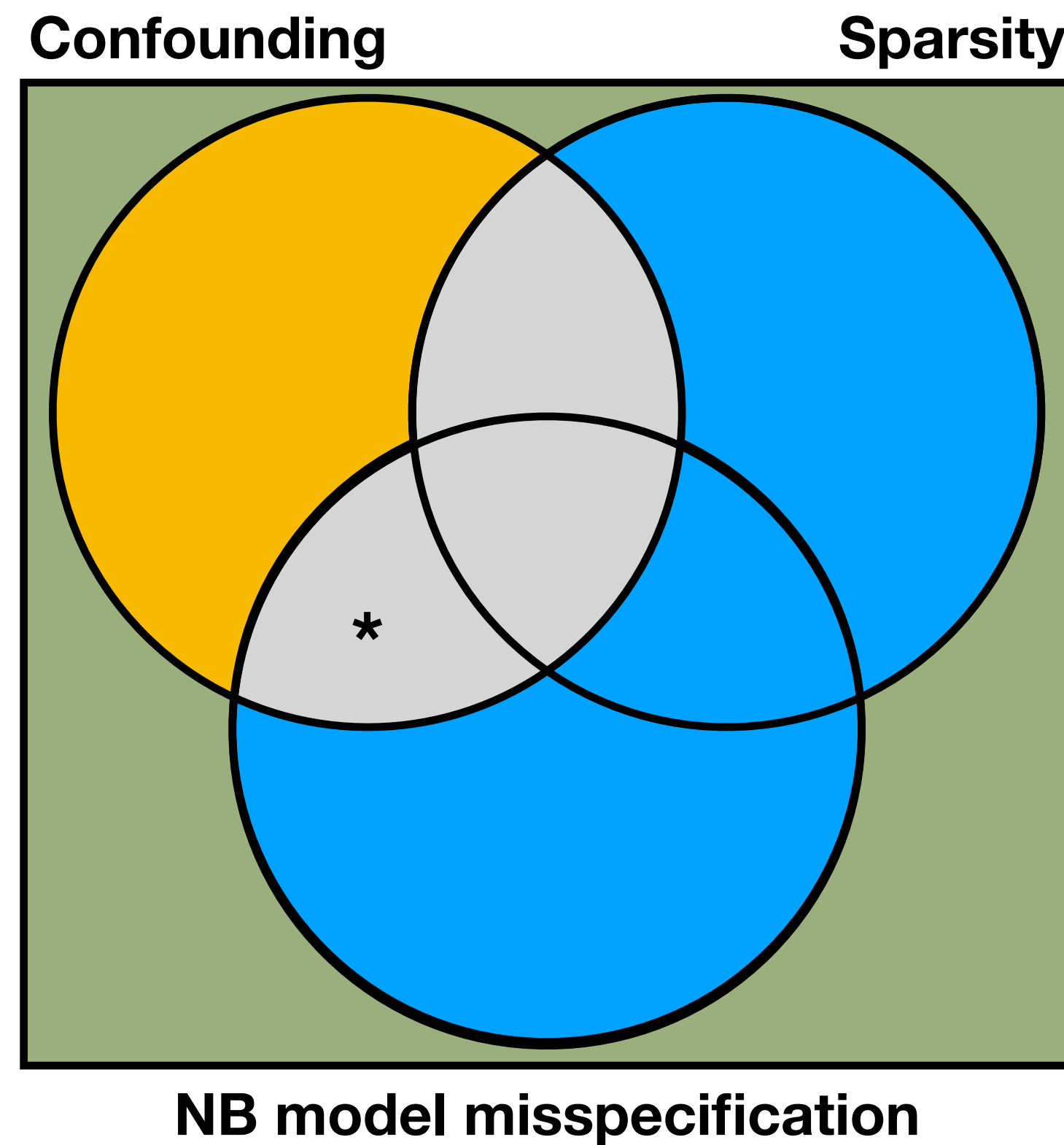
- a**
- 1 Obtain z-score from NB regression of gene expression on perturbation indicator and technical factors
 - 2 For $i = 1, \dots, M$:
Permute perturbation indicator and recompute z-score to obtain null z-score \tilde{z}_i
 - 3 Fit smooth curve to null z-scores \tilde{z}_i
 - 4 Obtain p-value by comparing original z-score z to fitted null distribution





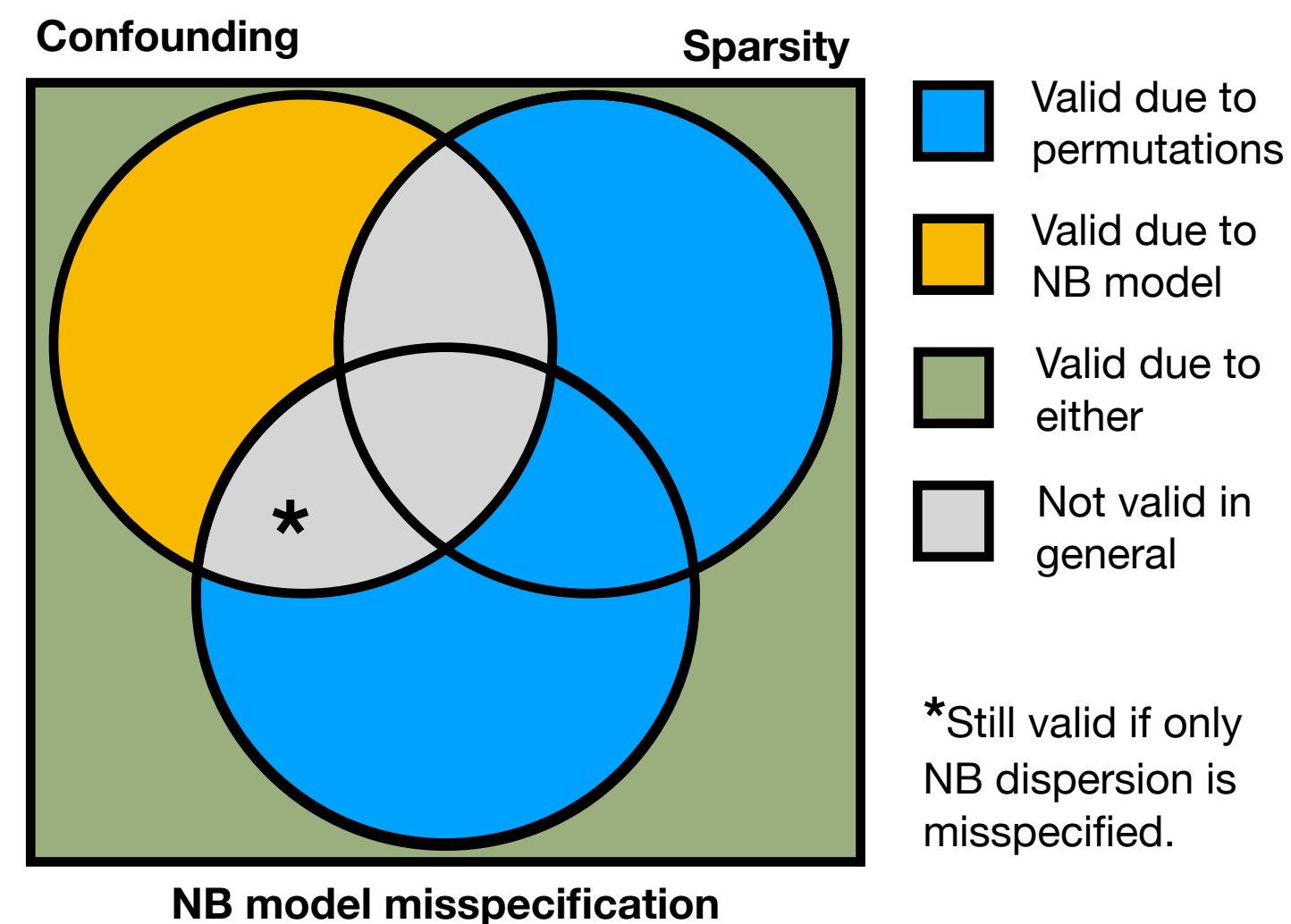
 Valid due to permutations  Valid due to NB model  Not valid





- Valid due to permutations
- Valid due to NB model
- Valid due to either
- Not valid in general

*Still valid if only NB dispersion is misspecified.



- Valid due to permutations
- Valid due to NB model
- Valid due to either
- Not valid in general

*Still valid if only NB dispersion is misspecified.