

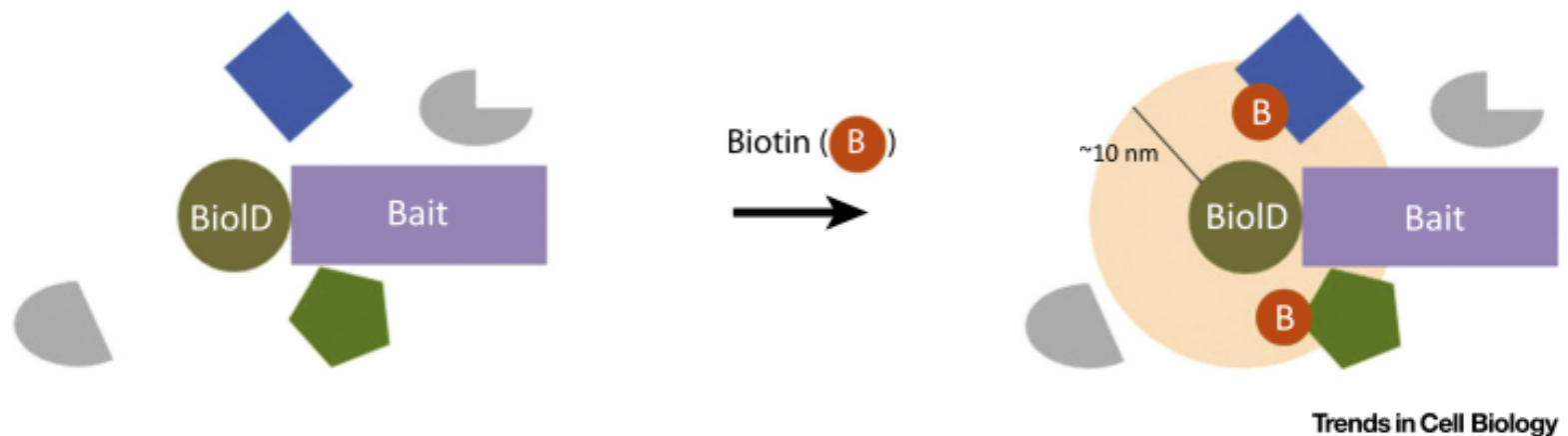
Differential Detection for Label-free Mass Spec Data

Constantin Ahlmann-Eltze

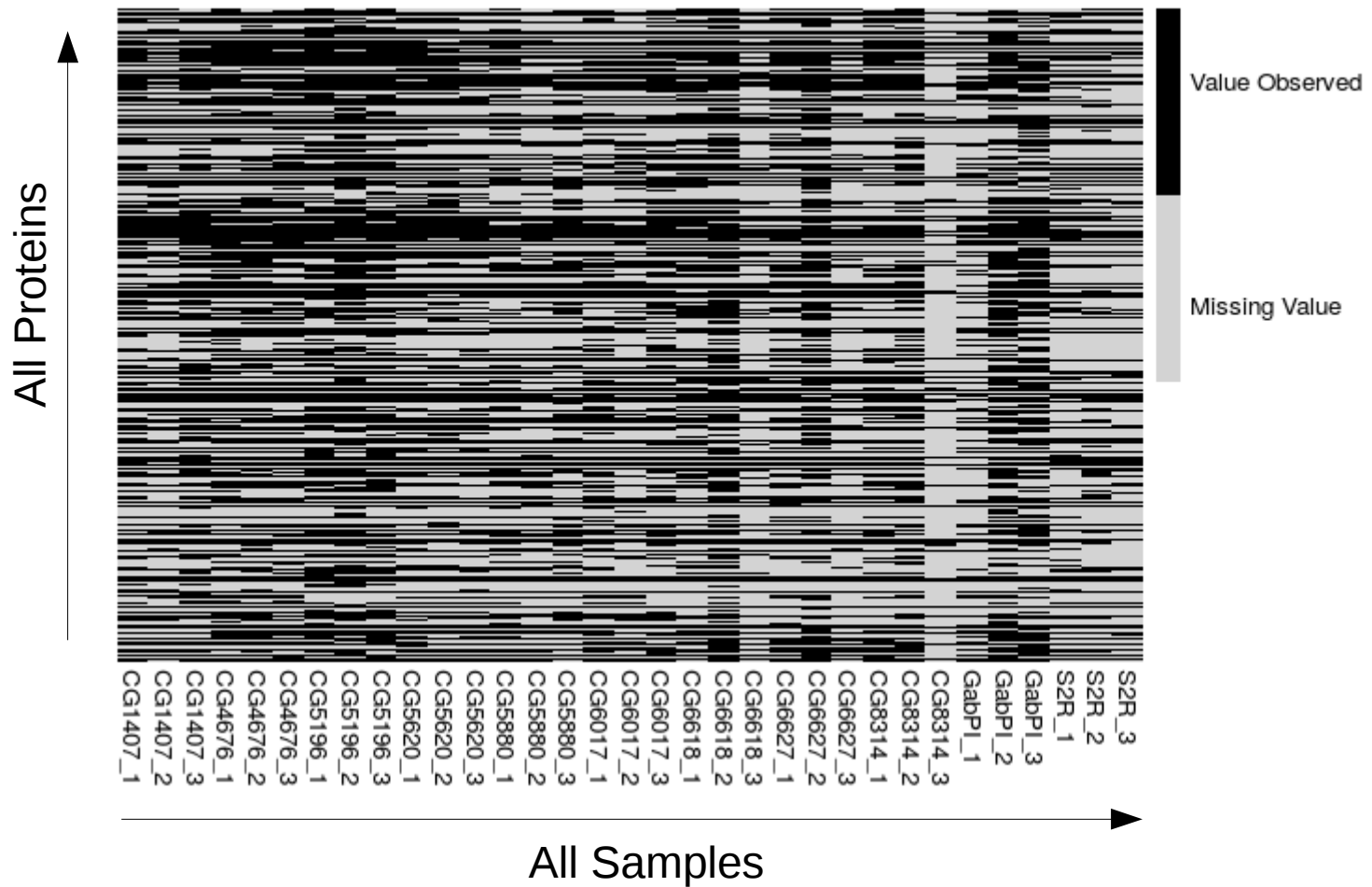
 @const-ae

 github.com/const-ae

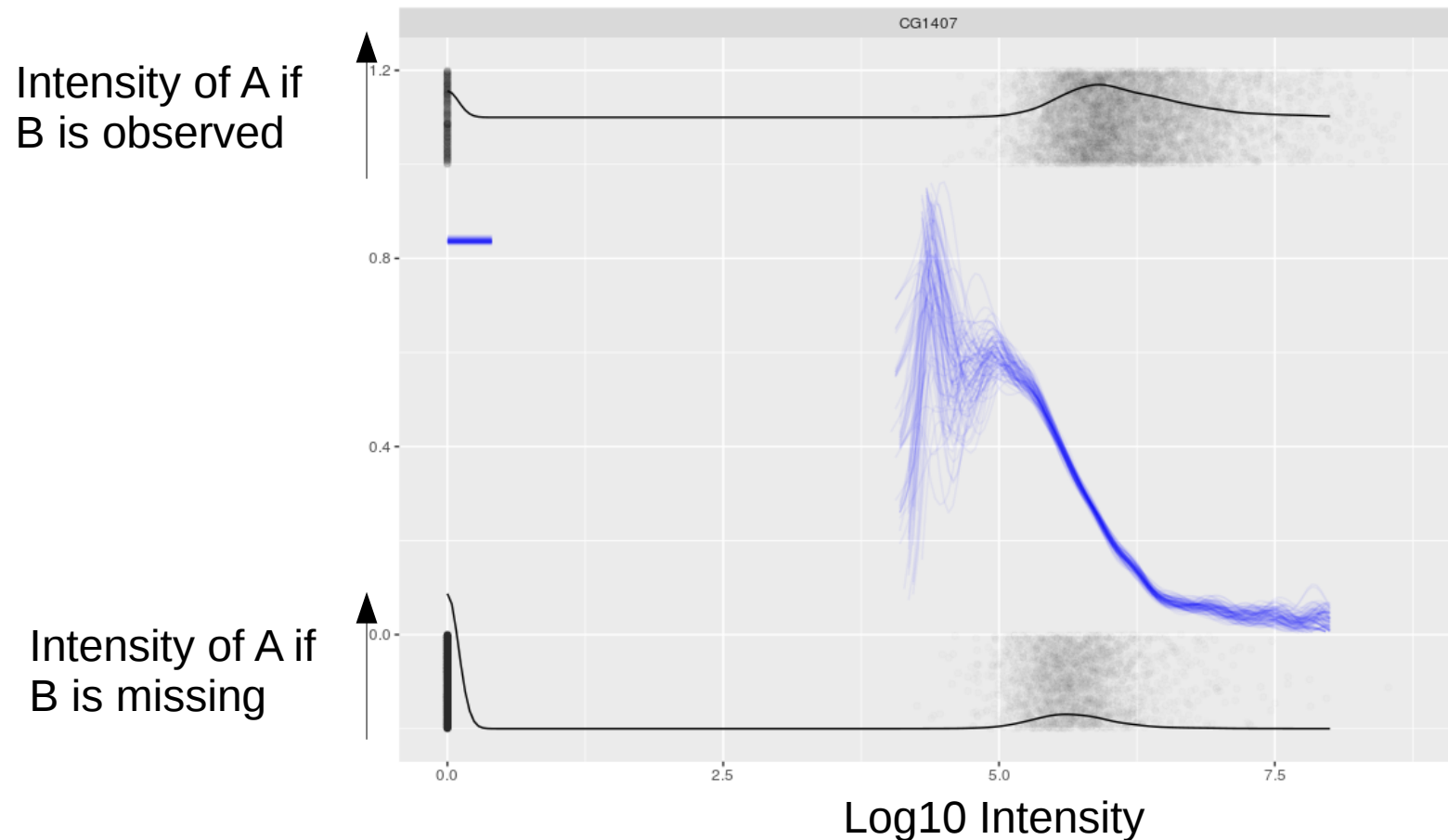
Finding Protein-Protein Interactions with BioID



A lot of values are missing...

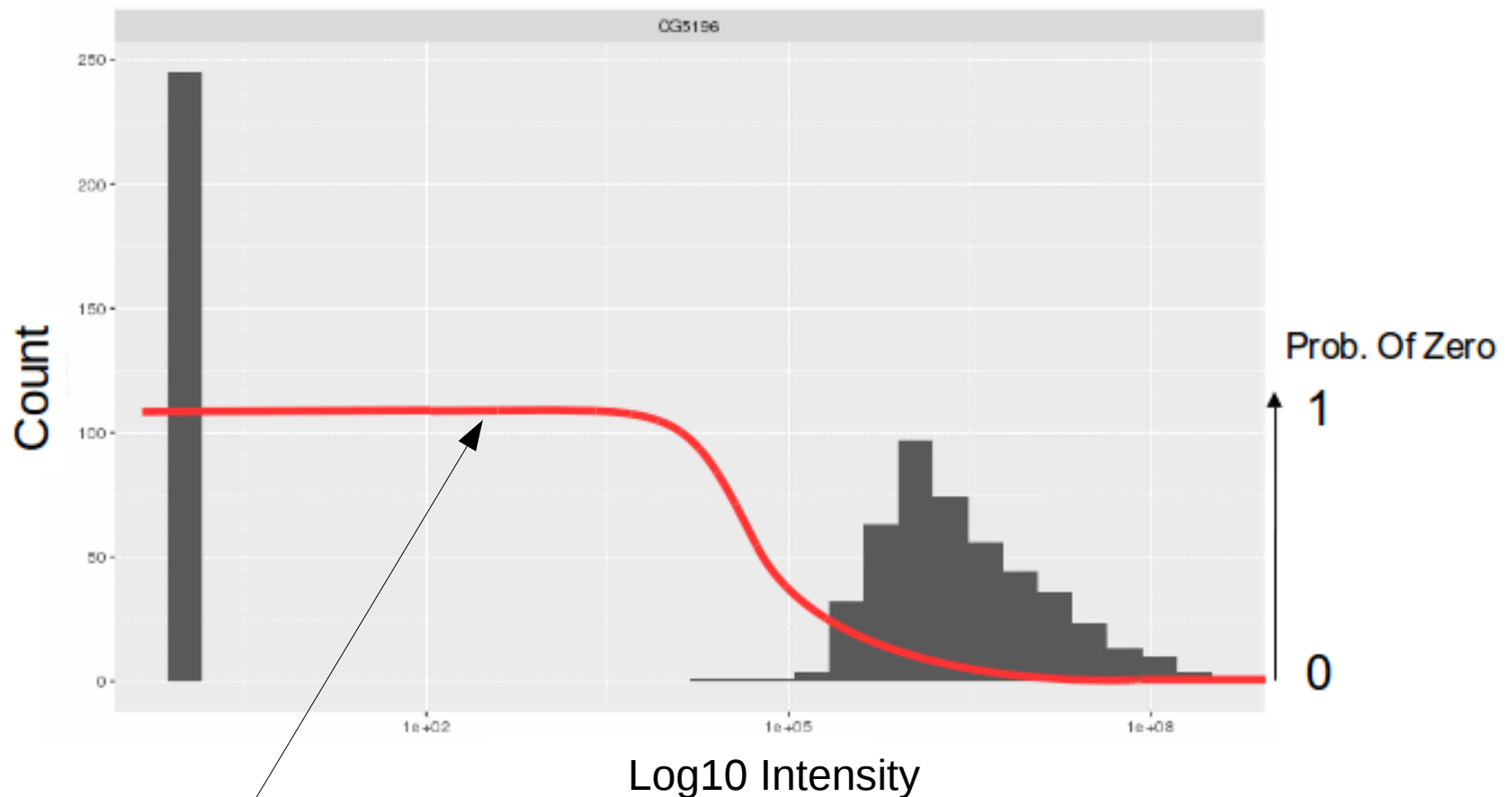


... but not at random



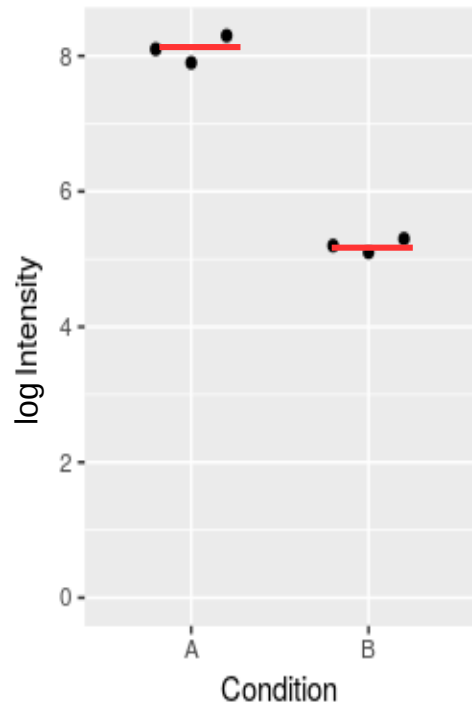
→ If the true intensity is lower,
the chance to miss a value is higher

Lognormal with sigmoidal hurdle



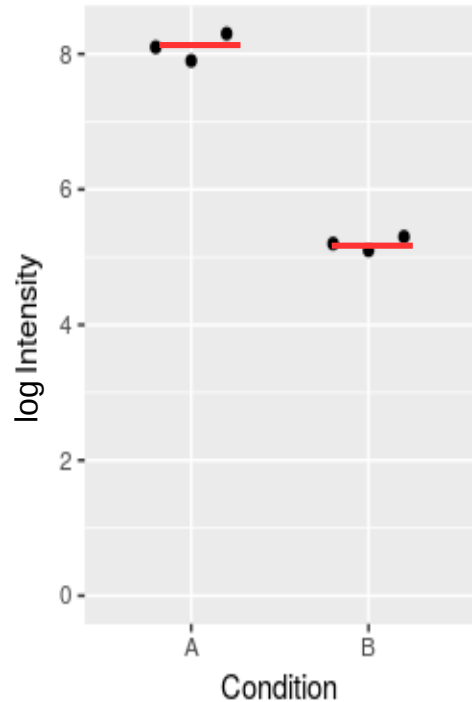
Proposition:
 $p(\text{Missing} \mid I_{\text{TM}}) = \text{sigmoid}(\text{location}, \text{scale})$
 $I_{\text{obs}} \sim \text{Normal}(I_{\text{TM}}, \sigma)$

Are differences just due to chance?

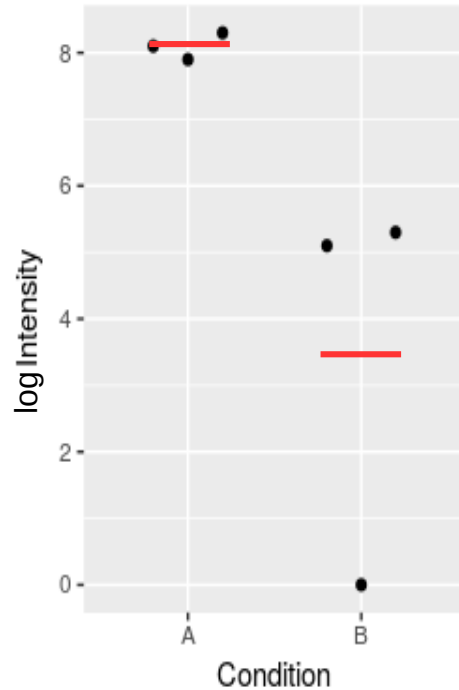


t-test
(variance
moderated)

Is the difference just due to chance?

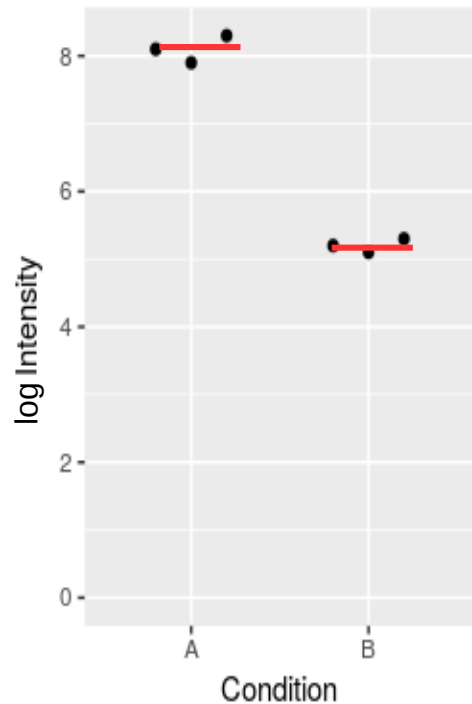


t-test
(variance
moderated)

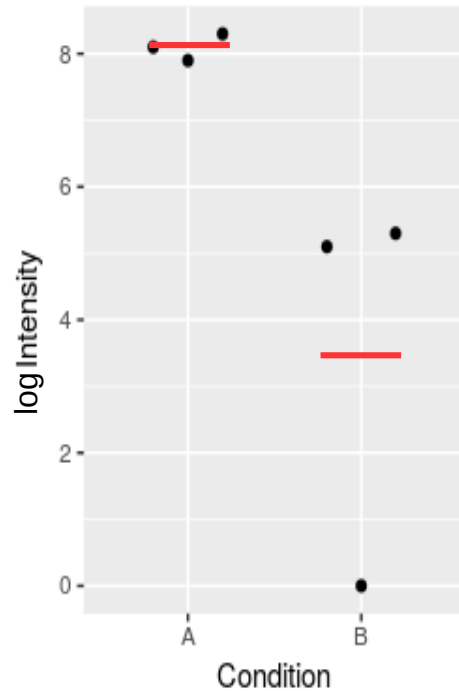


t-test?!

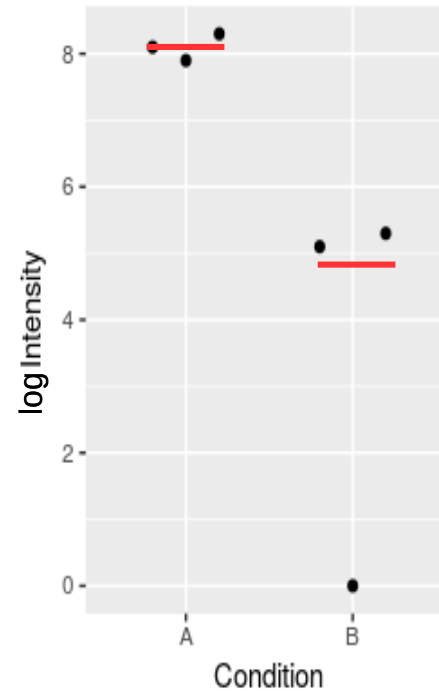
Is the difference just due to chance?



t-test
(variance
moderated)

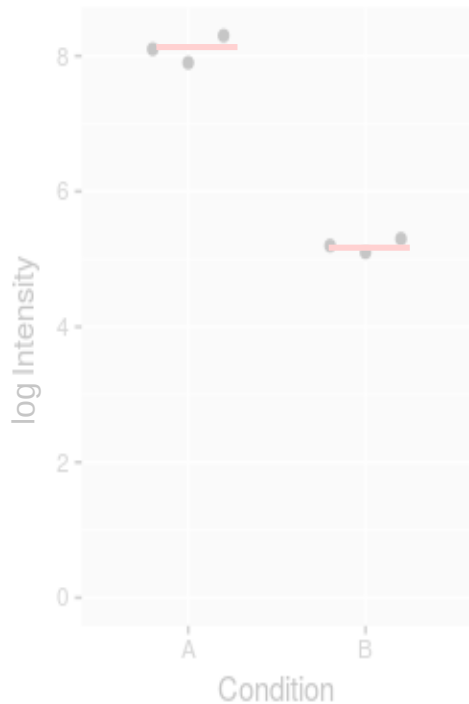


t-test?!



MLE of
group
means

Is the difference just due to chance?



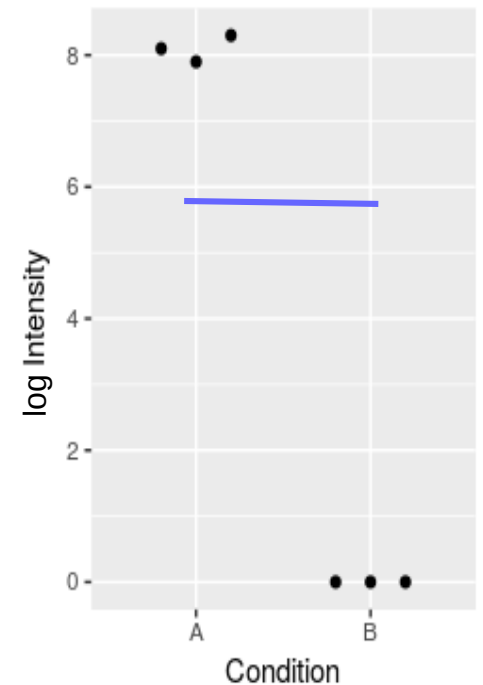
t-test
(variance
moderated)



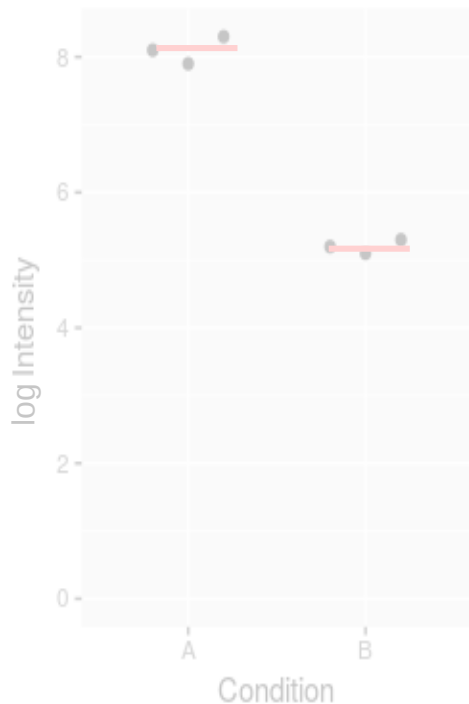
t-test?!



MLE of
group
means



Is the difference just due to chance?



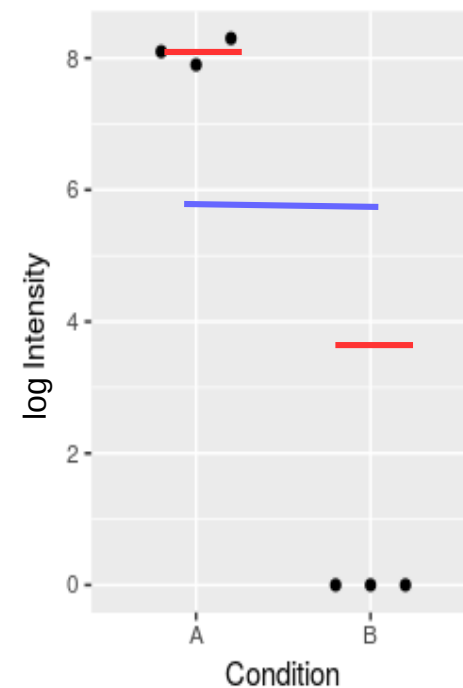
t-test
(variance
moderated)



t-test?!



MLE of
group
means



Groups are
symmetric
around global
mean

Conclusion

- Values in LFQ not missing at random (sigmoid)
- MLE of group means should be compared
- Symmetry can help if all values are missing

Implementation: github.com/const-ae/proDD