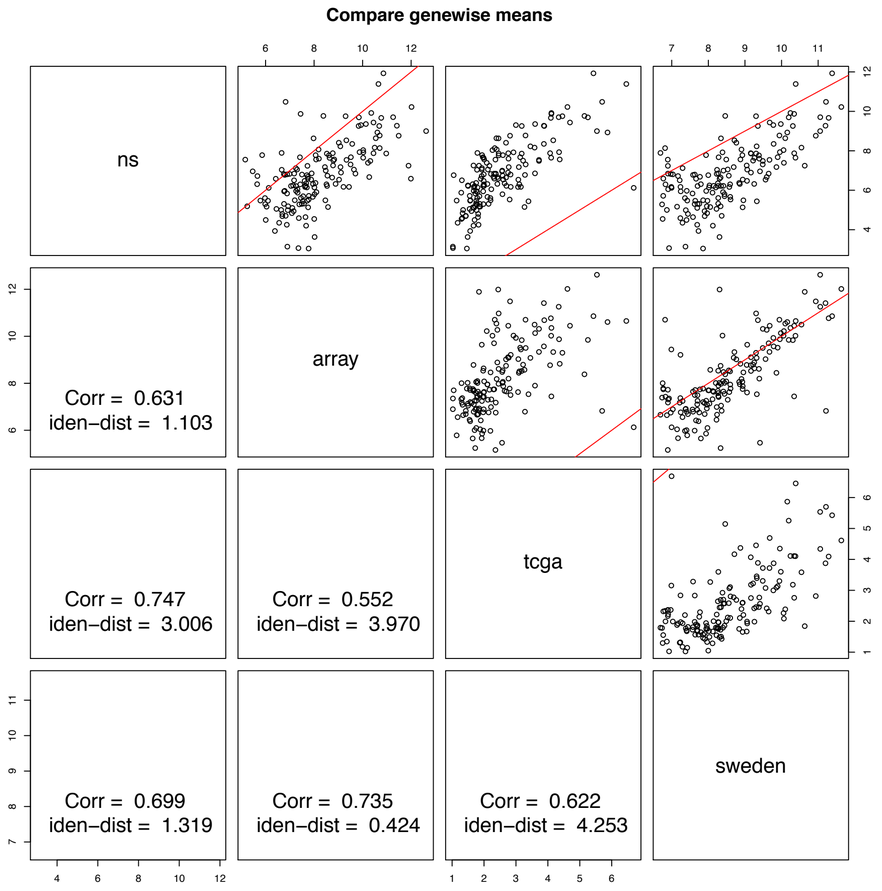
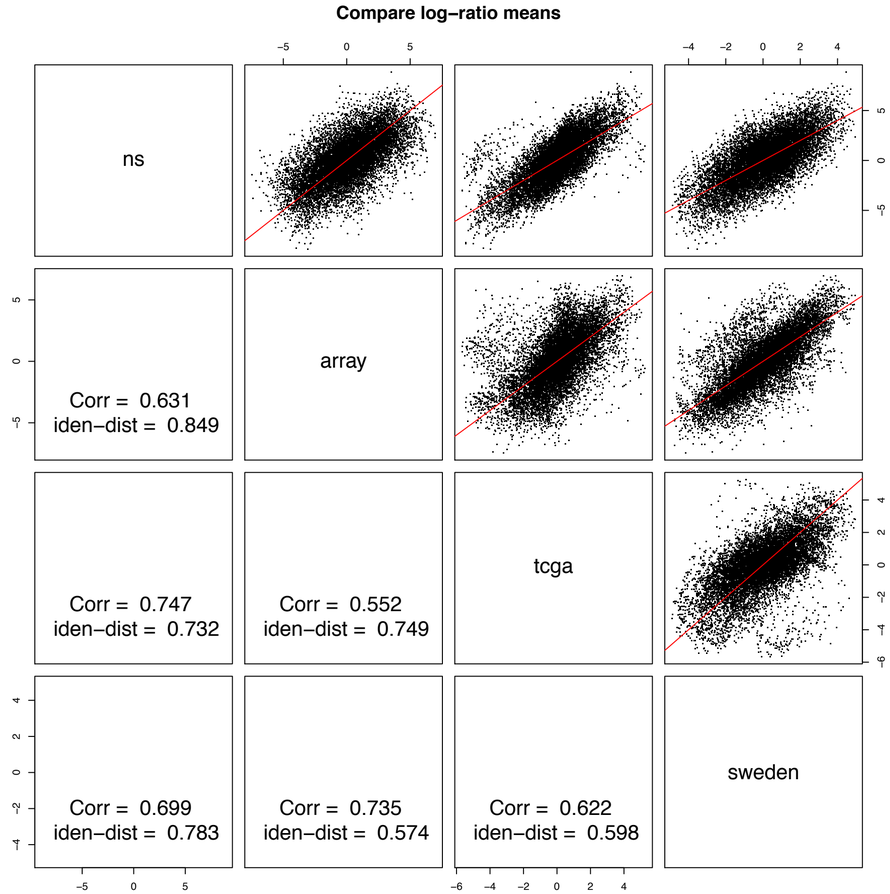
The solution is trivial.

- We have “standardised features” within every patient to build models

Log-ratio

log(gene A) – log(gene B)





The solution is trivial?

1. Single-patient prediction
2. Different scaling on genes between datasets
3. Concordance in feature selection/coefficient estimates