

# How to simulate a bad experiment?

Ho ho ho, I would like to simulate a very bad experiment. So far, the correlation between the expression level and the calculated FPKM generated from the FLUX-simulator has been too good to be true, around R-squared 0.8 to 0.9. I would like to generate an experiment full of biases (GC-bias) that has bad correlation between the gene expression level and observed reads number. Any suggestion on which parameters to tweak? Thanks.