

Noise while preparing library

I was trying to simulate two technical replicates from the same expression profiles. The noise between replicates A and B was smaller than I expected. I was trying to make it more realistic adjusting PCR probability but it didn't help. Increasing it from 0.1 to 1 of course made noise smaller, but decreasing this parameter, even to 0.00001, gave almost exactly the same noise level as at $p=0.1$. Actually, amount of fragments from certain gene in a cDNA library is very similar between PCR amplification, even for poorly expressed genes, eg. that have 2 copies. Is the little impact of PCR on amount of library fragments expected?

I would be grateful for a more through explanation on how PCR_DISTRIBUTION parameter affects the PCR efficiency. I thought that it goes along the explanation in Stolovitzky, G., & Cecchi, G. (1996). Efficiency of DNA replication in the polymerase chain reaction. PNAS, 93(23), 12947–52, (Fig. 3), but now I am somehow confused.

Thanks

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