Simultaneous quantification of multiple nucleic acid targets in complex rRNA mixtures using high density microarrays and nonspecific hybridization as a source of information

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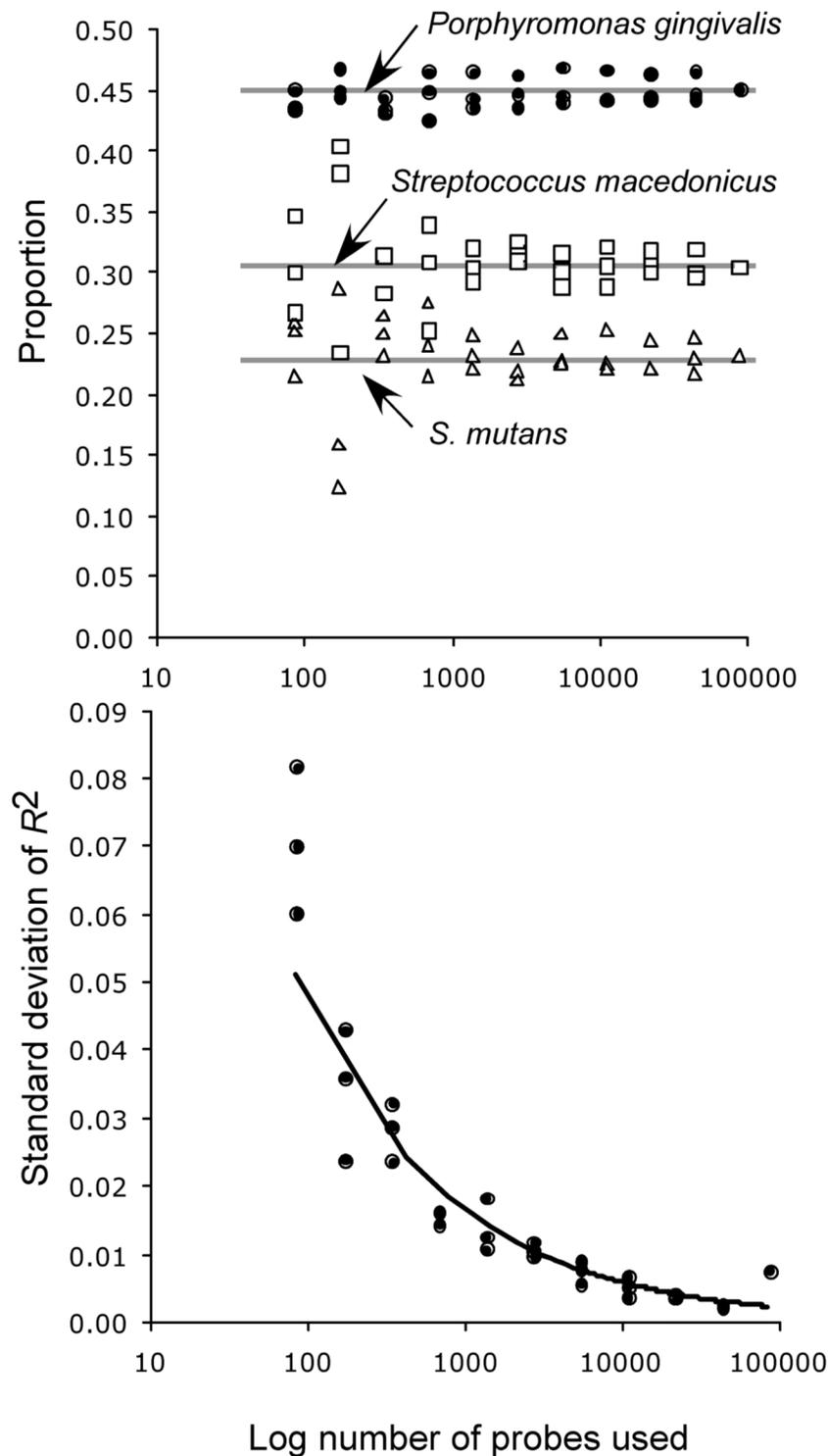PAN: panoble@washington.edu

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Figure 1. Effect of the number of oligonucleotide probes used by the numeric solution on predicted quantities of three different targets and their variability (see ref. 7 for details). Each datum point represents 10 replicated experiments randomly extracted from 86,652 probes. Results from the numeric solution were normalized to 1. Predicted proportions were more or less consistent until the number of oligonucleotide probes dropped to below ~1000 (upper panel). Standard deviation of the R^2 of the numeric solution decreased as the number of probes increased (lower panel)