

Supplemental Figures

Bayesian meta-analysis models for microarray data: a comparative study

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Figure S1 - Sensitivity analysis results for the two-study simulation data

Sensitivity analysis results for 3 and 40 degrees of freedom for the prior distributions of the slide and experiment variation parameters, ϕ_{jg}^2 and σ_{jg}^2 , respectively, for the two-study simulation data set with medium mean $\tau_g^2 = 0.3$ (differentially expressed); 0.03 (non-differentially expressed) and simulated percent differentially expressed genes $p_s = 10\%$. a) True integration-driven discovery rate ($tIDR$) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); b) True integration-driven revision rate ($tIRR$) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); c) The maximum number of true discovered genes versus posterior expected false discovery rate ($peFDR$) for the standardized expression integration model (blue circles), probability integration model (black diamonds), individual analyses of Study 1 (red checks) and Study 2 (green triangles).

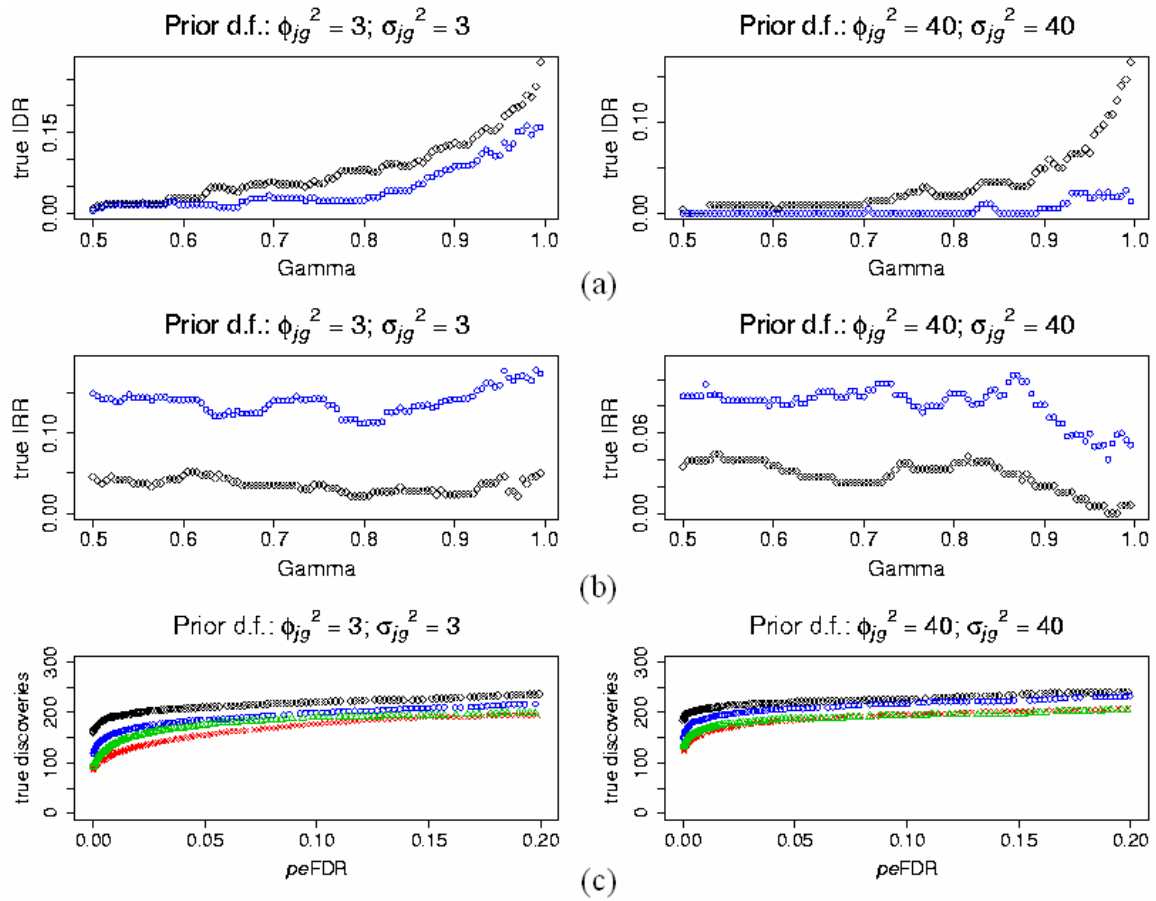


Figure S2 - Sensitivity analysis results for the five-study simulation data

Sensitivity analysis results for 3 and 40 degrees of freedom for the prior distributions of the slide and experiment variation parameters, ϕ_{jg}^2 and σ_{jg}^2 , respectively, for the five-study simulation data set with medium mean $\tau_g^2 = 0.3$ (differentially expressed); 0.03 (non-differentially expressed) and simulated percent differentially expressed genes $p_s = 10\%$. a) True integration-driven discovery rate ($tIDR$) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); b) True integration-driven revision rate ($tIRR$) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); c) The maximum number of true discovered genes versus posterior expected false discovery rate ($peFDR$) for the standardized expression integration model (blue circles), probability integration model (black diamonds), individual analyses of Study 1 (red checks), Study 2 (green triangles), Study 3 (turquoise pluses), Study 4 (pink inverted triangles) and Study 5 (gold stars).

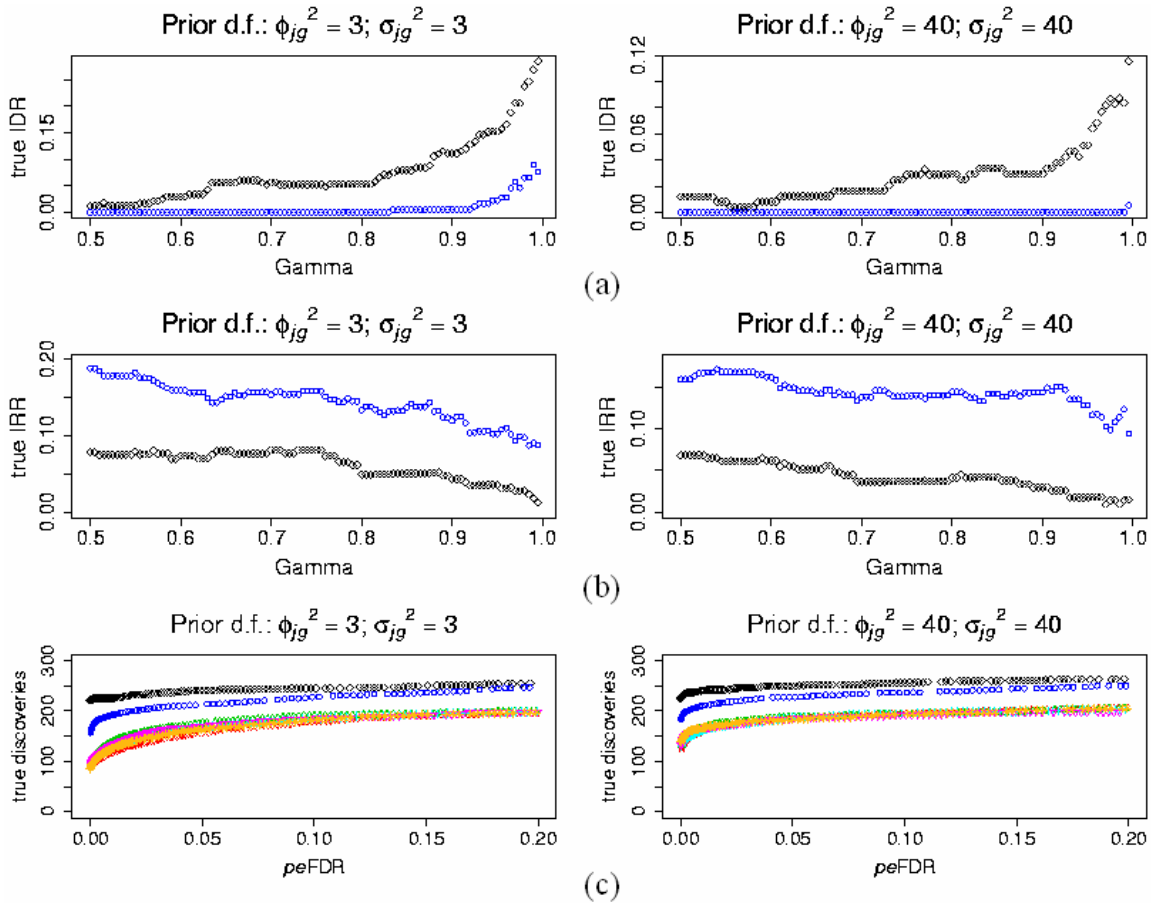


Figure S3 - Sensitivity analysis results for the biological data

Sensitivity analysis results for 3 and 40 degrees of freedom for the prior distributions of the slide and experiment variation parameters, ϕ_{jg}^2 and σ_{jg}^2 , respectively, for the *B. subtilis* mutant and induction biological study data. a) Integration-driven discovery rate (IDR) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); b) Integration-driven revision rate (IRR) versus threshold values of posterior probability of differential expression $\gamma \geq 0.50$, for the standardized expression integration model (blue circles) and probability integration model (black diamonds); c) The maximum number of differentially expressed genes versus posterior expected false discovery rate (*peFDR*) for the standardized expression integration model (blue circles), probability integration model (black diamonds), individual analyses of *B. subtilis* mutant study (red checks) and induction study (green triangles).

