Supplementary File 1 of the article
"Poisson-Tweedie mixed-effects model: a flexible approach for the analysis of longitudinal RNA-seq data"

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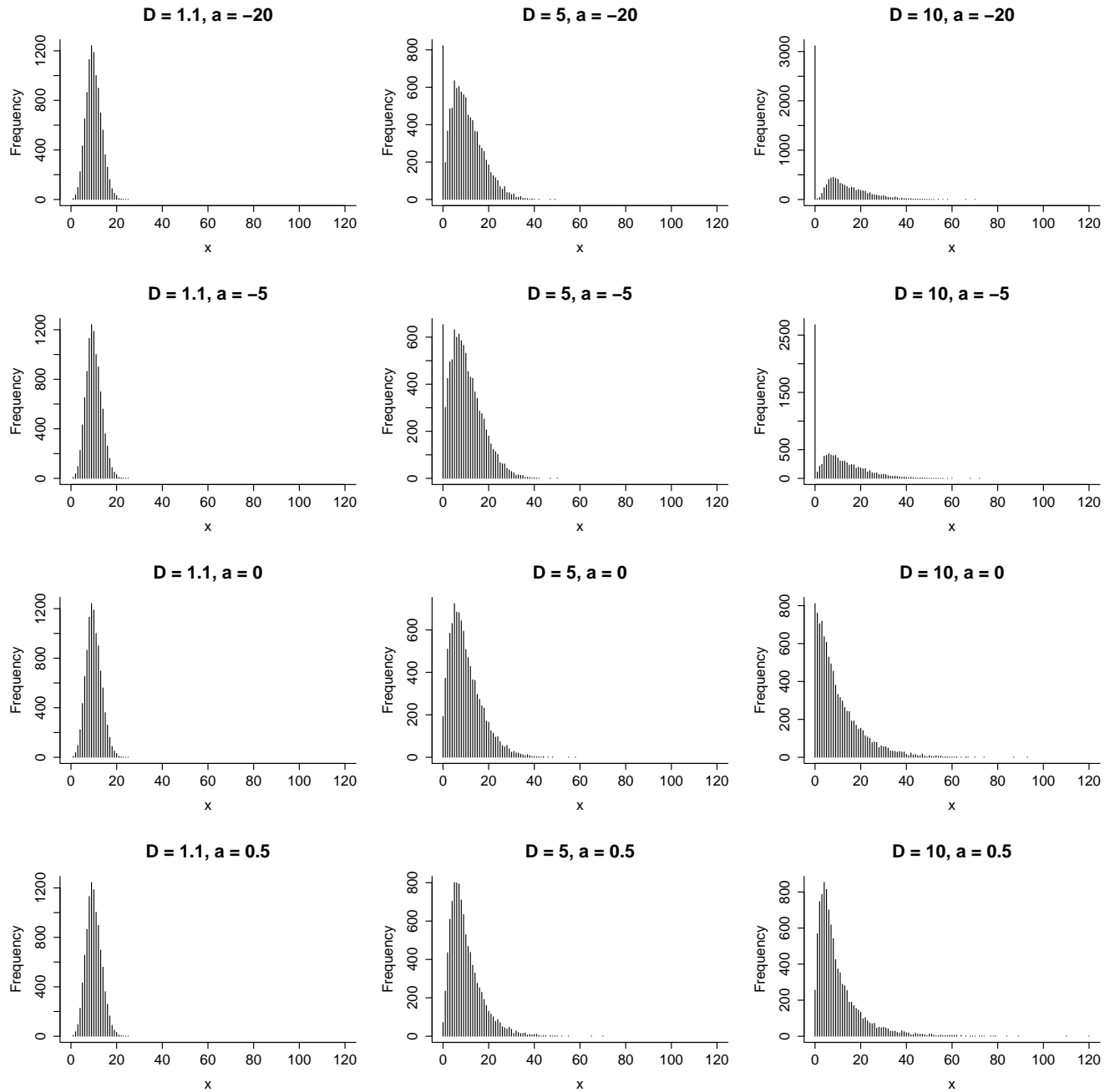
1 Supplementary Figures

Figure 1: Plots of the empirical probability mass function of the PT distribution for different values of the dispersion parameter D (1.1, 5, 10) and power parameter a (-20, 5, 0, 0.5) for fixed mean $\mu = 10$. Each plot is obtained based on 10000 random draws from the PT pmf.

2 Supplementary Tables

Table 1: Mean computing time (in minutes) in Simulation C. ptmixed and ShrinkBayes were fitted using 15 cores on a processor with 60 cores and 2.20 GHz CPU. All other methods, being much faster, were fitted using 1 core on the same processor.

Method	n = 10	n = 20	n = 40
DESeq2	0.05	0.07	0.09
DESeq2+FE	0.06	0.11	0.48
edgeR	0.01	0.02	0.04
edgeR+FE	0.02	0.06	0.31
limma-voom	0.00	0.00	0.00
limma-voom+FE	0.00	0.00	0.01
MaSigPro	0.15	0.17	0.21
ptmixed	30.61	59.20	117.68
ShrinkBayes	139.86	26.59	25.78
tweeDEseq	2.51	4.41	7.89

Table 2: Mean computing time (in minutes) in Simulation D. ptmixed and ShrinkBayes were fitted using 15 cores on a processor with 60 cores and 2.20 GHz CPU. All other methods, being much faster, were fitted using 1 core on the same processor.

Method	n = 10	n = 20	n = 40
DESeq2	0.06	0.07	0.09
DESeq2+FE	0.06	0.11	0.48
edgeR	0.01	0.02	0.04
edgeR+FE	0.03	0.07	0.33
limma-voom	0.00	0.00	0.00
limma-voom+FE	0.00	0.00	0.01
MaSigPro	0.12	0.14	0.18
ptmixed	30.32	59.39	118.94
ShrinkBayes	72.27	47.64	18.72
tweeDEseq	2.18	3.78	6.96