**Supplemental Table 1. Summary of Parameter Settings and Recommendations**

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| **Parameters** | **Default**  | **Description/Rationale** | **Recommendations** |
| Methods | ComBat | *ComBat* is relatively quick and can be selected as comparison method or used to investigate suitable values for the range of *M*. *ComBat* usually has lower power and higher type I error rate than *BRIDGE.* | Four methods (*BRIDGE-1, BRIDGE-2, ComBat, Longitudinal ComBat*) are provided. Please refer to Table 1 to estimate the running time before choosing. *BRIDGE-1* is preferred if multiplicative batch effect is >= 1; *BRIDGE-2* is preferred if multiplicative batch effect < 1; relatively quick and can be selected as comparison method or used to investigate suitable values for the range of *M*; *Longitudinal ComBat* best controls the type-1 error rate but is computationally expensive. |
| Multiplicative Batch Effect | 0.93 | The empirical Bayes estimate of the multiplicative batch effect from a publicly available rheumatoid arthritis data set consisting of longitudinal whole blood RNAseq data used in Xia et al. (Xia et al., 2021)  | Consider using this default value if batch 2 has better quality; if batch 1 is better, consider using 1/0.93; or use 0.8-1.2 to be more general. |
| Additive Batch Effect  | 3.0 | Our exploratory analyses of *pwrBRIDGE* suggest that the additive batch effect parameter has little effect on statistical power for a fixed *M,* and thus users of *pwrBRIDGE* can leave this parameter at its default value with little impact on the results | Use default |
| Effect Size  | 0.4 | The effect size (logFC) for three top-ranked differentially expressed genes, C4A, C4B, and GFAP in ROSMAP, is around 1 (e.g., 1.05, 1.00, 0.89, respectively) between AD and control. We set a lower effect size (e.g., 0.4) to detect difference between AD and aMCI. The latter represents an intermediate stage between normal aging and AD. | Study specific |
| Standard Deviation for timepoint 1 or 2 | 1.0 | The standard deviation of gene expression for each of the previously mentioned genes is around 0.25 in RNA-seq derived from post-mortem samples of the dorsolateral prefrontal cortex area. As whole blood is likely a more heterogeneous tissue type, we set at the standard deviation for timepoint 1 or 2 assuming a slightly higher value of 1.0. | Study specific |
| Within-subject Correlation between Timepoint | 0.9 | The empirical Bayes estimate of the within-subject correlation of time from a publicly available Rheumatoid arthritis data set consisting of longitudinal whole blood RNAseq used in Xia et al. (Xia et al., 2021).  | Study specific |
| Within-subject Correlation between Batch | 0.9 | The empirical Bayes estimate of the within-subject correlation of batch from a publicly available Rheumatoid arthritis data set consisting of longitudinal whole blood RNAseq used in Xia et al. (Xia et al., 2021)  | Consider using as default value if designing an RNAseq study. |
| Total Genes | 1000 | The total number of genes/features that will be tested for their difference between timepoints. A sufficient number of total genes is needed for information borrowing via empirical Bayes step.  | Study dependent. Note increasing the number of total genes will increase the running time. |
| Total Differential Genes | 200 | Total number of genes expected to be differentially expressed between timepoints 1 and 2. Our hypothetical study assumed 200 to allow for a sufficient number of genes in which to calculate power and type-I error rate. | Study and context dependent.  |
| Total Participants | 100 | Total number of participants, *N*, for the study being planned. Must be > *M.* | Consider use default |
| Bridging sample size  | [5,10,15,20,25,30,35,40] | The assumed bridging sample sizes, *M*, to compute power and type 1 error rate. The number of elements in the set will affect the running time for *BRIDGE-1, BRIDGE-2, ComBat* and *Longitudinal ComBat*. The bridging sample size affects the precision of estimates of batch effects. | >5 |
| Simulations | 30 | Number of simulations in which to estimate power and type 1-error rates for the suppled value(s) of *M*. Variance of estimates of power and type 1 error rates stabilizes around 30 | Consider using as default |