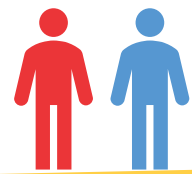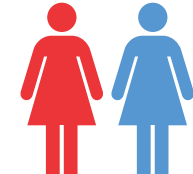# Our Personalised approach

Preprocess data

Fit GP models independently to each probe-set of case-control pair #1

Fit GP models independently to each probe-set of case-control pair #N

Time-window analysis

Time-course analysis

Time-course analysis

Time-window analysis

Identify differentially expressed probe-sets using BF-score for case-control pair #1, map probe-sets to genes, and compute overlaps with pathways

Identify differentially expressed probe-sets using BF-score for case-control pair #N, map probe-sets to genes, and compute overlaps with pathways

Use the KL-score to identify differentially expressed probe-sets, map probe-sets to genes, and compute pathway overlaps in a given time window

Use the KL-score to identify differentially expressed probe-sets, map probe-sets to genes, and compute pathway overlaps in a given time window
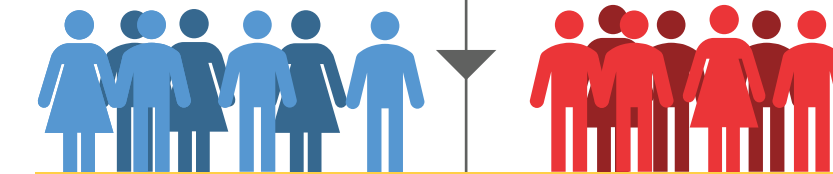
Combine using adjusted geometric mean and compute statistical significance using permutation test

Report significant pathways after FDR correction

Combined method

Preprocess data

Fit GP models independently to each probe-set of combined data from all cases and controls

Time-course analysis

Time-window analysis

Identify differentially expressed probe-sets using BF-score, map probe-sets to genes, and compute overlaps with pathways using e.g., Fisher's test

Use the KL-score to identify differentially expressed probe-sets, map probe-sets to genes, and compute overlaps with pathways using e.g., Fisher's test

Report significant pathways after FDR correction