

Single-Omics

RNA-seq

Gene Quantification

FeatureCounts

Batch Removal

RUVSeq

Normalization

TMM UQua FQua

Differential Expression

NOISeq DESeq2 edgeR

NOISeq

Filtering

ChIP-seq

Peak Calling

csaw

Differential Binding

NOISeq DESeq2 edgeR

ATAC-seq

Region Detection

DEScan2

Batch Removal

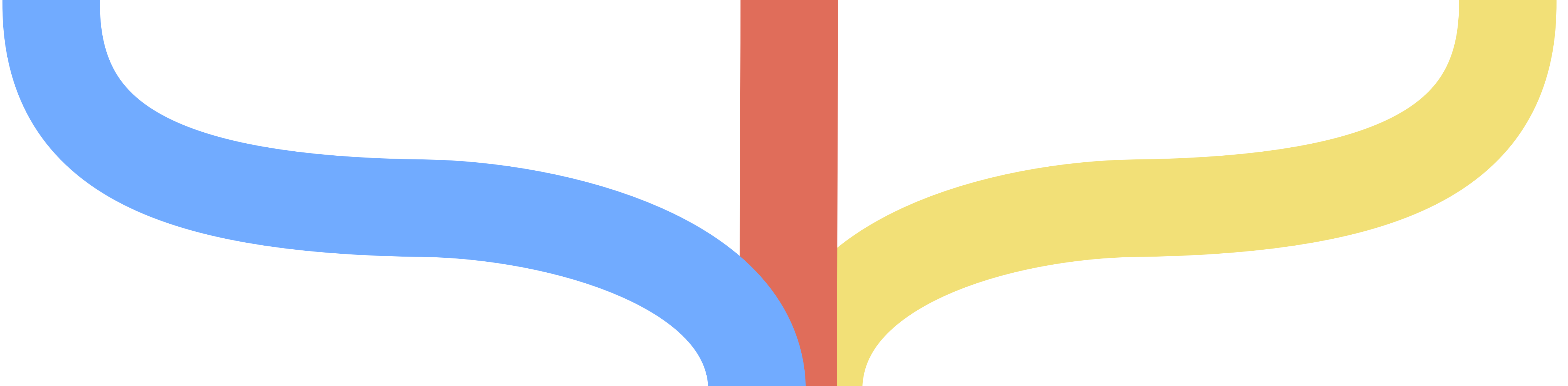
RUVSeq

Normalization

TMM UQua FQua

Differential Enrichment

NOISeq DESeq2 edgeR



Multi-Omics

Functional Analysis

Pathway

gProfiler clusterProfiler

Gene Ontology

gProfiler clusterProfiler

Annotation

Peak-Gene

ChIPpeakAnno