Top level

Genotypes -> Missing value imputation -> SML analysis

Phenotypes -> Scale environments -> Calculate mean

\[ \Delta r^2 \]

Post-processing visualisation

Local summation -> Genetic map -> QTL profile

SML analysis

Processed genotypes -> Repeated bootstrap sample & test

Create bootstrap splits

Training data -> Test data

Train model

Model = Evaluate model

\[ \Delta r^2 \]

Calculate bootstrap mean

\[ \Delta r^2 \]