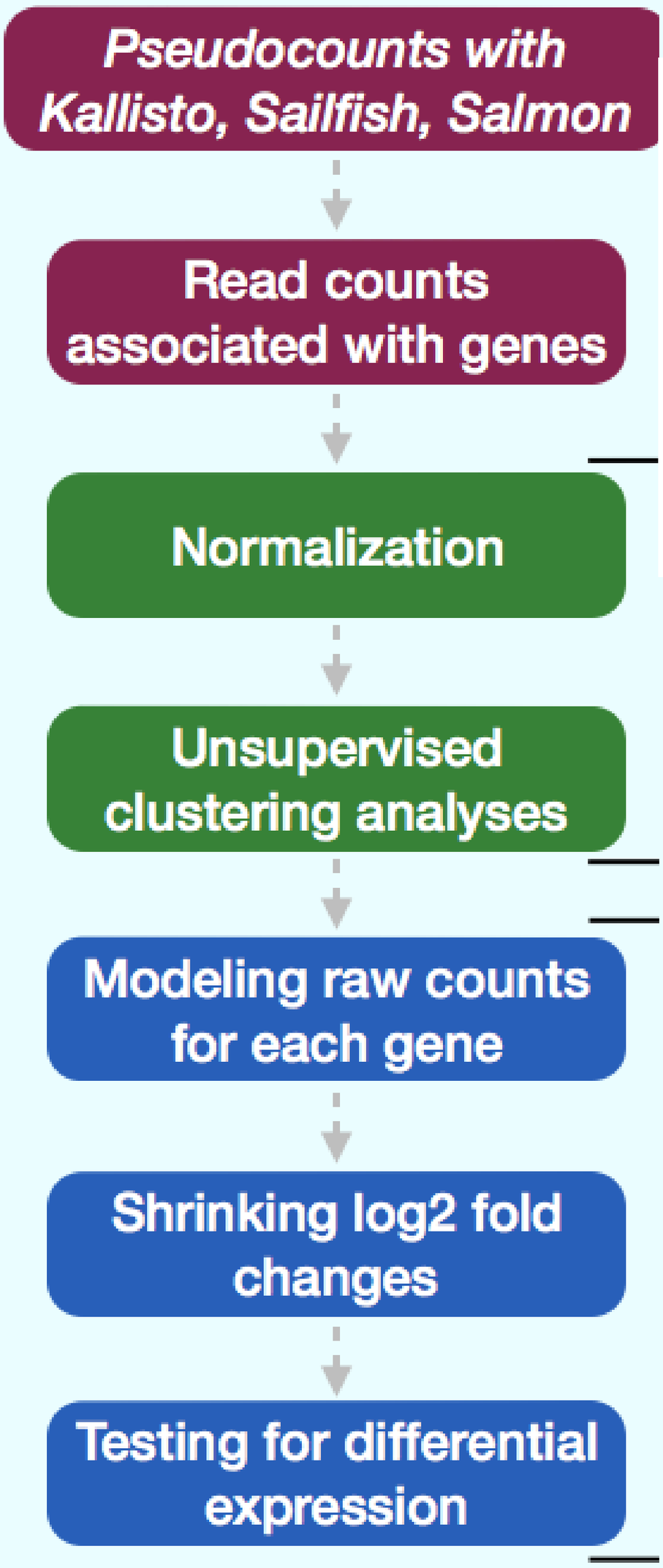
Python Port of DESEQ2

What is DESeq2?

DESeq2 is a tool used after alignment/quantification to analyze RNA-seq count data. Its goal is to find which genes change expression between conditions (e.g., treated vs. control). It normalizes sequencing depth, models counts with a negative binomial distribution, and identifies genes that are significantly up- or down-regulated.



Metric	Value
Size Factor Correlation	1.000000
Size Factor MAE	1.71e-15
Dispersion Correlation (log)	0.4949
Median Dispersion Ratio (Py/R)	0.68x
LFC Correlation (High Expr)	0.9530
Significant Gene Match (%)	98.7%
Top-500 DE Gene Overlap	80.4%
P-value Correlation	0.6897
LFC Sign Agreement	99.7%
LFC MAE	0.1102
LFC RMSE	0.3027
BaseMean Correlation	1.0000
Spearman (p-values)	0.9874
Spearman (|LFC|)	0.9595

DESeq2 in the RNA-Seq Pipeline

DESeq2 normalizes counts using size factors, estimates gene dispersions, fits a smooth dispersion trend, shrinks dispersions toward this trend, and then applies a Negative Binomial model to compute log2 fold changes, p-values, and adjusted p-values. Then an optional LFC shrinkage provides more stable effect-size estimates for visualization.