Introduction to single-cell RNA-seq analysis - Data sets and analyses

November 2025

Data sets

- Childhood acute lymphoblastic leukemia (cALL)
  - Caron et al. 2020
  - The most common pediatric cancer
  - Characterized by bone marrow lymphoid precursors that acquire genetic alterations,resulting in disrupted maturation and uncontrollable proliferation
  - Up to 85–90% of patients are cured
  - Others do not respond to treatment or relapse and die
  - **Aim**: characterise the heterogeneity of gene expression at the cell level, within and between patients
  - **cells**: Bone Marrow Mononuclear cells (BMMCs)

Samples

Five types of sample are considered:

- B-ALL patients:
  - **'ETV6-RUNX1'**, or 't(12;21)', four patients
  - **'HHD'**, or 'High hyper diploid', two patients
- T-ALL patients
  - **'PRE-T'**, two patients
- Healthy controls,
  - **Healthy pediatric controls**, three individuals

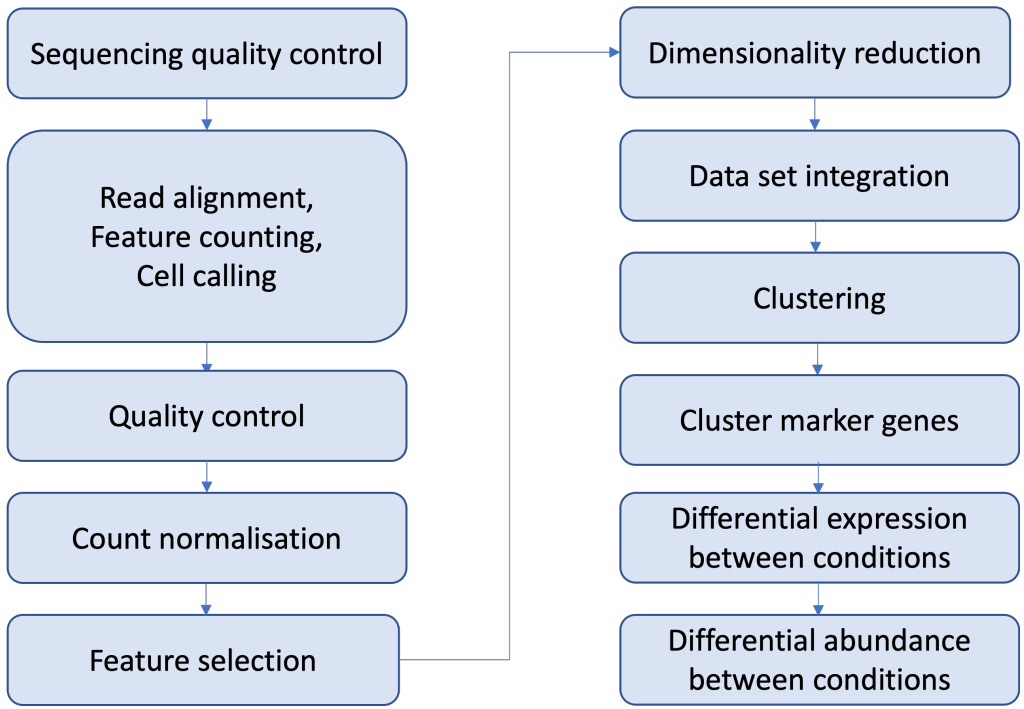
As the study aims at identifying cell populations, large numbers of cells were sequenced with the droplet-based 10x Chromium assay.

Analyses

We will follow several steps:

- Sequencing quality check
- Alignment of reads to the human genome with 10x software cellranger
- Quality control (filter poor quality cells and remove uninformative genes)
- UMI count normalisation
- Feature selection and dimensionality reduction
- Data set integration
- Clustering
- Identification of cluster marker genes
- Differential expression and abundance between conditions

Workflow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Feature counting,
Cell calling
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Count normalisation
Feature selection
Dimensionality reduction
Data set integration
Clustering
Cluster marker genes
Differential expression
between conditions
Differential abundance
between conditions

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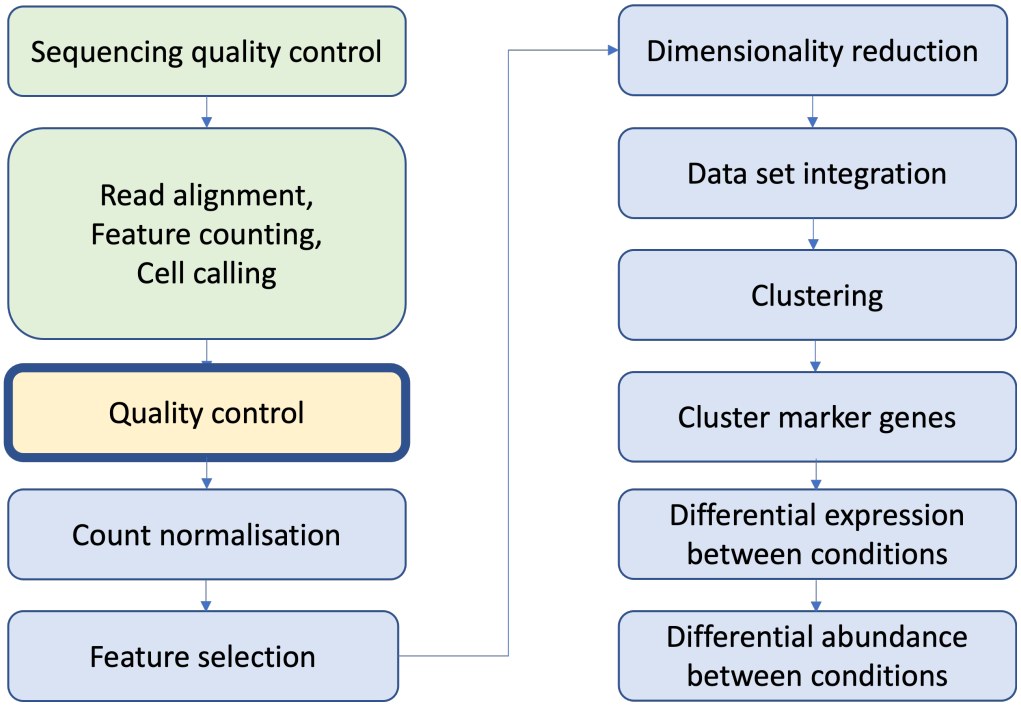
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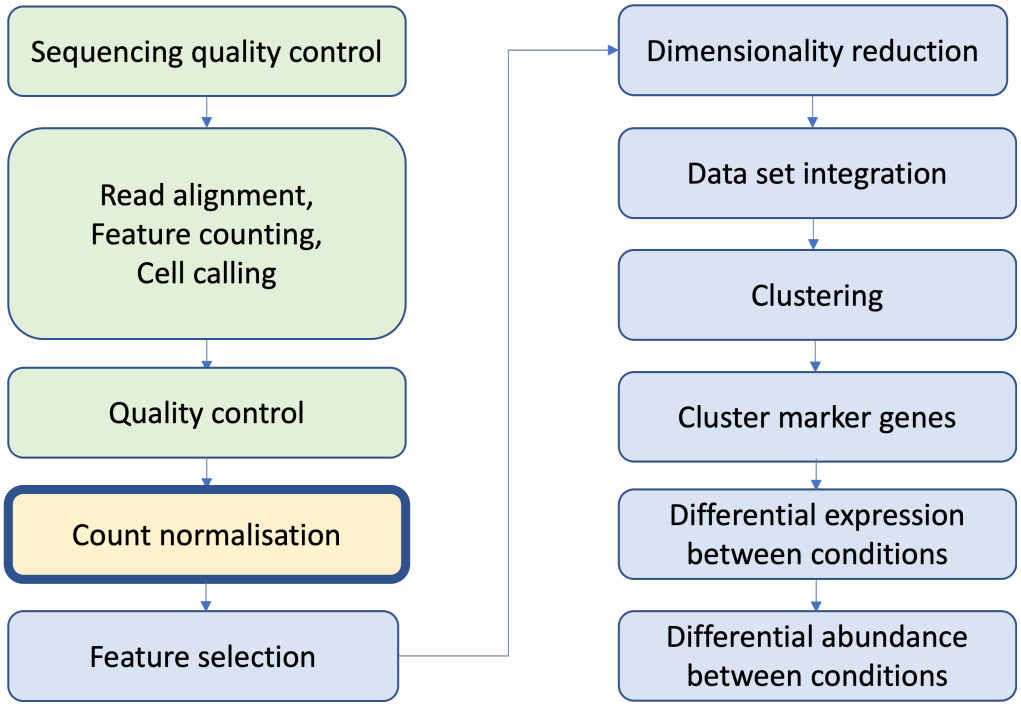
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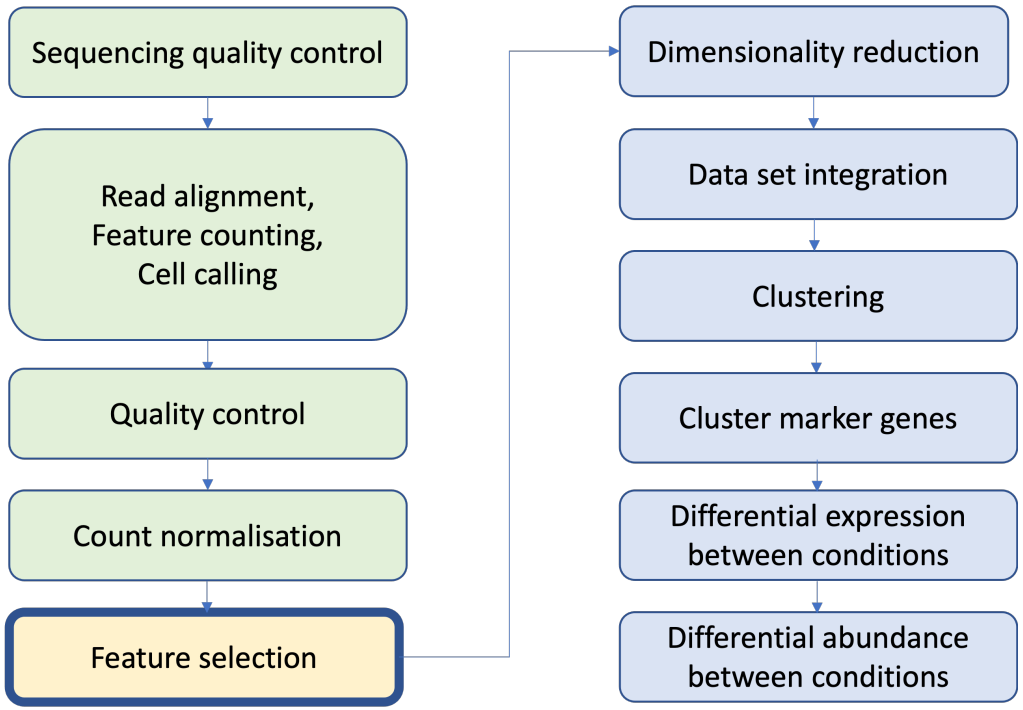
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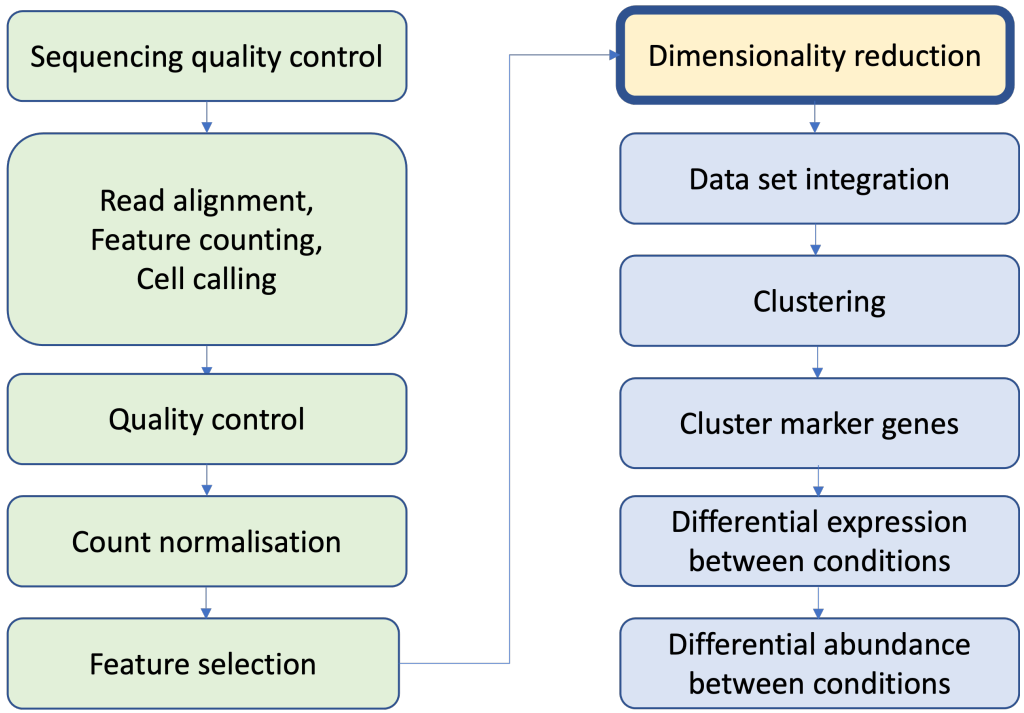
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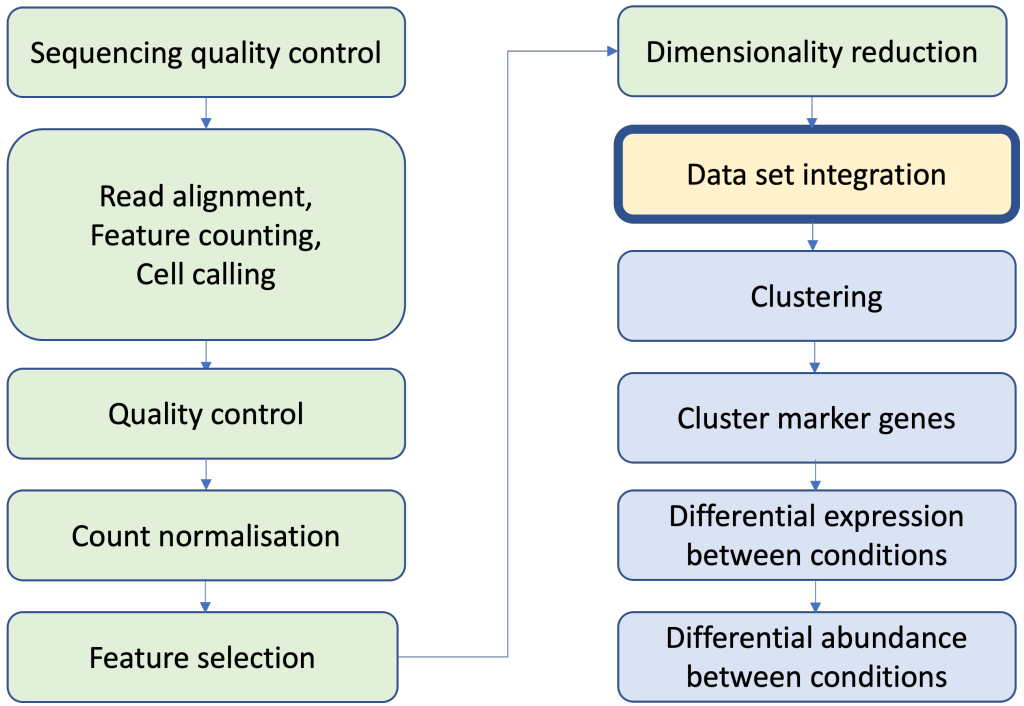
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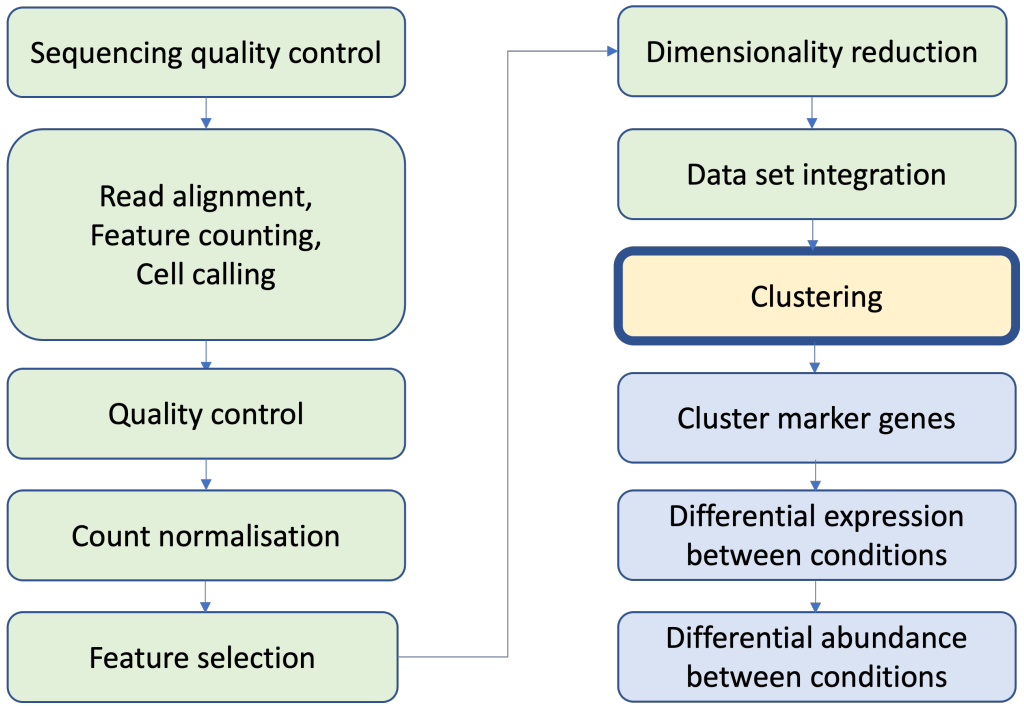
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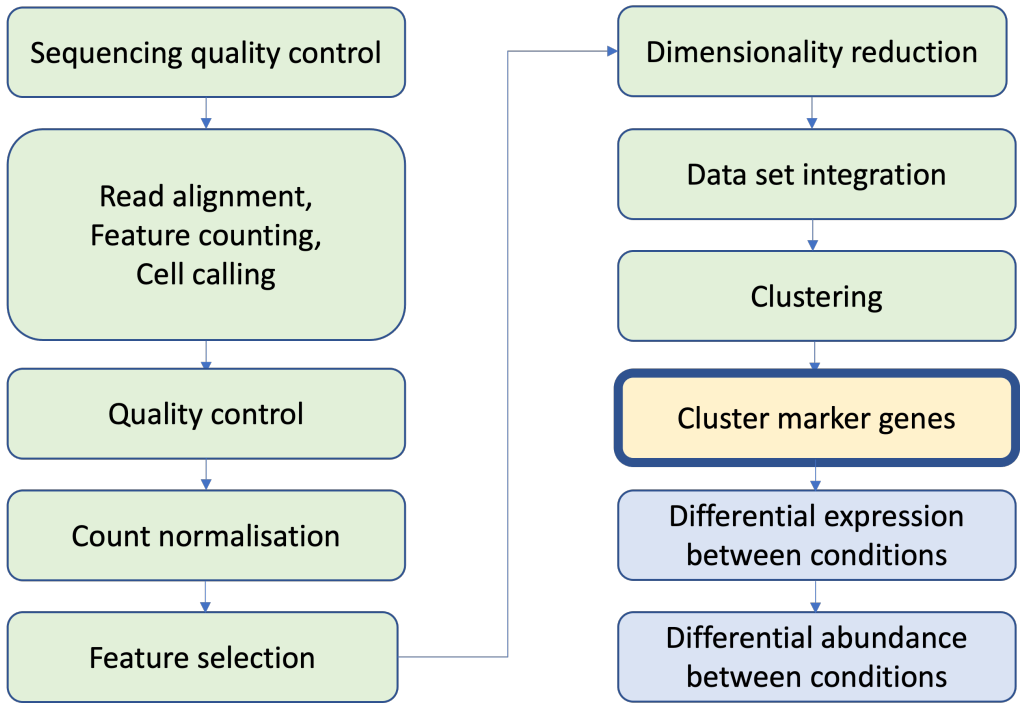
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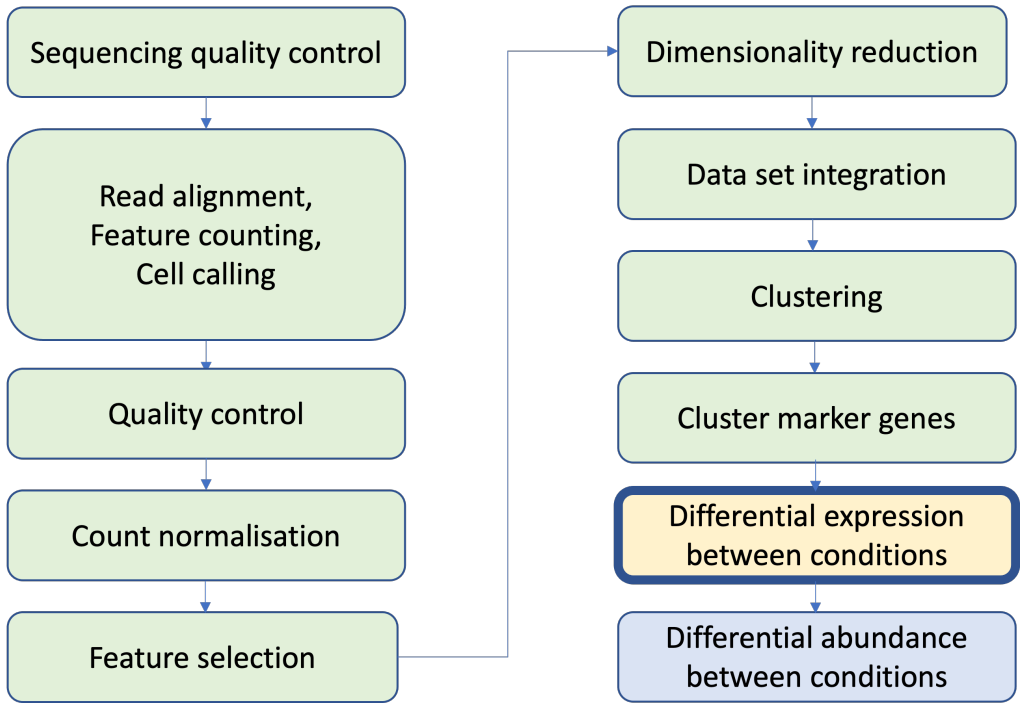
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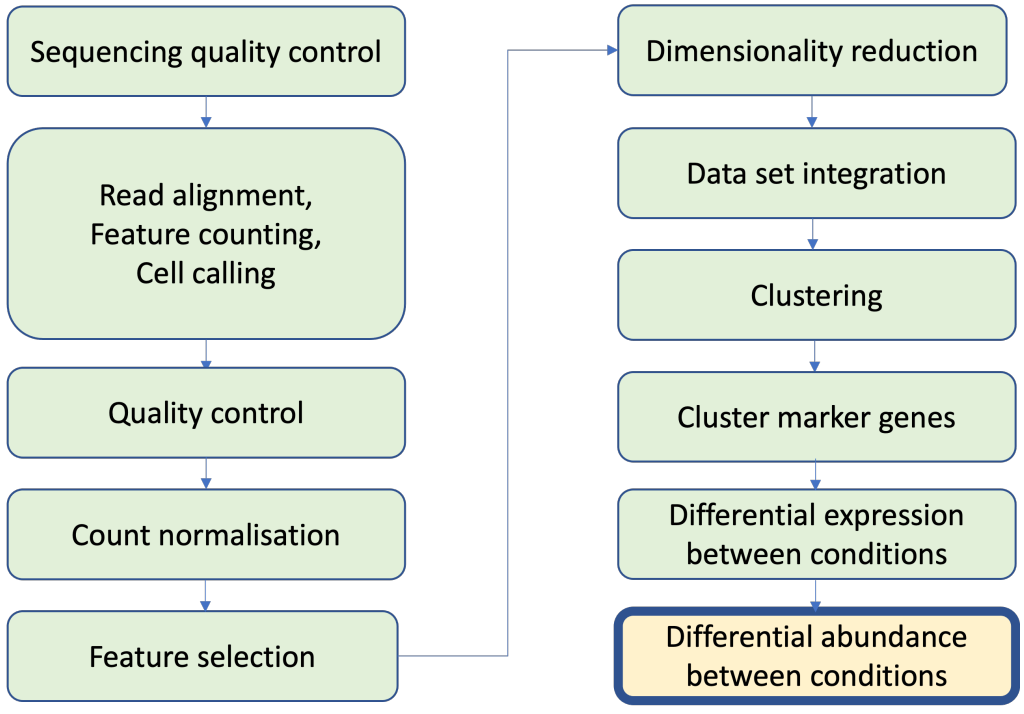
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