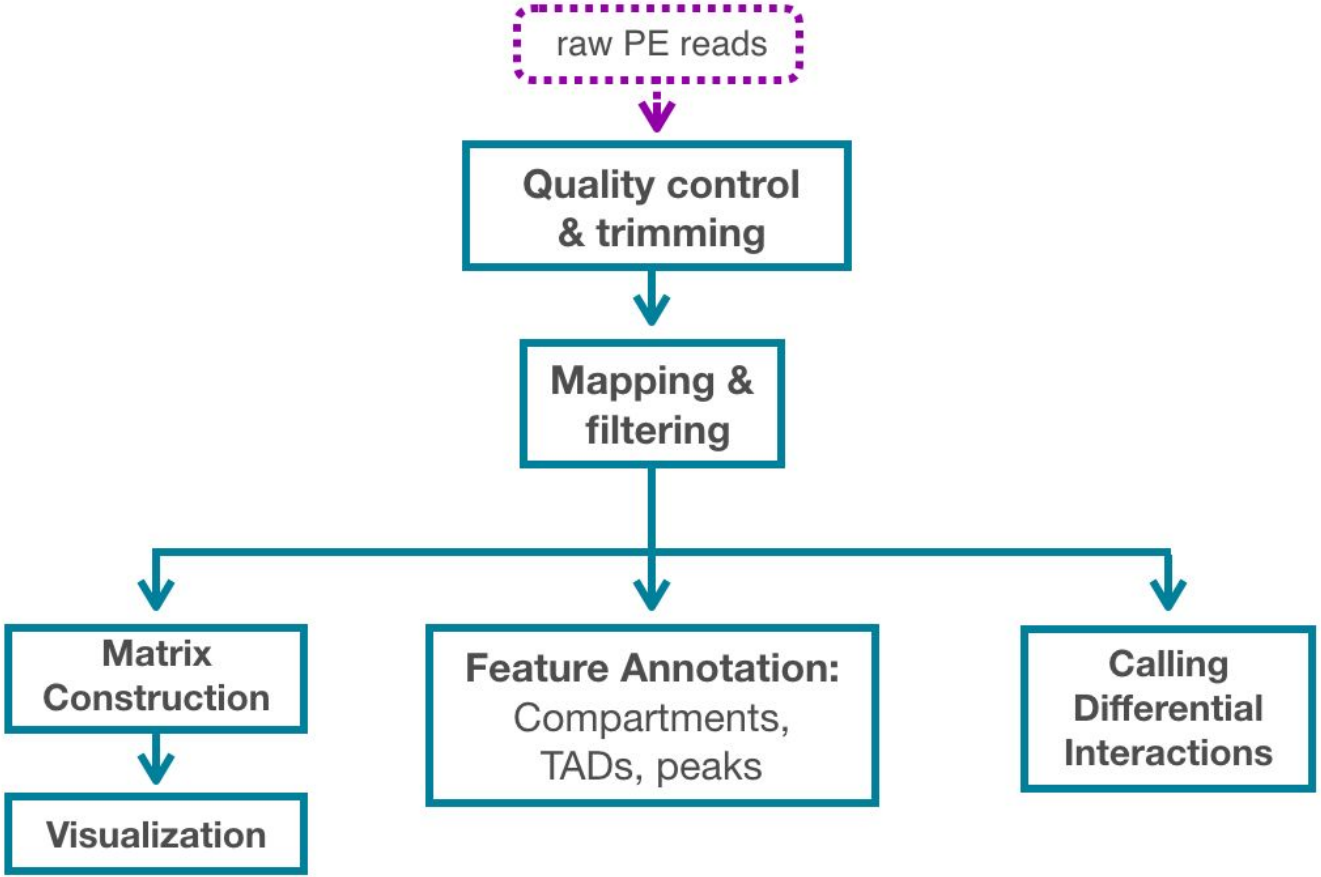
Matrix Visualization

Recap


raw PE reads
Quality control & trimming
Mapping & filtering
Matrix Construction
Visualization
Feature Annotation: Compartments, TADs, peaks
Calling Differential Interactions

Learning objectives

- Interpret a Hi-C heatmap
- Use visualization to explore different chromatin features
- Get acquainted with different visualization tools

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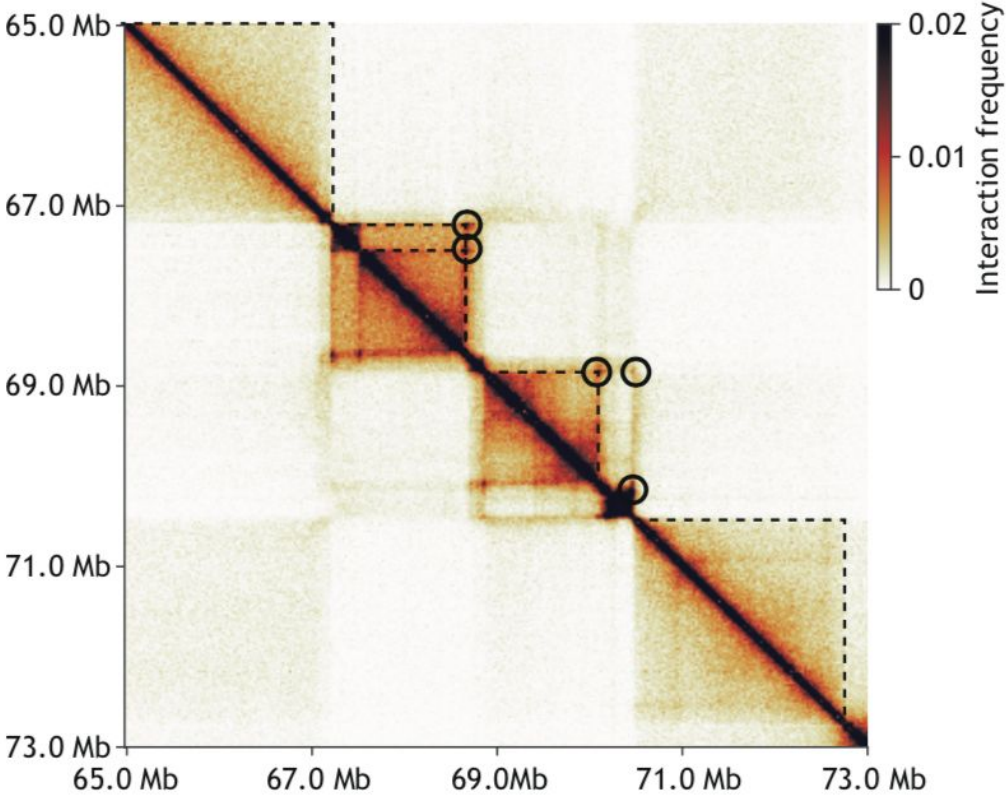
REVIEW

Visualising three-dimensional genome organisation in two dimensions

Elizabeth Ing-Simmons* and Juan M. Vaquerizas*

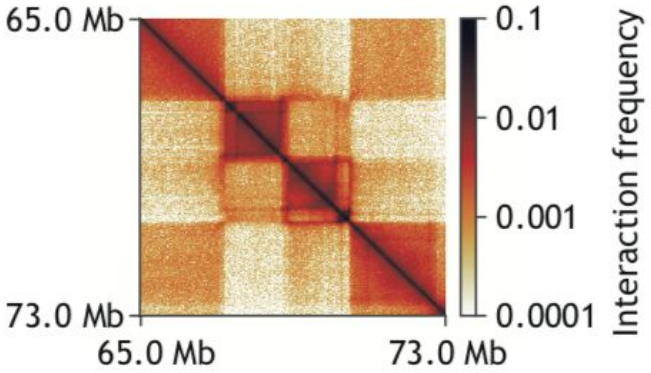
Interpreting a HiC heatmap

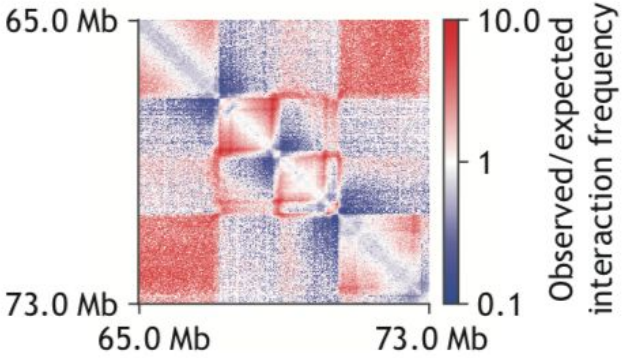
- Axes represent genomic coordinates
- Interaction frequency is mapped to color
- Diagonal has higher interaction frequency



Common scales and data transformations

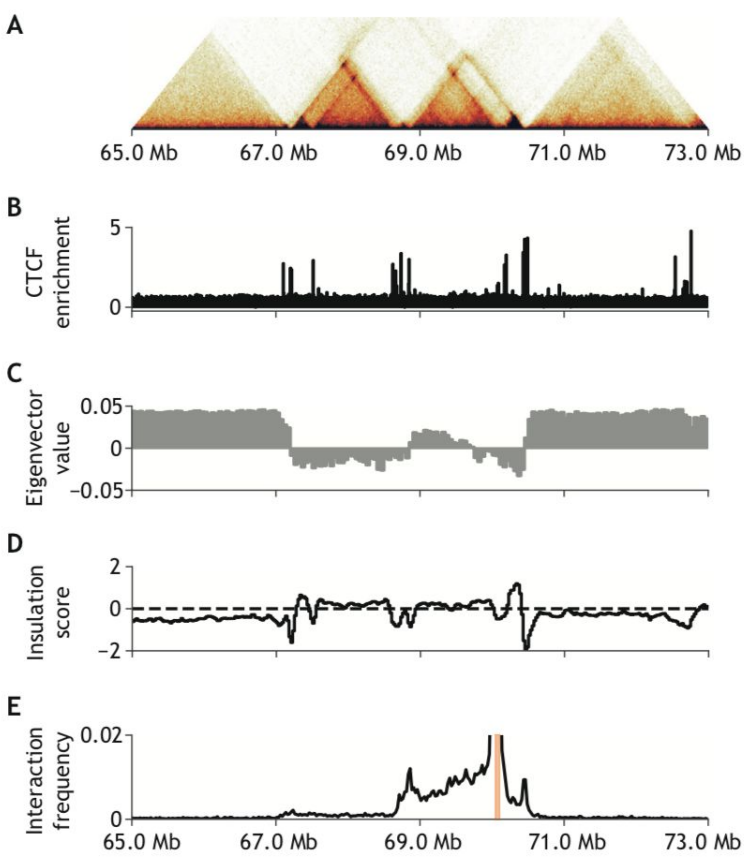
- HiC data varies across orders of magnitude
  - Linear color scale only works for a range of interaction frequencies
  - Min and max values affect which features are discernible
- To emphasize both near and far diagonal features:
  - Log scale
  - Distance normalization
- Comparative
  - LogFC
  - Between matrix normalization





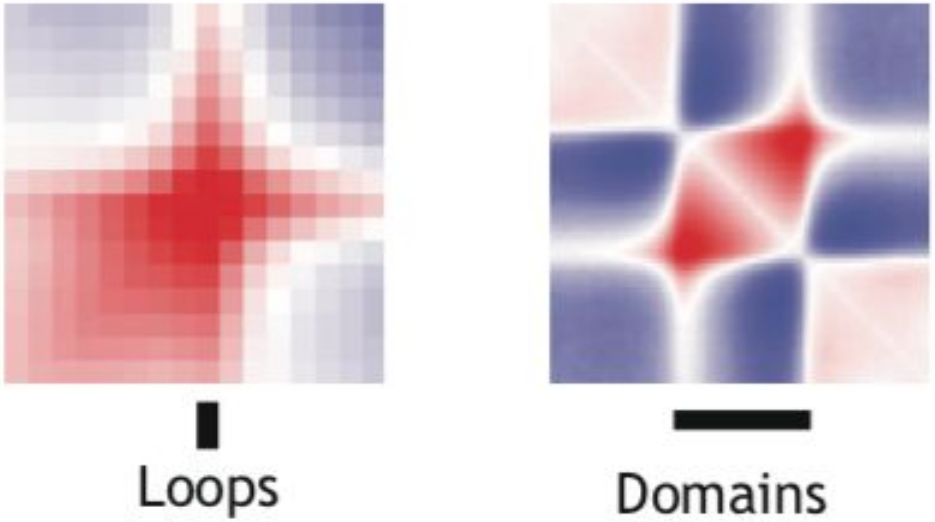
Integration with other tracks

- Half matrix
- Architectural proteins
- Compartments
- TADs
- Viewpoint



Aggregate analysis

- Global overview
- QC
- Comparison of overall features



Common HiC data visualization tools

- Heatmap
  - **Juicebox**, HiGlass, HiCExplorer
- Triangular heatmap
  - HiGlass, WashU epigenome browser
- Linear tracks
  - UCSC genome browser, HiCExplorer
- Arcs
  - WashU epigenome browser

Command Line Tools

Use in reproducible workflows

- HiCexplorer
- HiPlotter

Practical

- Juicebox
- HiCExplorer

Resources

- http://aidenlab.org/juicebox/
- http://higlass.io/
- https://hicexplorer.readthedocs.io/en/latest/