

Exploring genomic interactions in 3D using Hi-C

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Overview

1 Introduction

- Why we study 3D genome organization?
- How Hi-C works
- Representative Hi-C results

2 Methods

3 Results

4 Conclusion

Why we study 3D genome organization?

- How chromosomes are organized?
- Where active genes are located?
- Is there a tendency for co-regulated genes to co-localize in the nucleus?
- How important and how frequent *cis* and *trans* genomic interactions are for gene transcription?

How Hi-C works

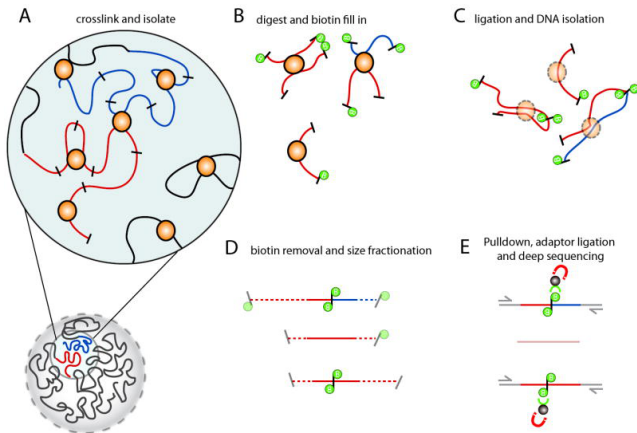


Figure : An overview of the Hi-C technique. Source: Belton, J.-M. *et al. Methods* 58, 268–276 (2012).

Representative Hi-C results (1MB resolution)

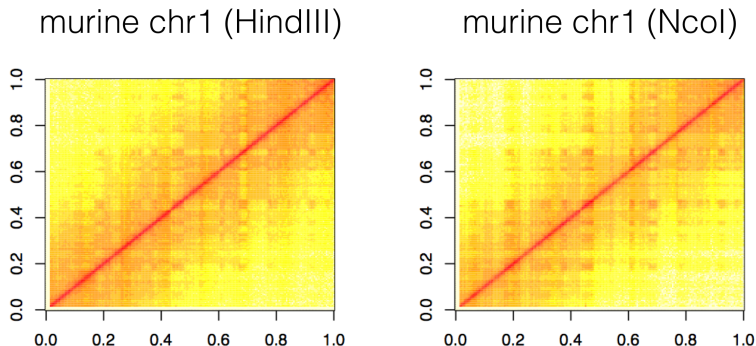
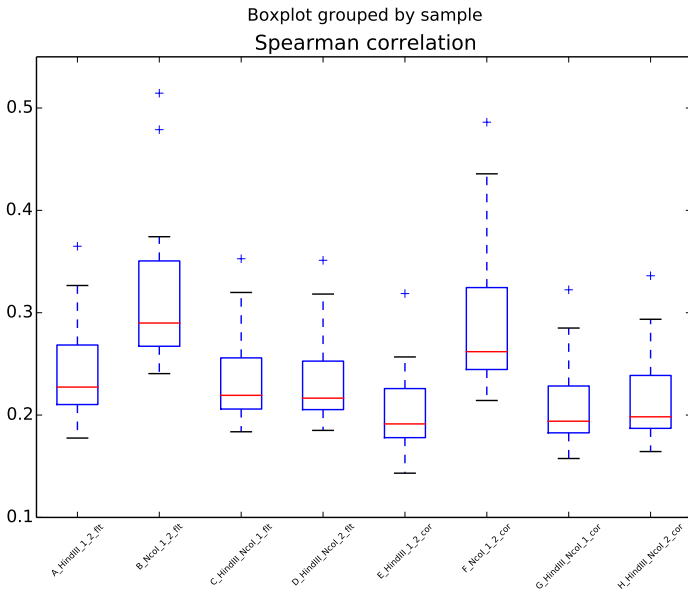


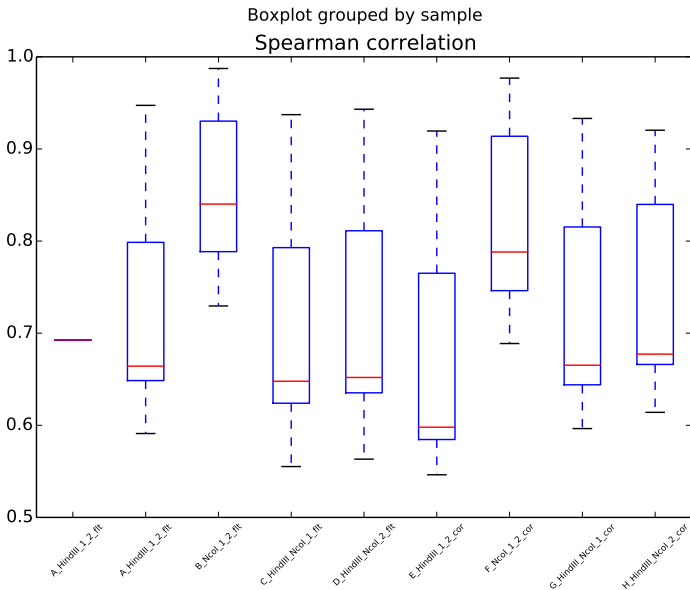
Figure : Heatmaps depicting genomic interactions in murine chromosome 1

- 1 Python script using Numpy to generate and export genome interaction matrix.
- 2 R scripts and Python scripts (matplotlib) to generate heatmap.
- 3 Python Pandas to generate boxplots for correlations.

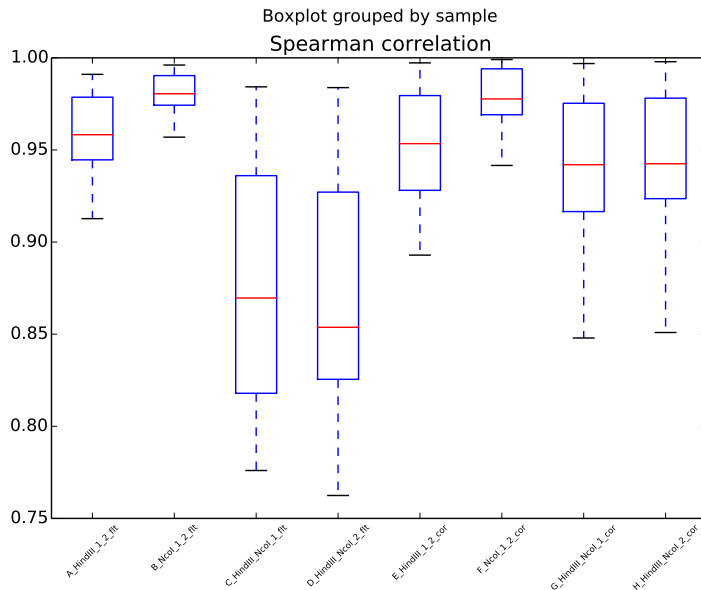
Correlation of Hi-C results (HindIII vs. NcoI, 128kb)



Correlation of Hi-C results (HindIII vs. NcoI, 1024kb)



Correlation of Hi-C results (HindIII vs. NcoI, 4096kb)



Conclusion

- New methods are required to achieve even better consistency of results in replicates.
- Main bottleneck in scripts → IO
- Pandas and matplotlib very interesting but:
 - Need time to learn
 - Problems with running on cluster. Many requirements.
 - Not easily customizable graphs.

Q & A