

TADbit

Comparing experiments

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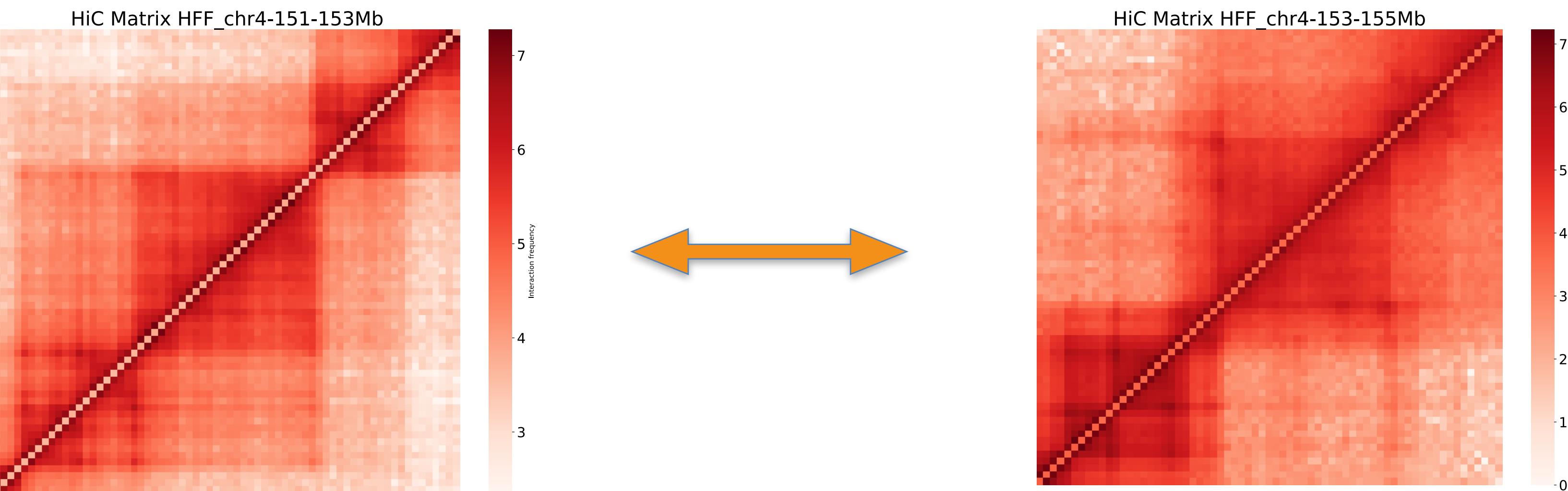
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Comparing Hi-C experiments

- Assess reproducibility (replicates)
- Identify structural differences (different conditions)



Traditional metrics

Pearson and Spearman correlation of each value in the matrix

Drawbacks:

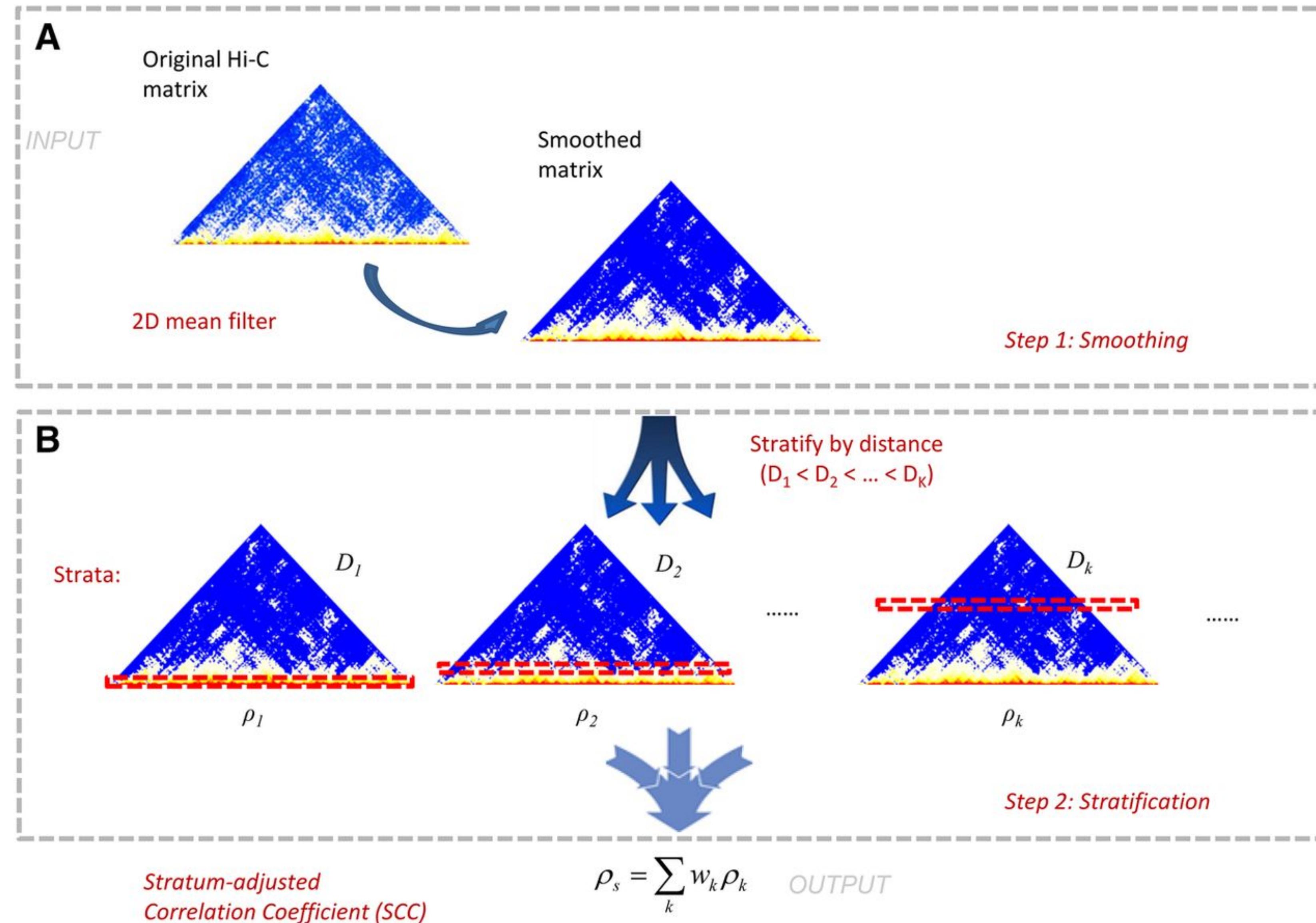
- Susceptible to outliers
- Treats all elements of the Hi-C matrix as independent measurements
- Most of the signal comes from pairs that are less than 1Mb apart. Correlation coefficient is dominated by these short-range interactions

Tailored metrics

- Based on correlation
 - HiCRep (<https://pubmed.ncbi.nlm.nih.gov/28855260/>)
- Based on decomposition
 - HiC-spector (<https://academic.oup.com/bioinformatics/article/33/14/2199/3078603>)

HICRep

Stratum-adjusted Correlation Coefficient (SCC)



HiC-spector

Reproducibility score Q

Laplacian

$$\mathcal{L} = D - W$$

$$D_{ii} = \sum_j W_{ij} \begin{pmatrix} D_{11} & 0 & 0 & 0 & \dots \\ 0 & D_{22} & 0 & 0 & \dots \\ 0 & 0 & D_{33} & 0 & \dots \\ 0 & 0 & 0 & D_{44} & \dots \end{pmatrix}$$

Normalized Laplacian

$$l = D^{-1/2} L D^{-1/2}$$

↓
n first eigenvectors

$$\{\nu_0, \nu_1, \dots, \nu_{n-1}\}$$

$$S_d(A, B) = \sum_{i=0}^{n-1} \|\nu_i^A - \nu_i^B\|$$

Q is $S_d(A, B)$ linearly rescaled

Reproducibility metrics

- Do not provide a systematic approach to identify structural changes
- Visual inspection is needed to pinpoint the differences

chess-hic

<https://github.com/vaquerizaslab/chess>

pypi package 0.3.7 docs passing

CHESS is a tool for the comparison and automatic feature extraction for chromatin contact data, developed in the [Vaquerizas Lab](#).

If you use CHESS in your research, please cite the [CHESS paper](#).

Please check out the [online documentation](#) for detailed installation and usage instructions.



TECHNICAL REPORT

<https://doi.org/10.1038/s41588-020-00712-y>

CHESS enables quantitative comparison of chromatin contact data and automatic feature extraction

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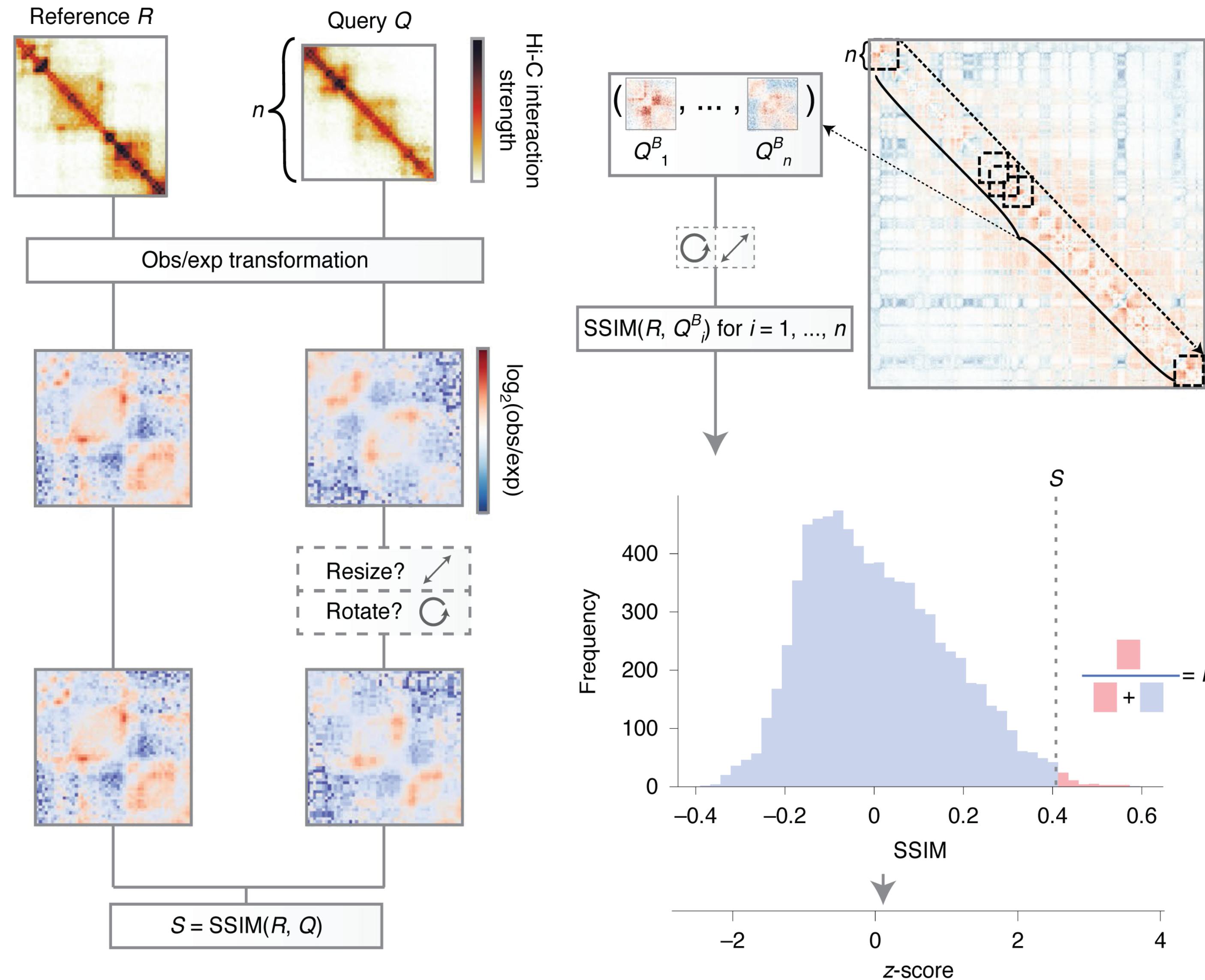
CHESS

- Systematic and quantitative comparison of 3C regions
- Identify and classify specific similarities or differences and features:
 - feature-free approach: not specifically looking for tads or loops.

Structural similarity index (SSIM)

- Widely used in image analysis
- SSIM score is a single value combining:
 - brightness: mean of the signal intensity
 - contrast: variance in signal
 - structure differences: correlation between signal values of two matrices

Identify regions that are significantly different between two conditions



Identify features that change between two conditions

