Context-Driven Exploration with Scalable Insets

Scalable Insets is a feature-centric technique to visually explore many local contact features within genome interaction maps. Exploration of sparsely-distributed features is challenging as context and navigational cues get lost upon zooming and navigation is time consuming. Our technique visualizes features too small to be identifiable using magnified thumbnail views called insets. These insets are dynamically placed either within the viewport or along the boundary of the viewport to improve search and navigation. Features are interactively clustered and piled up showing the average and variance of features to scale to thousands of features.

Context-Free Exploration with HiPiler

HiPiler lets you explore many local chromatin features in isolation as snippets. Snippets are 2D cut-outs from a Hi-C map. They can be automatically or manually arranged and piled up in a 2D canvas by the underlying data or custom attributes for quality control and stratification.

Loop patterns arranged by t-SNE and manually aggregated. The central pile up shows a pronounced loop pattern.

Left: Rao et al. 2014, Cell. Right: © OpenStreetMap
Live: higlass.io/app/?config=hi-c-scale-ismb

Contact Patterns

Commonly studied chromatin interaction patterns of increasing size representing different biological features.

Scale of Patterns

Loop, Domain, Chromosome, Genome
Park, City, Country, Globe

Bedpe, Csv

Feature-Centric
Visual Exploration of
Genome Interaction Maps

Fritz Lekschas¹, Benjamin Bach¹, Peter Kerpedjiev², Michael Behrisch¹, Nils Gehlenborg², and Hanspeter Pfister¹
¹Harvard John A. Paulson School of Engineering and Applied Sciences and ²Harvard Medical School

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scalable-insets.lekschas.de
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