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



Context-Driven Exploration



FIND OUT MORE scalable-insets.lekschas.de hipiler.lekschas.de

and the second

Visual

Computing

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 **INSETS** get lost upon zooming and navigation is time consuming. technique visualizes Uur

too small to be features

identifiable using magnified thumbnail **PLACEMENT** views called insets. These insets are Annotated dynamically placed either within the viewport or along the boundary of the to improve search and viewport navigation. Features are interactively clustered and piled up showing the average and variance of features to scale to thousands of features.

Commonly studied chromatin interaction patterns of increasing size representing



INTERACTIONS





Inset

Origin

different biological 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=hic-scale-ismb