HiPiler: Visual exploration of large genome interaction matrices with interactive small multiples

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http://hipiler.higlass.io/

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Some background
Three billion characters long
Genome is 3D

You wish -_-  

More like it :-/
3D Genome of single* cell reconstructed

What data are we dealing with?

Matrices!
Edited Fig. 3 from HiPiler paper
Interaction Matrix

Millions of regions

Diagonally symmetric

Interaction value
**Why: Regions of Interest (ROI)**

Remade from Fig. 4 of HiPiler paper
## Interaction Matrix

### Task
- View ROI's
- Examine pattern of ROI
- Compare patterns of different ROI's
- Preserve global context

### Challenge
- Too many ROI's
- Need to zoom
- Often far away
Task abstraction (abridged)

1. Search for known patterns
2. Examine one instance
3. Compare instances
The How

Matrix → Snippets → Interaction

Reannotated from Fig. 7 of HiPiler paper
The How

Context

Snippets layout
The How

Context (mainly HiGlass)  Snippets layout
Layout (using user specified metrics/attributes)

1D sorting

2D scatterplot

+3D tSNE clustering

Remade from Fig. 5 of HiPiler paper
Layout: Multi-dimensional clustering

- tSNE clustering
- Configurable

Remade from Fig. 5 of HiPiler paper
Selection, aggregation, filtering

- Lasso selection
- Combine snippets into a pile
- Delete snippet (pile)
Aggregation

Pile cover

In stack preview

Inspection

Remade from Fig. 5 of HiPiler paper
Stated Limitations

- Only square ROI
- Fixed rows/cols order
- Scalability (beyond 2000 snippets)
Evaluation

● Five domain experts/users
● 1-2 hours interview
  ○ Training
  ○ Pre-prepared data
  ○ Own data
Evaluation feedback

- Good snippet/matrix linking
- Validated (behaviourally) task abstractions
- Easy to learn
- Big improvement on state-of-the-art
Summary
Summary

**What?**
Interaction matrix

**Why?**
Explore and validate

**How?**
Snippets:
- Linked
- Laid out
- Select/Aggregate/Filter
Critique
Great!

● **Tool:**
  ○ Open source
  ○ Nice aesthetic
  ○ Does what it says!

● **Paper:**
  ○ Easy to read
  ○ Great online resources (demo, video, slides, docs, etc...)

Not so great :-(

- Software:
  - Selection sucks, real bad
  - Slow (too much on-the-go computation)
  - Heavy on client-side memory
  - Unintuitive settings
  - Very buggy
  - Too much installation overhead (server)
Thanks!

Questions?