



HiPiler

Exploring Many Hi-C Features Through Visual Decomposition

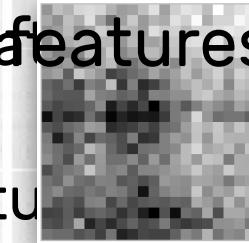
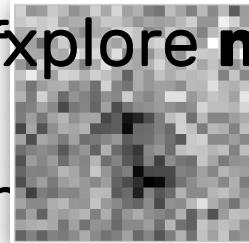
Fritz Lekschas, Benjamin Bach, Peter Kerpeljiev,
Nils Gehlenborg, and Hanspeter Pfister

... and special thanks to N. Abdennur, B. Alver, H. Belaghzal, A. van den Berg, J. Dekker, G. Fudenberg, J. Gibcus, A. Goloborodko, D. Gorkin, M. Imakaev, Y. Liu, L. Mirny, J. Nübler, P. Park, H. Strobelt, and S. Wang for their invaluable feedback during the development of HiPiler.

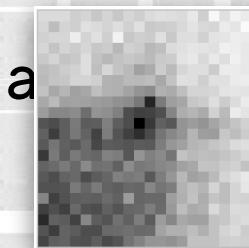
Rao et al. "A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping." *Cell*, 159(7):1665–1680, 2014.

How to visualize and explore many local features?

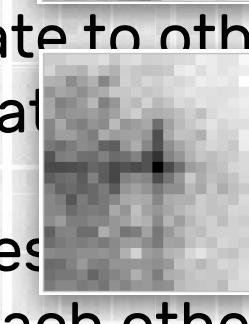
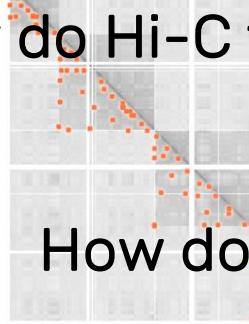
How variant are



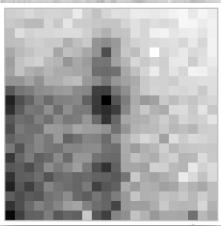
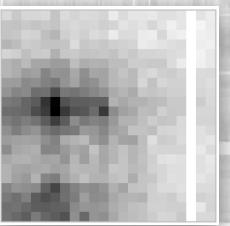
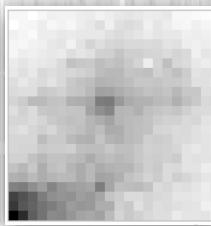
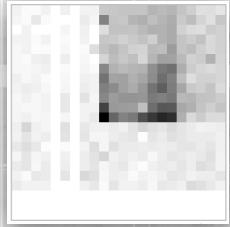
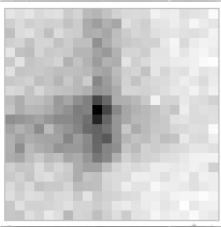
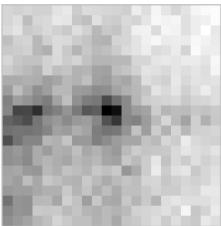
Are there subgroups a



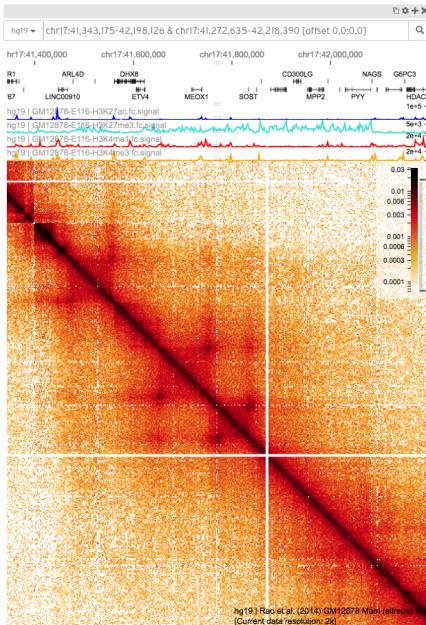
How do Hi-C features relate to other
derived at



How do Hi-C features
each other?



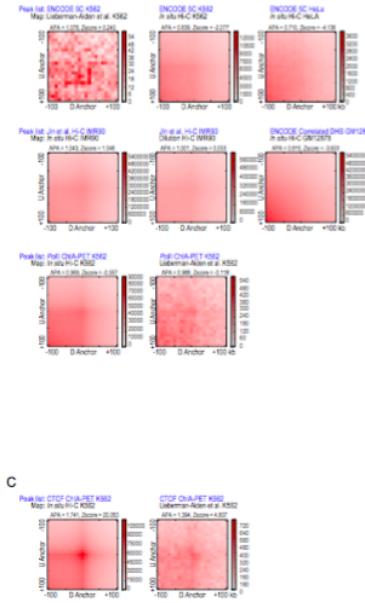
Single View



Multi View



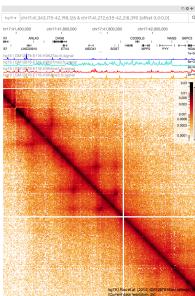
Custom View



Rao et al. "A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping." *Cell*, 159(7):1665–1680, 2014.

Single View

Simple to use



No comparisons

Multi View

Comparison*



No aggregation

Custom View

Highly flexible



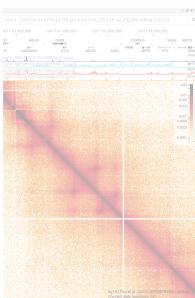
No interactions
Time consuming

*) Of up to dozens of features

Rao et al. "A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping." *Cell*, 159(7):1665–1680, 2014.

Single View

Simple to use



No comparisons

???

Compare thousands
of features

Use metadata

Find subgroups

Inspect aggregates

Interactive

Custom View

Highly flexible



No interactions
Time consuming

Rao et al. "A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping." *Cell*, 159(7):1665–1680, 2014.



Cut Matrix into Pieces!

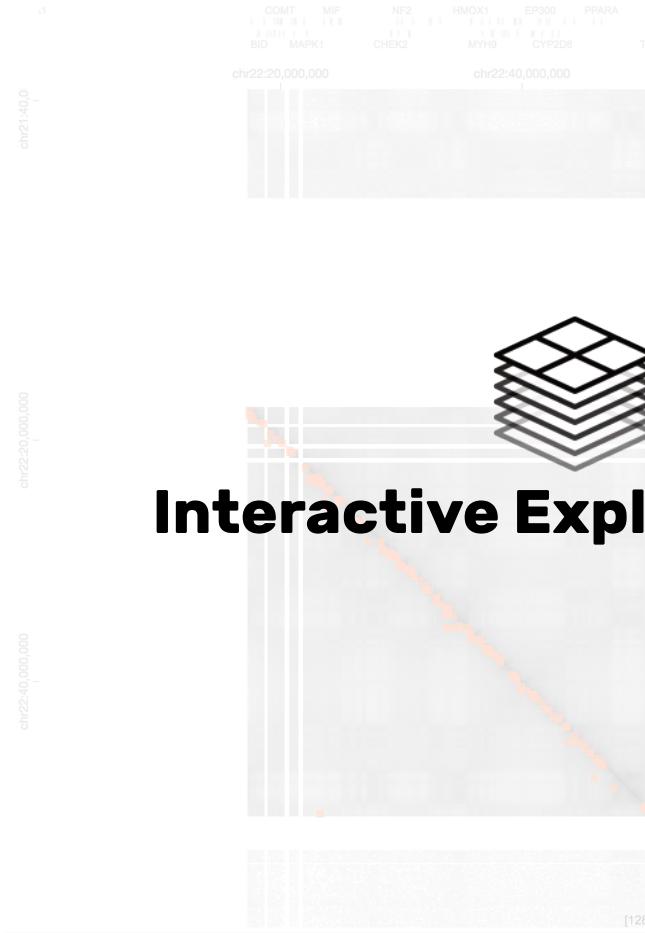
The Snippets Approach

Okay

but...



MATRIX



SNIPPETS



ARRANGE: Choose measures...

Cluster MORE

MATRIX



SNIPPETS



OVERVIEW, FILTERING, GROUPING

Understand and filter results based on derived metrics

ARRANGE: Choose measures...

Cluster MORE

AGGREGATION

Assessing individual, average, and variance patterns

MATRIX

d



SNIPPET MATRIX LINKING

Correlation of features in their context

MATRIX

SOD1
COL18A1
RUNX1
ITGB2

chr21:40,000,000

COMT MIF
NF2 HMOX1 EP300 PRARA
BID MAPK1 CHEK2 MYH9 CYP2D6
STS TLR7 F

chr22:20,000,000

SNIPPETS

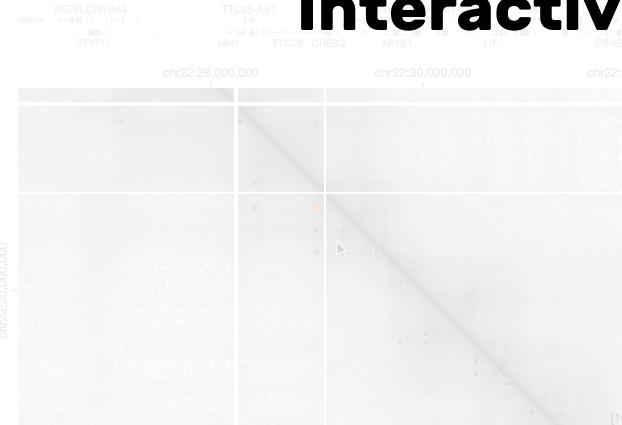
105000

Distance to diagonal

1820000



chr22:26,185,136-32,021,553 & chr22:28,091,635-31,271,609 [offset 0,0:0,0]

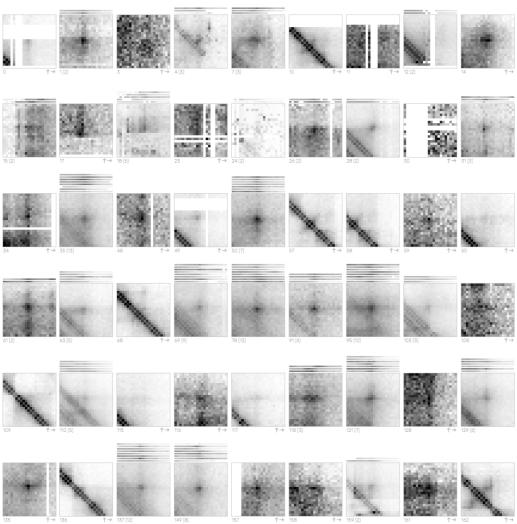


SNIPPET CLUSTERING

Interactive Subgroup Exploration

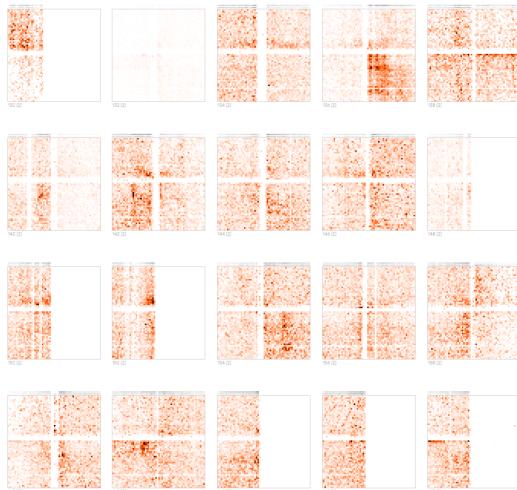
Loops

AVERAGES SUBGROUP FILTERING



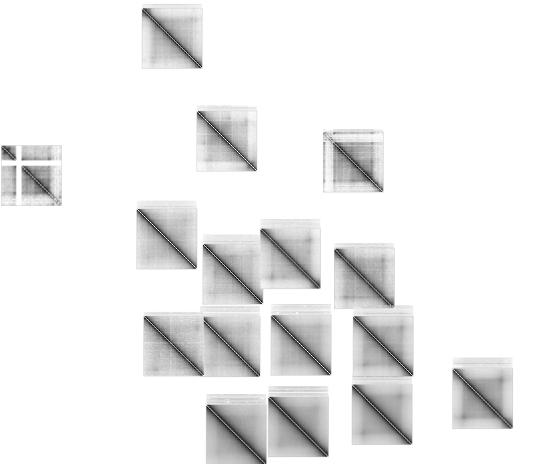
Telomeres

VARIANCES PAIRWISE COMPARISION



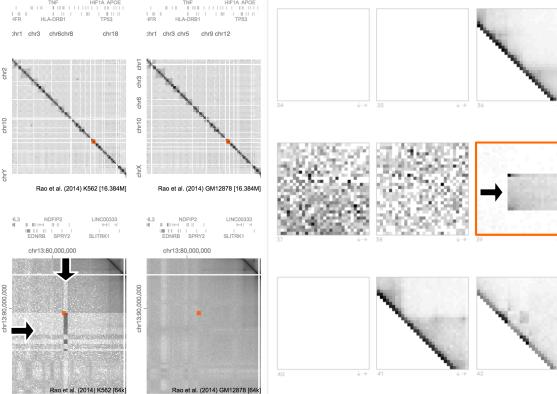
Domains

AVERAGES RESCALED CLUSTERING



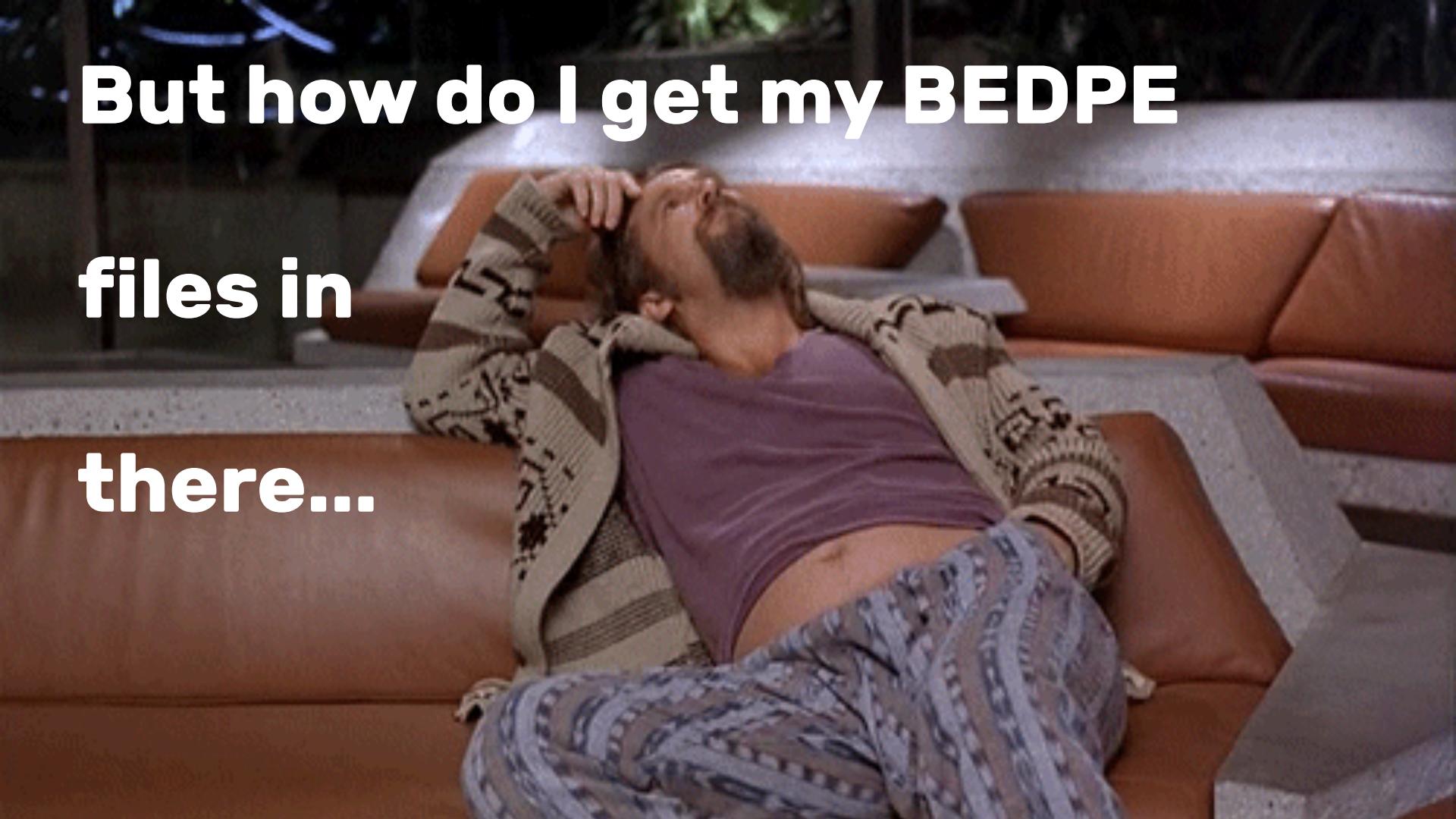
Structural Variation

EXPLORATION PAIRWISE COMPARISON



Use Cases

- Studying Hi-C features (one pattern type)
E.g.: Loops, TADs, compartments, ...
- Studying other genomic features (many pattern types)
E.g.: Genes, SNPs, protein-binding sites, ...
- HiPiler currently renders up to 2000 snippets in your browser
- Export data as JSON with CMD + S

A man with short brown hair is lying on his back on a brown leather couch. He is wearing a purple t-shirt and patterned pajama bottoms. He is holding a newspaper over his head with both hands, looking up at it. The couch has a decorative, tufted headrest. In the background, there's a grey sofa and some green plants.

**But how do I get my BEDPE
files in
there...**

Requirements

1. Multi-resolution cooler file
2. BEDPE-like set of 2D regions (including derived metrics)
3. HiGlass Server
4. A modern web browser

Create View Config for HiPiler

1. Create or convert BEDPE* to JSON
2. Define how features should be cut out
3. Create HiGlass view for the matrix

Links

Examples:

<http://hipiler.higlass.io>

Example View Config:

<https://gist.github.com/flekschas/8b0163f25fd4ffb067aaba2a595da447>

Docs:

<https://github.com/flekschas/hipiler/wiki/Data#config-file>



MIT



HiGlass



HiPiler

POSTER: #41 and #31

TUTORIAL: [github.com/4dn-dcic/
2017-annual-meeting-higlass-hipiler-tutorial](https://github.com/4dn-dcic/2017-annual-meeting-higlass-hipiler-tutorial)

DEMO: higlass.io
hipiler.higlass.io

DOCS: github.com/hms-dbmi/higlass/wiki
hipiler.higlass.io/docs

CODE: github.com/hms-dbmi/higlass
github.com/flekschas/hipiler

HiPiler

View Config

```
{  
    "fgm": {  
        "fragmentsServer": "http://higlass.io/api/v1/", // HiGlass server  
        "fragmentsNoBalance": false, // Cooler balancing  
        "fragmentsPrecision": 2, // Float precision  
        "fragmentsBaseRes": 1000, // Base resolution in KB  
        "fragmentsDims": 20, // Number of pixels, e.g., 20x20px  
        "fragmentsPercentile": 100, // Upper percentile capping  
        "fragmentsIgnoreDiags": 0, // Number of diagonals to ignore  
        "fragmentsNoCache": false, // Don't cache (dev only)  
        "fragments": [ ... // BEDPE-like loci ]  
    },  
    "hgl": { ... // HiGlass view config }  
}
```

BEDPE JSON ARRAY

REQUIRED
NUMERICAL
_CATEGORICAL

[
 ["chrom1", "start1", "end1", "strand1", "chrom2", "start2",
 "end2", "strand2", "dataset", "zoomOutLevel", "corner-score",
 "U-var", "L-var", "U-sign", "L-sign", "_group"],
 ["22", 17425000, 17545000, "+", "22", 17425000, 17545000,
 "+", "rao-gm12878-1kbmr", 1, 0.91491, 0.061801, 0.033795,
 0.60558, 0.6278, 1],
 ["22", 17555000, 17645000, "+", "22", 17555000, 17645000,
 "+", "rao-k563-1kbmr", 1, 0.89306, 0.035257, 0.020245,
 0.54321, 0.69136, 1],
 ...
]
]

LOCI

BEDPE JSON ARRAY

REQUIRED
NUMERICAL
_CATEGORICAL

Pandas DataFrame:

```
json.dumps([list(df.columns)] + df.values.tolist())
```

R Data Frame:

```
library(jsonlite)  
noquote(paste("[", toJSON(c(colnames(df), "name")), ",  
substring(toJSON(df, dataframe='values'), 2), sep=""))
```

[

```
["chrom1", "start1", "end1", "strand1", "chrom2", "start2", "end2", "strand2", "dataset",  
"zoomOutLevel", "corner-score", "U-var", "L-var", "U-sign", "L-sign", "_group"],  
["22", 17425000, 17545000, "+", "22", 17425000, 17545000, "+", "rao-  
gm12878-1kbmr", 1, 0.91491, 0.061801, 0.033795, 0.60558, 0.6278, 1],
```

...

]

HiGlass

View

Config

1 Row Only
Disable editing
(recommended)

