

# Orchestrating Hi-C analysis with Bioconductor

Package demonstration

Jacques Serizay

Bioconductor Conference 2023

# Orchestrating Hi-C analysis with Bioconductor

## Welcome

This is the landing page of the “**Orchestrating Hi-C analysis with Bioconductor**” book. **The primary aim of this book is to introduce the R user to Hi-C analysis.** This book starts with key concepts important for the analysis of chromatin conformation capture and then presents **Bioconductor** tools that can be leveraged to process, analyze, explore and visualize Hi-C data.

**Authors:** Jacques Serizay [aut, cre]

**Version:** 1.1.0

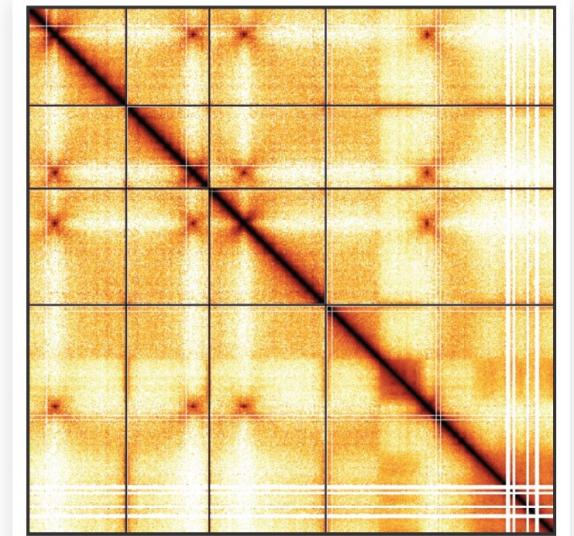
**Modified:** 2023-04-14

**Compiled:** 2023-07-24

**Environment:** R version 4.3.1 (2023-06-16), Bioconductor 3.18

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<https://js2264.github.io/OHCA/>

# Outline

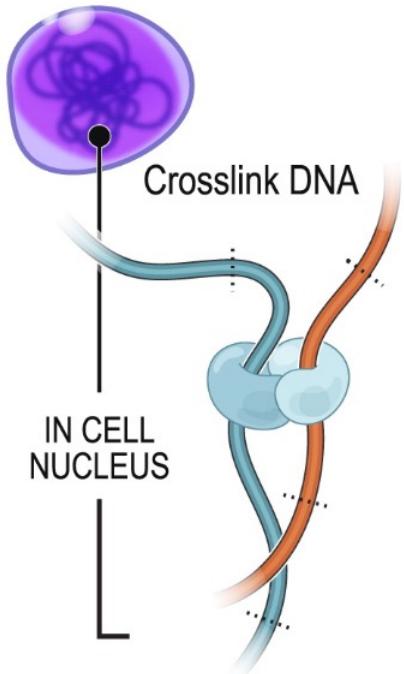
- ❑ Overview of Chromosome Conformation Capture technical aspects
- ❑ Introduction to the OHCA ecosystem
- ❑ Importing Hi-C data with `HiCExperiment`
- ❑ Manipulating and visualizing Hi-C data with `HiContacts`
- ❑ Inter-operability with existing Hi-C packages
- ❑ Wrapping-up

# Outline

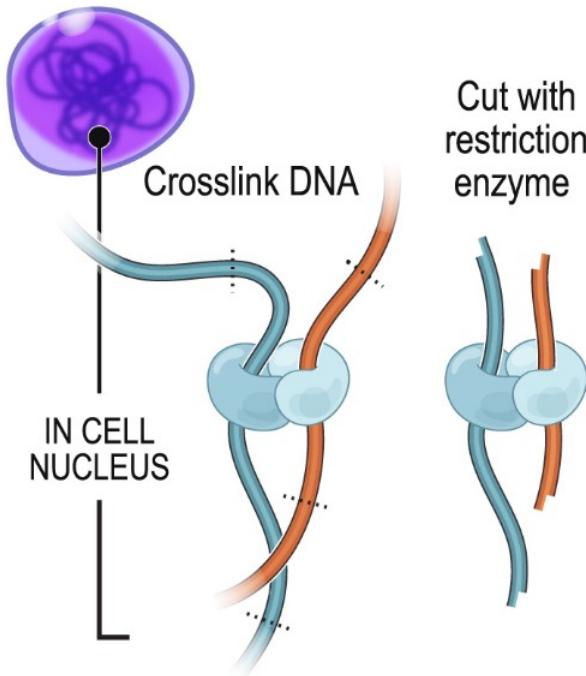
## ❑ Overview of Chromosome Conformation Capture technical aspects

- ❑ Introduction to the OHCA ecosystem
- ❑ Importing Hi-C data with HiCExperiment
- ❑ Manipulating and visualizing Hi-C data with HiContacts
- ❑ Inter-operability with existing Hi-C packages
- ❑ Wrapping-up

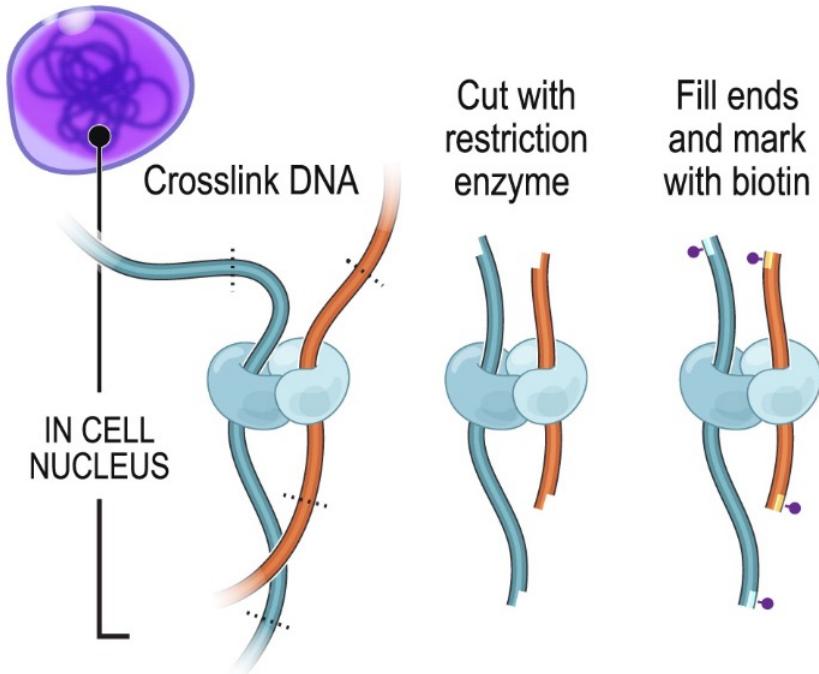
# Chromosome Conformation Capture



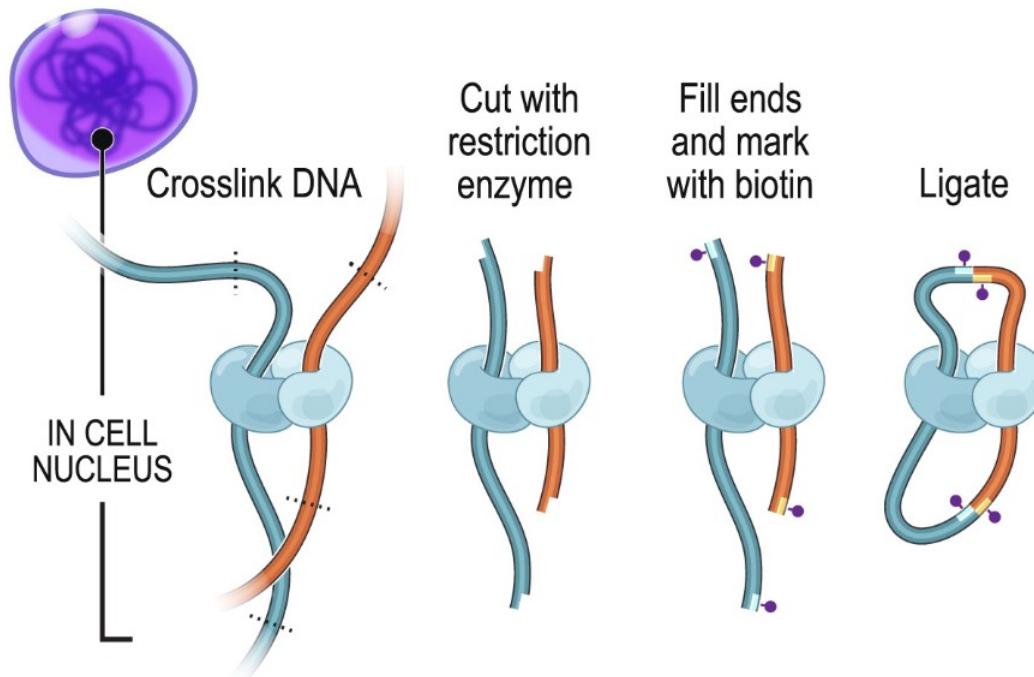
# Chromosome Conformation Capture



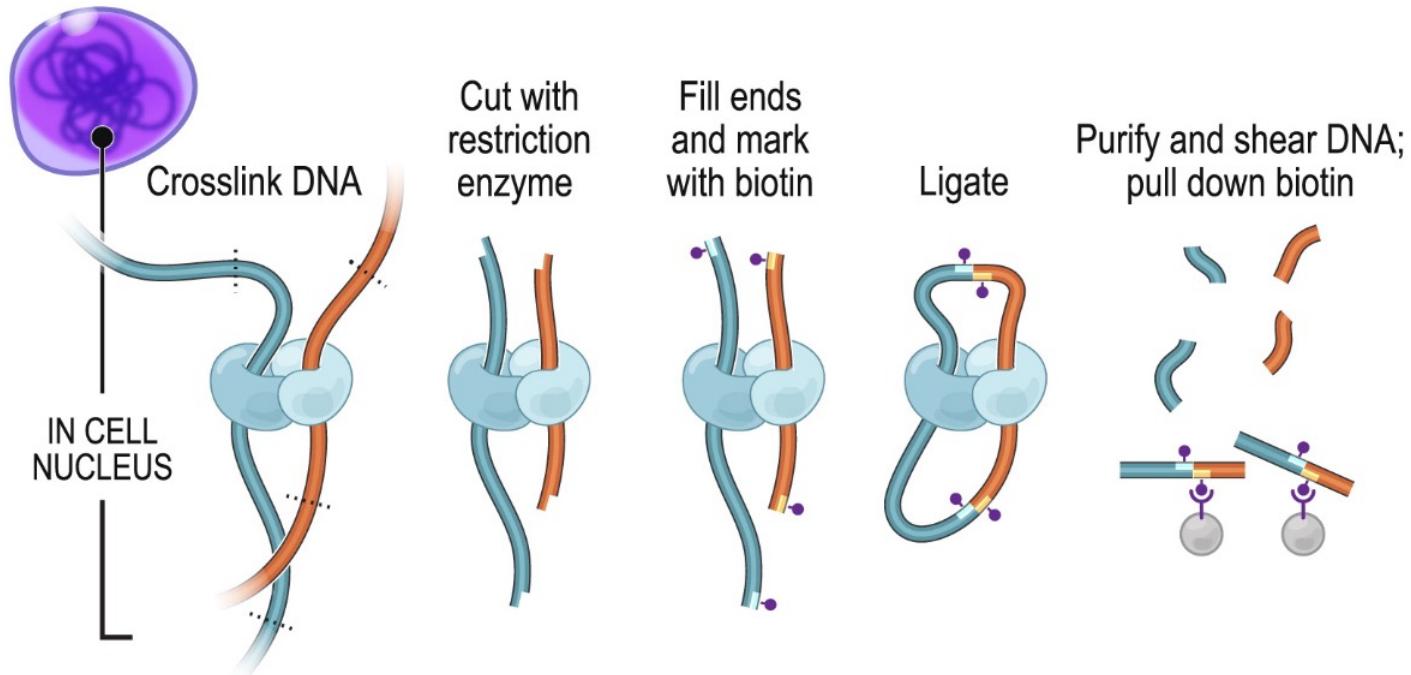
# Chromosome Conformation Capture



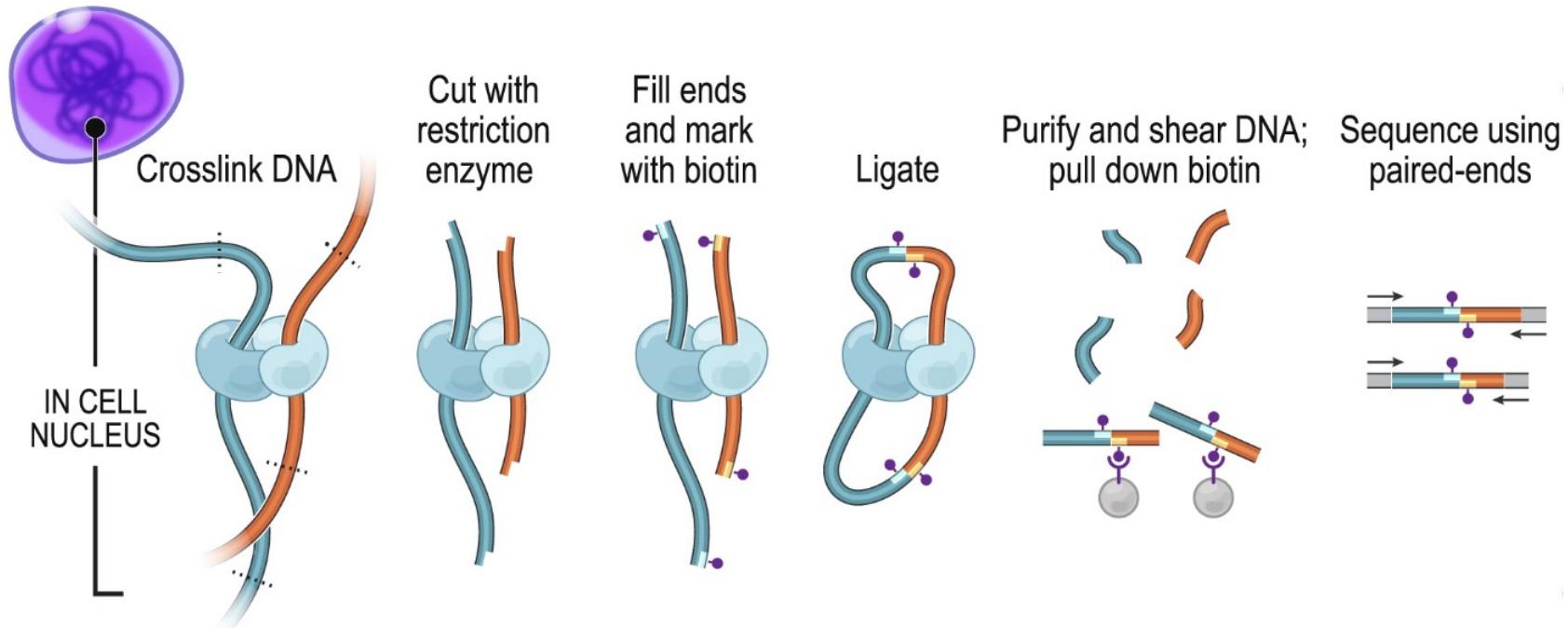
# Chromosome Conformation Capture



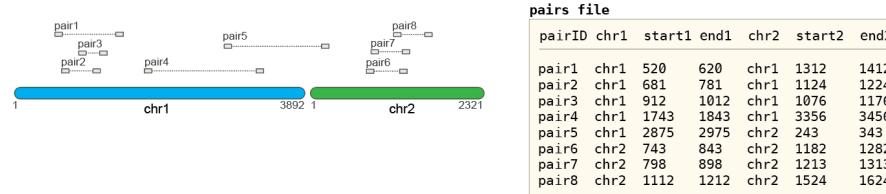
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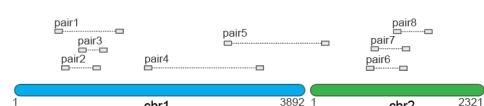
# Chromosome Conformation Capture processing



# Chromosome Conformation Capture processing

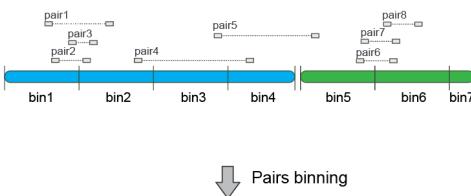


# Chromosome Conformation Capture processing



Chromosome binning

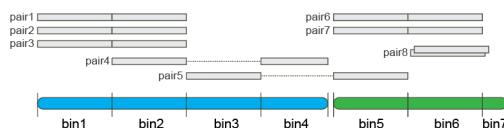
pairs file						
pairID	chr1	start1	end1	chr2	start2	end2
pair1	chr1	520	620	chr1	1312	1412
pair2	chr1	681	781	chr1	1124	1224
pair3	chr1	912	1012	chr1	1076	1176
pair4	chr1	1743	1843	chr1	3356	3456
pair5	chr1	2875	2975	chr2	243	343
pair6	chr2	743	843	chr2	1182	1282
pair7	chr2	798	898	chr2	1213	1313
pair8	chr2	1112	1212	chr2	1524	1624



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pair8	chr2	1112	1212	chr2	1524	1624

regions file			
binID	chr	start	end
bin1	chr1	1	1000
bin2	chr1	1001	2000
bin3	chr1	2001	3000
bin4	chr1	3001	3892
bin5	chr2	1	1000
bin6	chr2	1001	2000
bin7	chr2	2001	2321



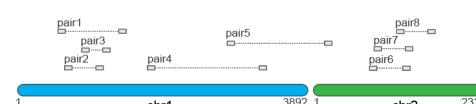
binned pairs file (temp.)

pairID	binID_1	binID_2
pair1	bin1	bin2
pair2	bin1	bin2
pair3	bin1	bin2
pair4	bin2	bin4
pair5	bin3	bin5
pair6	bin5	bin6
pair7	bin5	bin6
pair8	bin6	bin6

regions file

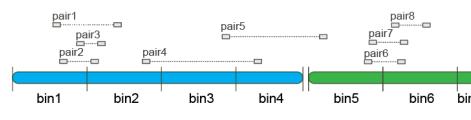
binID	chr	start	end
bin1	chr1	1	1000
bin2	chr1	1001	2000
bin3	chr1	2001	3000
bin4	chr1	3001	3892
bin5	chr2	1	1000
bin6	chr2	1001	2000
bin7	chr2	2001	2321

# Chromosome Conformation Capture processing



Chromosome binning

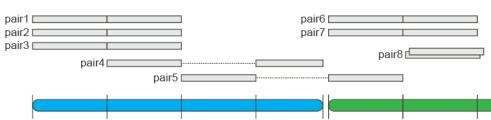
pairs file						
pairID	chr1	start1	end1	chr2	start2	end2
pair1	chr1	520	620	chr1	1312	1412
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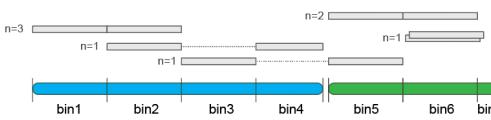
binned pairs file (temp.)

pairID	binID_1	binID_2
pair1	bin1	bin2
pair2	bin1	bin2
pair3	bin1	bin2
pair4	bin2	bin4
pair5	bin3	bin5
pair6	bin5	bin6
pair7	bin5	bin6
pair8	bin6	bin6

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bin4	chr1	3001	3892
bin5	chr2	1	1000
bin6	chr2	1001	2000
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Pairs counting



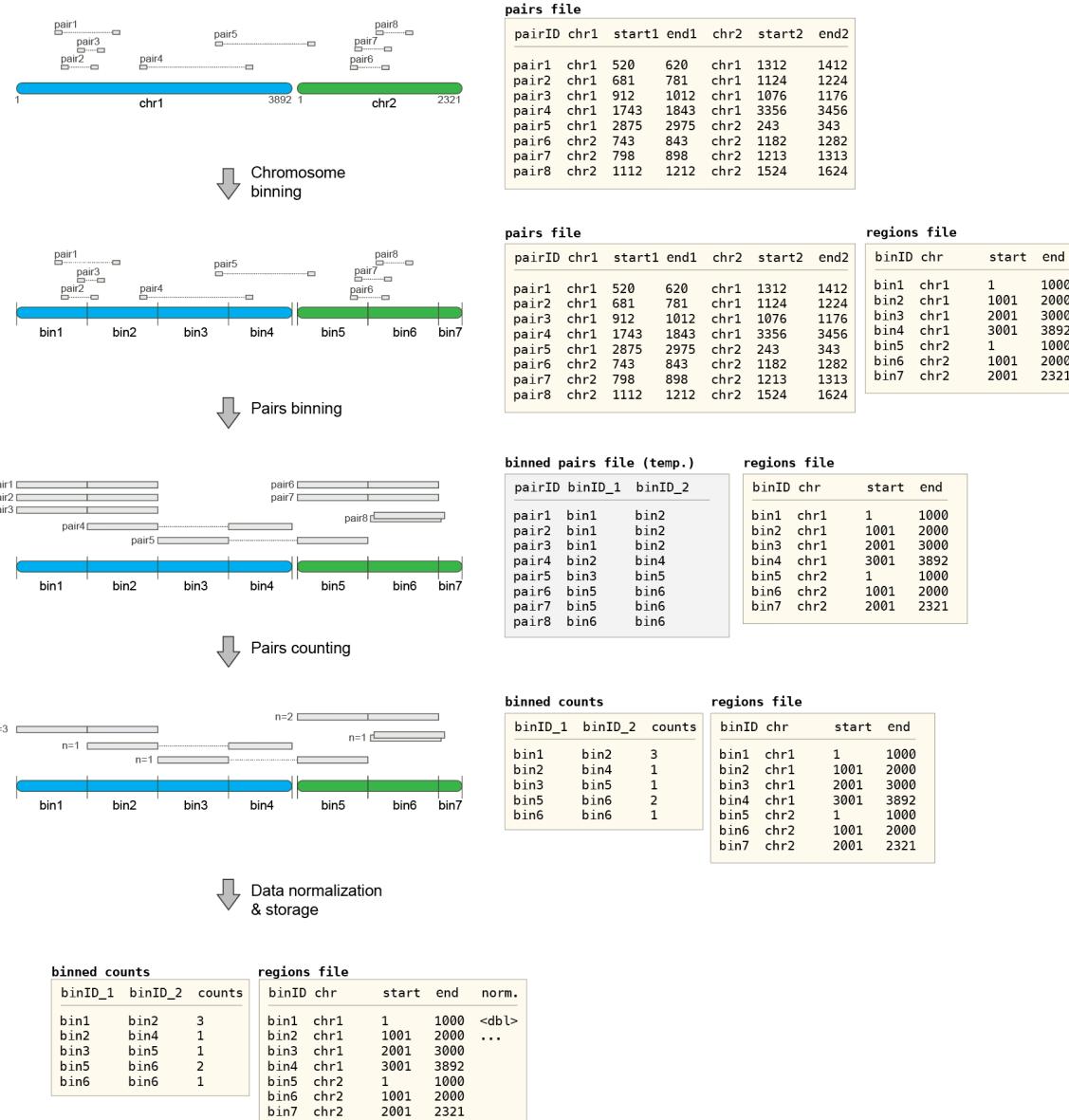
binned counts

binID_1	binID_2	counts
bin1	bin2	3
bin2	bin4	1
bin3	bin5	1
bin5	bin6	2
bin6	bin6	1

regions file

binID	chr	start	end
bin1	chr1	1	1000
bin2	chr1	1001	2000
bin3	chr1	2001	3000
bin4	chr1	3001	3892
bin5	chr2	1	1000
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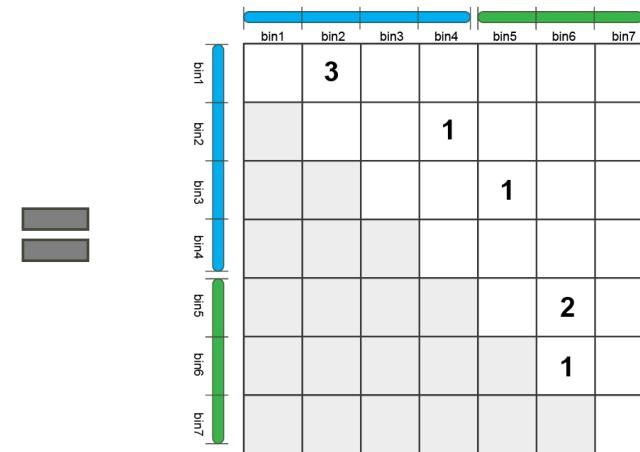
# Chromosome Conformation Capture processing



# Chromosome Conformation Capture processing

binned counts		
binID_1	binID_2	counts
bin1	bin2	3
bin2	bin4	1
bin3	bin5	1
bin5	bin6	2
bin6	bin6	1

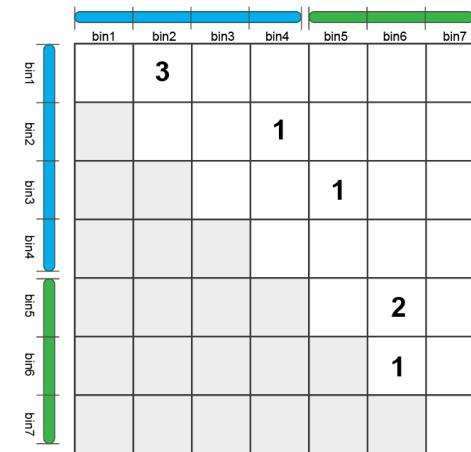
regions file				
binID	chr	start	end	norm.
bin1	chr1	1	1000	<dbl>
bin2	chr1	1001	2000	...
bin3	chr1	2001	3000	
bin4	chr1	3001	3892	
bin5	chr2	1	1000	
bin6	chr2	1001	2000	
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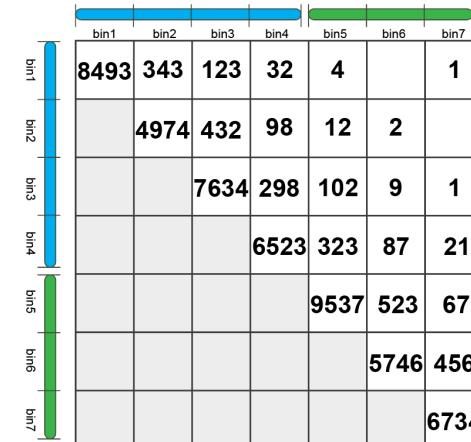
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bin5	chr2	1	1000	
bin6	chr2	1001	2000	
bin7	chr2	2001	2321	



binned counts		
binID_1	binID_2	counts
bin1	bin2	343
bin2	bin4	943
bin3	bin5	201
bin5	bin6	438
bin6	bin6	8493
...		
...		
...		

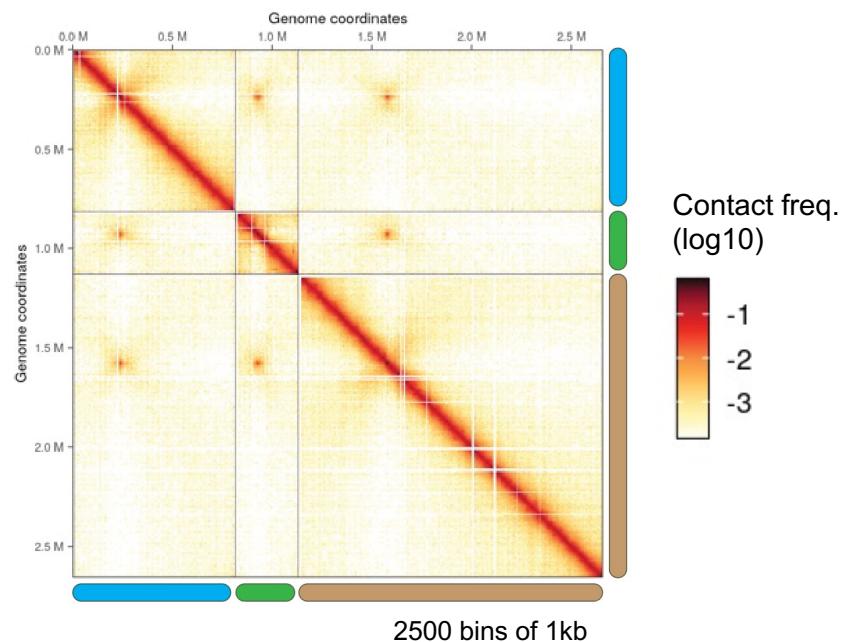
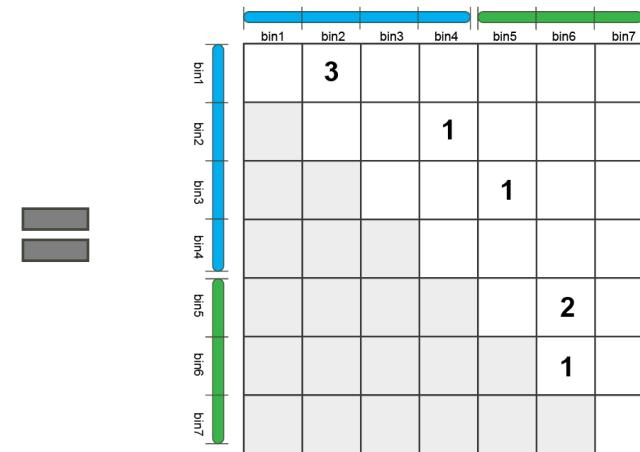
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# Chromosome Conformation Capture processing

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regions file				
binID	chr	start	end	norm.
bin1	chr1	1	1000	<dbl>
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bin4	chr1	3001	3892	
bin5	chr2	1	1000	
bin6	chr2	1001	2000	
bin7	chr2	2001	2321	



## Hi-C data file formats (1): human-readable files

### ❖ .pairs:

- Lossless format
- Human-readable
- No random access supported by Bioconductor (could be implemented by the 4DN-provided Rpairix package)

### ❖ HiC-Pro files:

- Two text files: a regions.txt and a counts.txt
- Human-readable
- Can take up significant space
- Does not support normalization along with raw counts
- No natively supported random access

## Hi-C data file formats (2): binarized files

### ❖ .cool:

- Stores binned matrices in a **binarized, HDF5-based** archive
- Supports random access (`rhd5lib`)
- Supports multi-resolution matrices
- Handles a **single** normalization vector (can be tweaked)
- Well-documented, robust `cooler` API, **compatible** with `pairtools`, `cooltools` & `coolpuppy`

### ❖ .hic:

- Stores binned matrices in a **binarized proprietary** format
- Supports random access (`strawr`)
- Supports multi-resolution matrices
- Handles **multiple** normalization vectors
- Somewhat documented, monolith `juicer` tools API.

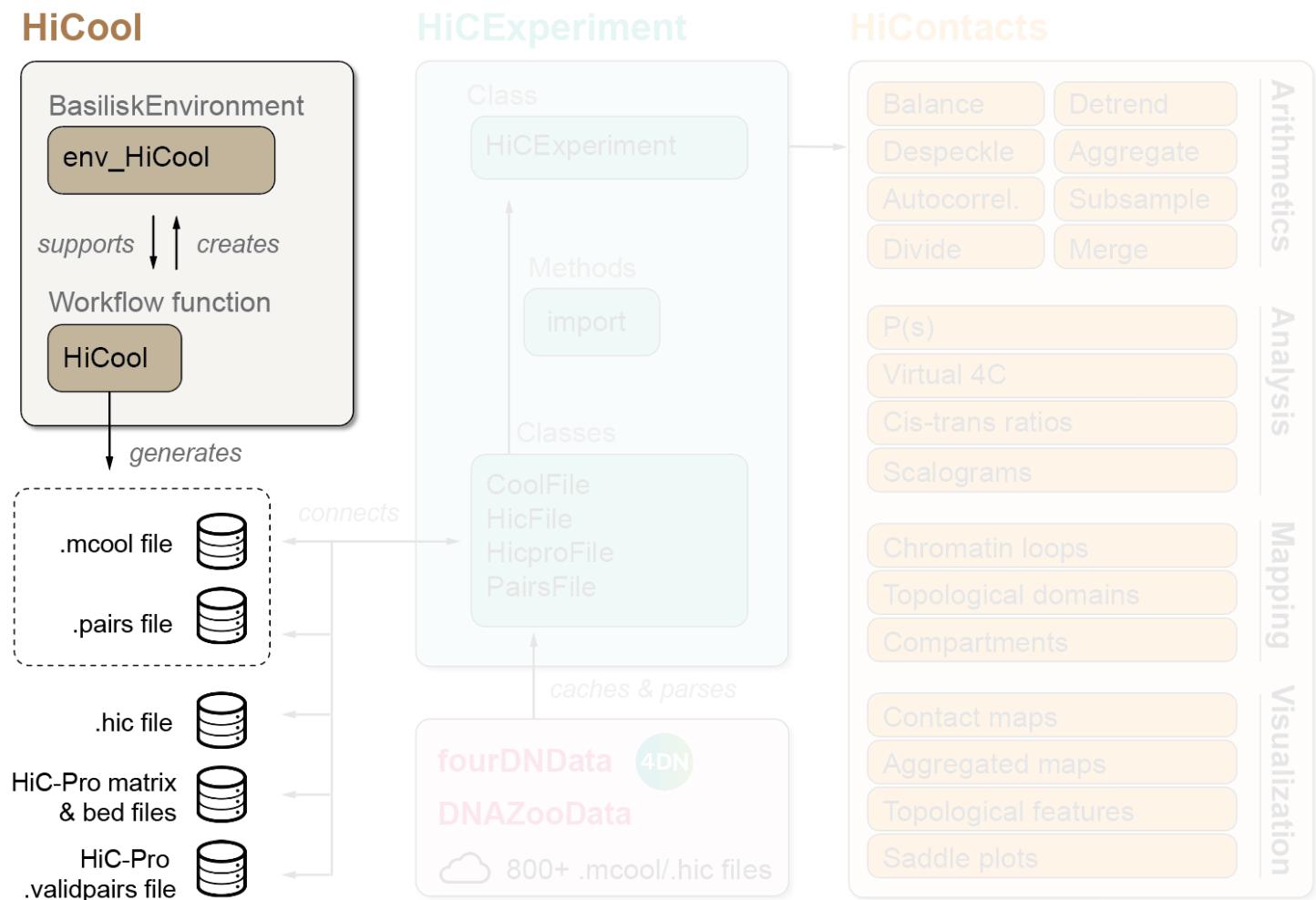
# Outline

- ❑ Overview of Chromosome Conformation Capture technical aspects
- ❑ **Introduction to the OHCA ecosystem**
- ❑ Importing Hi-C data with `HiCExperiment`
- ❑ Manipulating and visualizing Hi-C data with `HiContacts`
- ❑ Inter-operability with existing Hi-C packages
- ❑ Wrapping-up

# The OHCA ecosystem

## ❖ HiCool

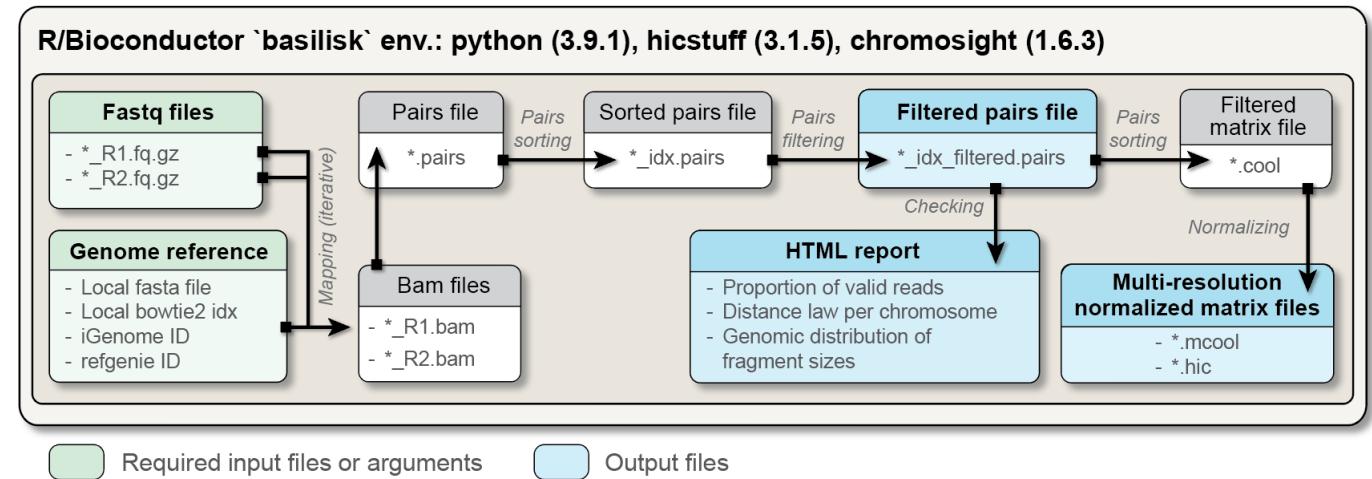
- Processing fastq files into .pairs files and binned .hic/.cool files
- Wraps hicstuff, a lightweight python Hi-C processing library
- Based on basilisk



# The OHCA ecosystem

## ❖ HiCool

- Processing fastq files into .pairs files and binned .hic/.cool files
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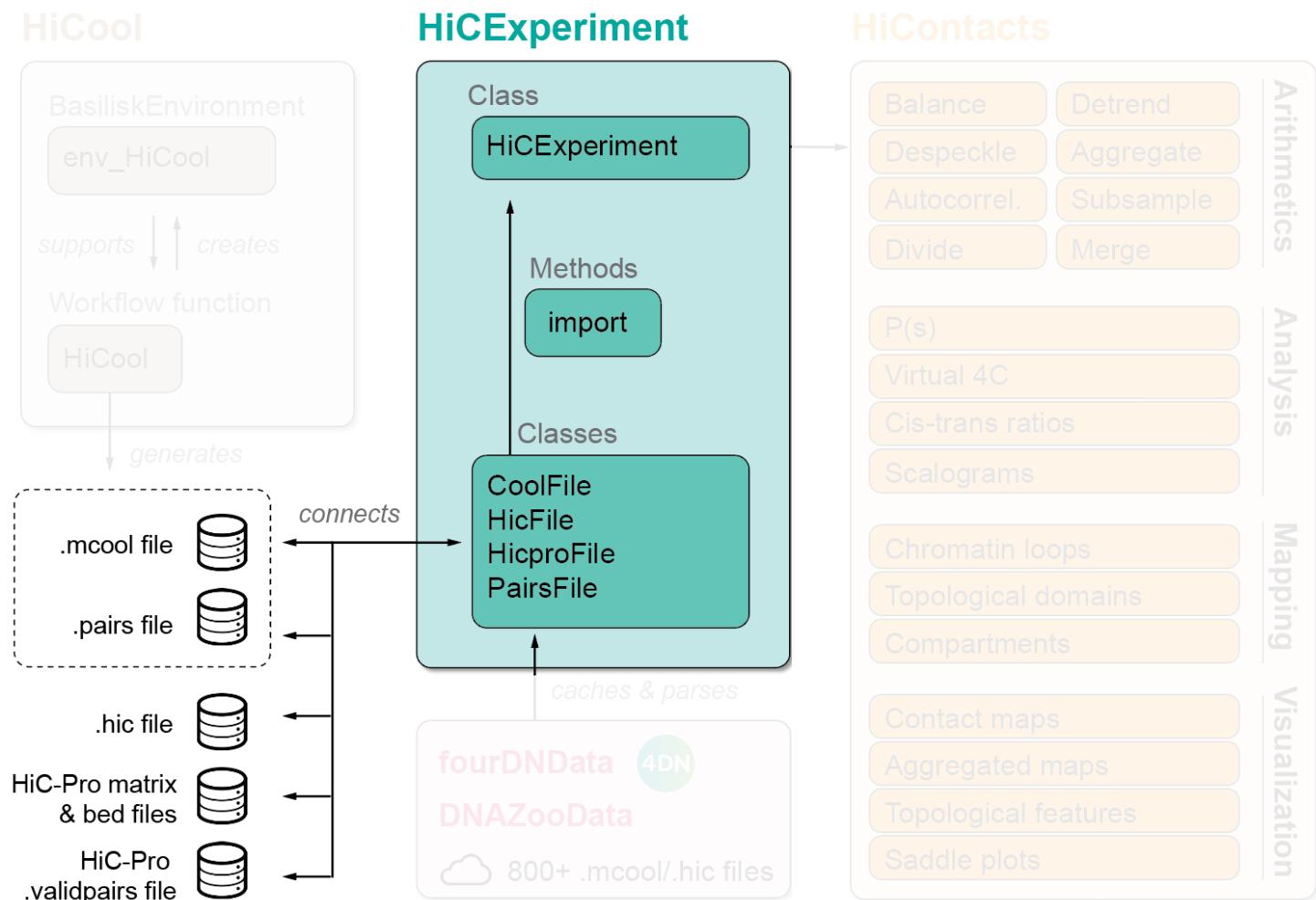


# The OHCA ecosystem

## ❖ HiCool

## ❖ HiCExperiment

- Defines the HiCExperiment class of object and associated methods, including subsetting of in memory Hi-C data
- Based on Ginteractions and BiocFile classes
- Import methods for all Hi-C data file formats
- Supports random access for .hic and .cool files

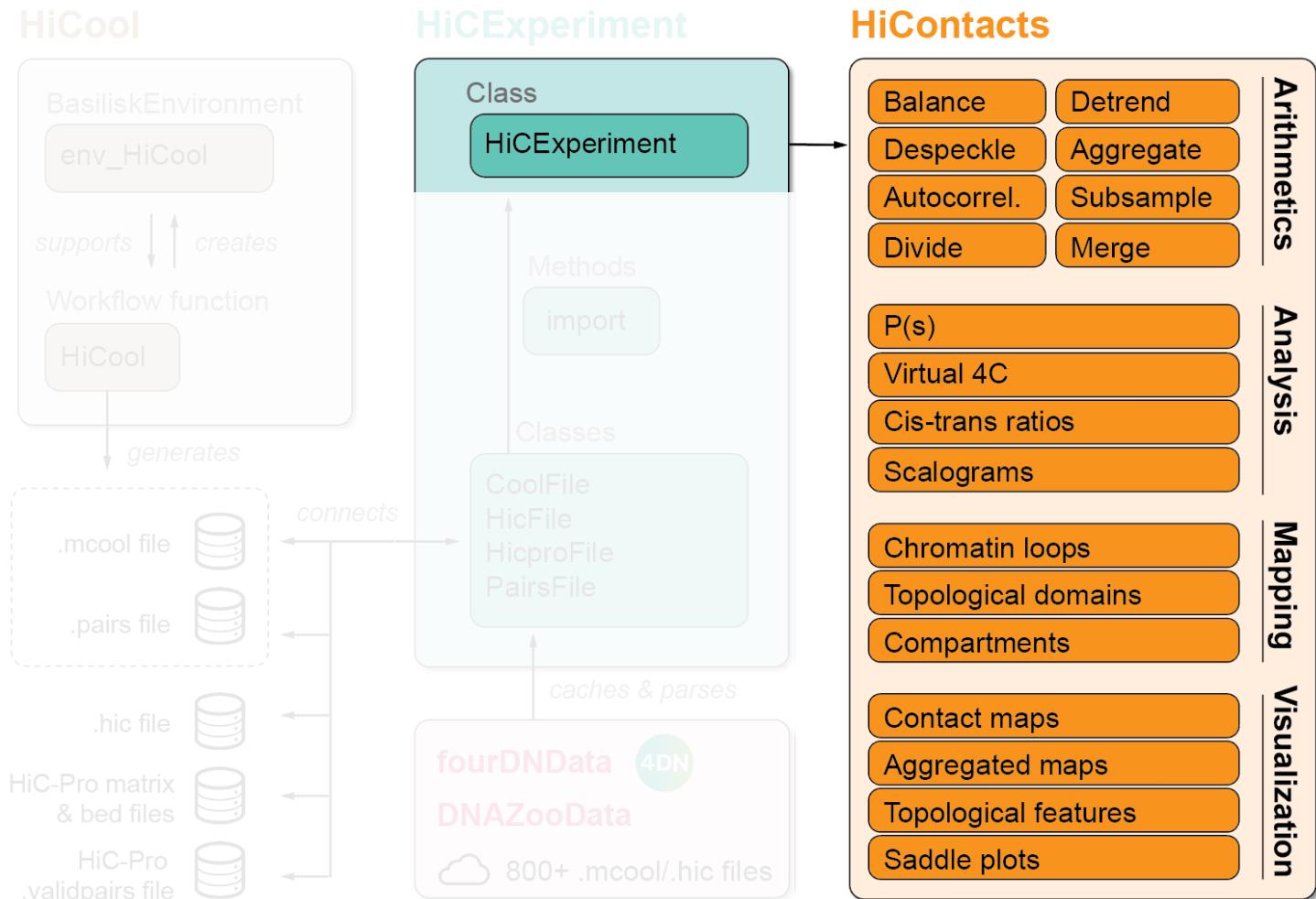


# The OHCA ecosystem

- ❖ HiCool
- ❖ HiCExperiment

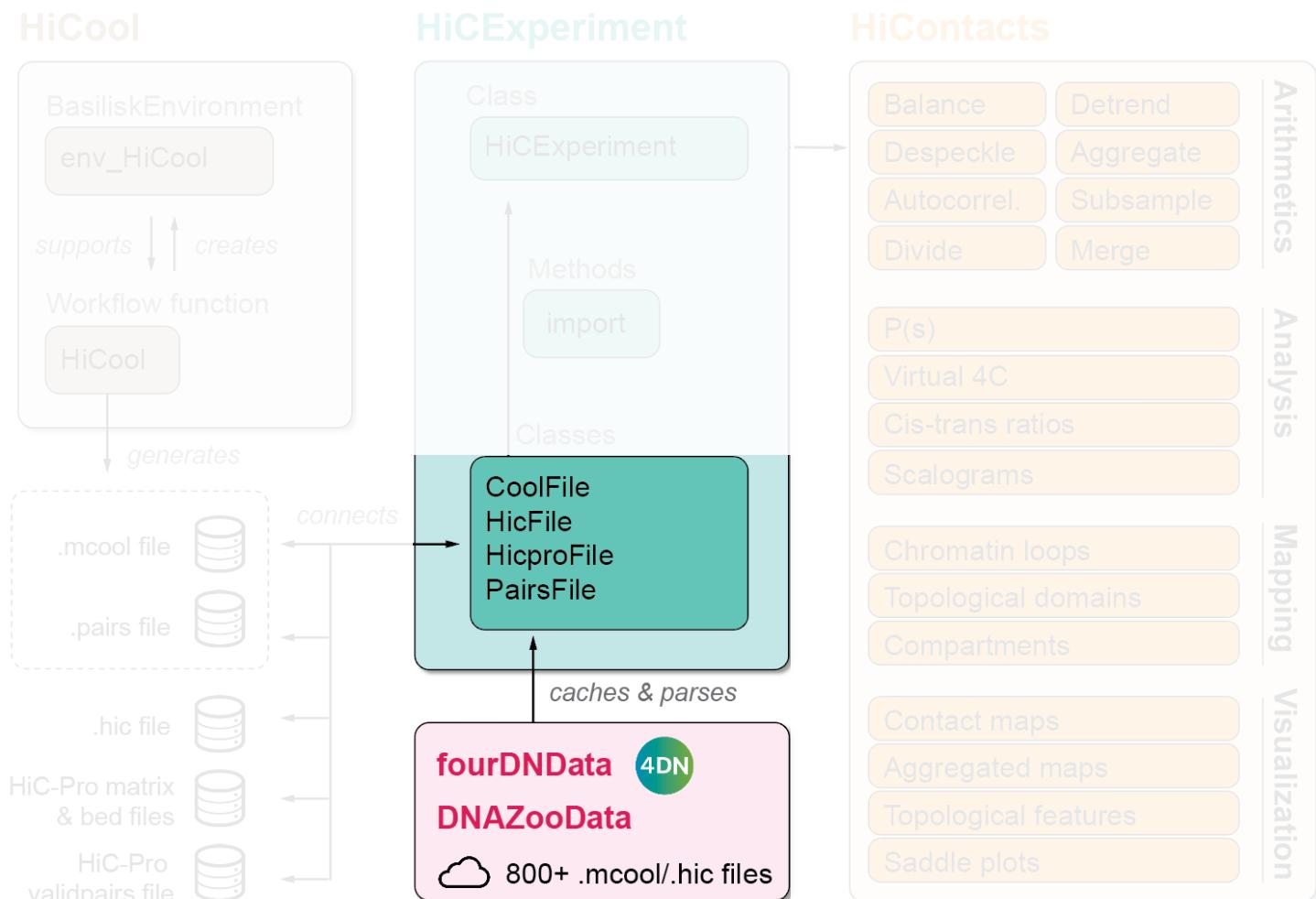
- ❖ HiContacts

- Genomic arithmetic for Hi-C maps
- Genomic interactions analytical tools
- Implementations of algorithms to annotate 3D features (compartments, TADs, loops)
- Extensive ggplot2-based visualization methods



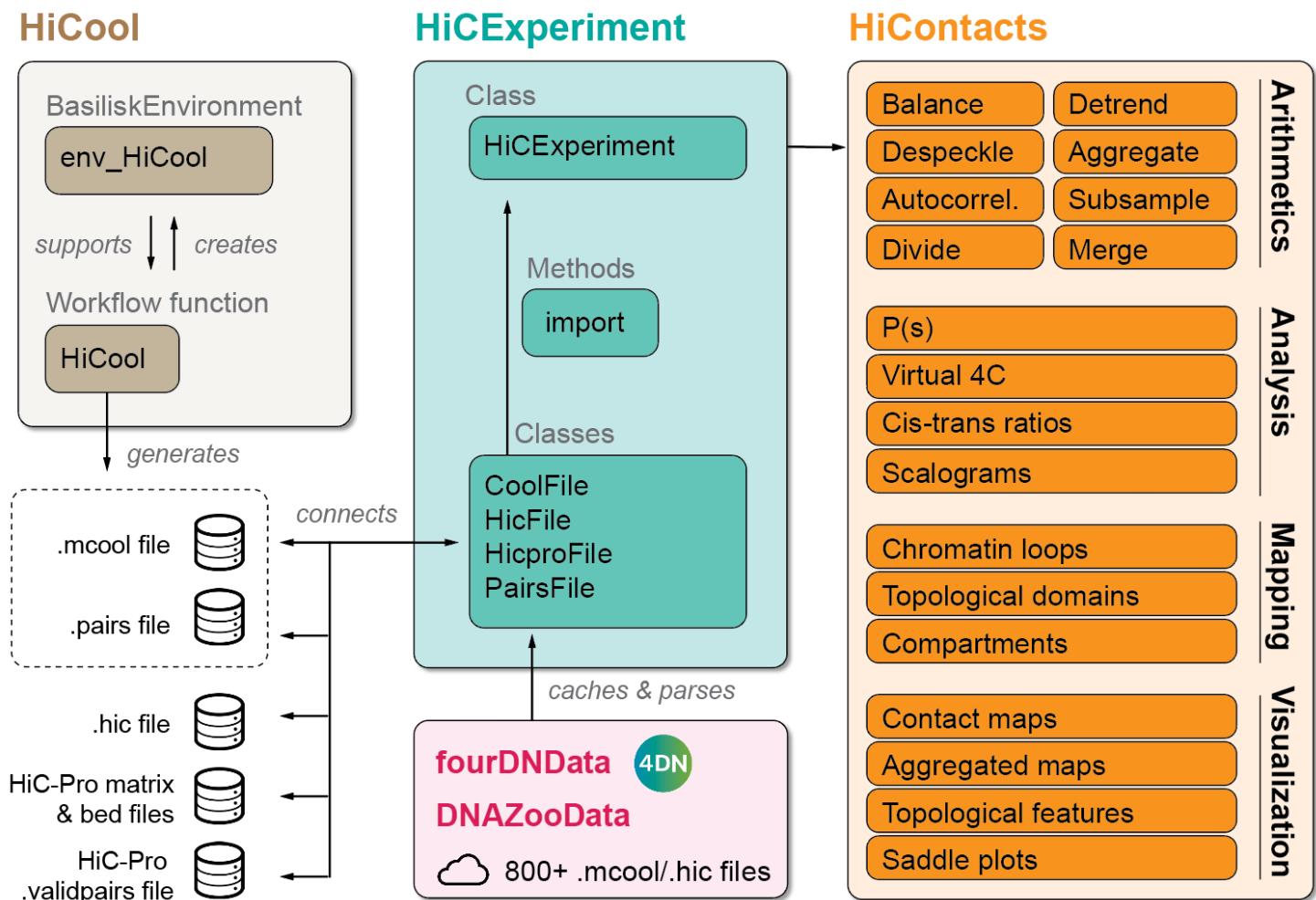
# The OHCA ecosystem

- ❖ HiCool
- ❖ HiCExperiment
- ❖ HiContacts
- ❖ fourDNDData / DNAZooData
  - Data packages
  - Gateways to 2 major Hi-C consortia
  - ExperimentHub-based file accession
  - Support BiocFileCache



# The OHCA ecosystem

- ❖ HiCool
- ❖ HiCExperiment
- ❖ HiContacts
- ❖ fourDNDData / DNAZooData



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# ContactFile et PairsFile: connection to disk-stored Hi-C data

<ContactFile> .(m)cool, .hic, HiC-Pro

ContactFile:

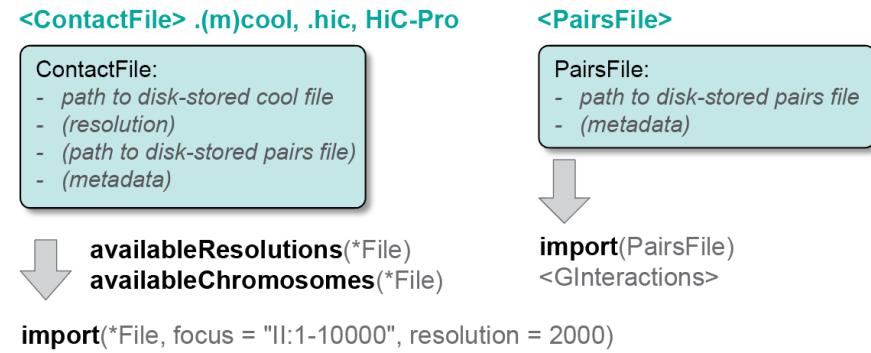
- *path to disk-stored cool file*
- *(resolution)*
- *(path to disk-stored pairs file)*
- *(metadata)*

<PairsFile>

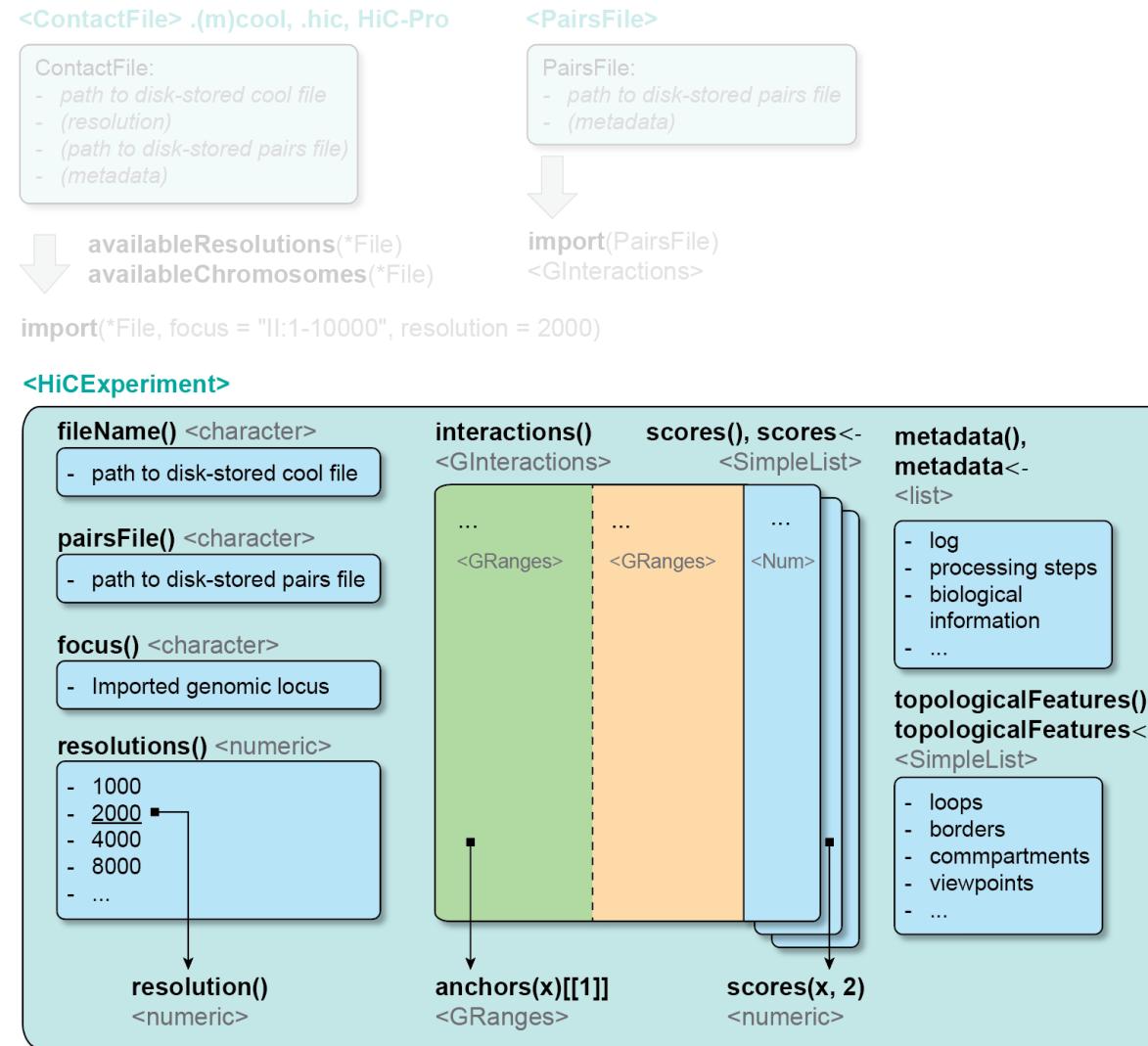
PairsFile:

- *path to disk-stored pairs file*
- *(metadata)*

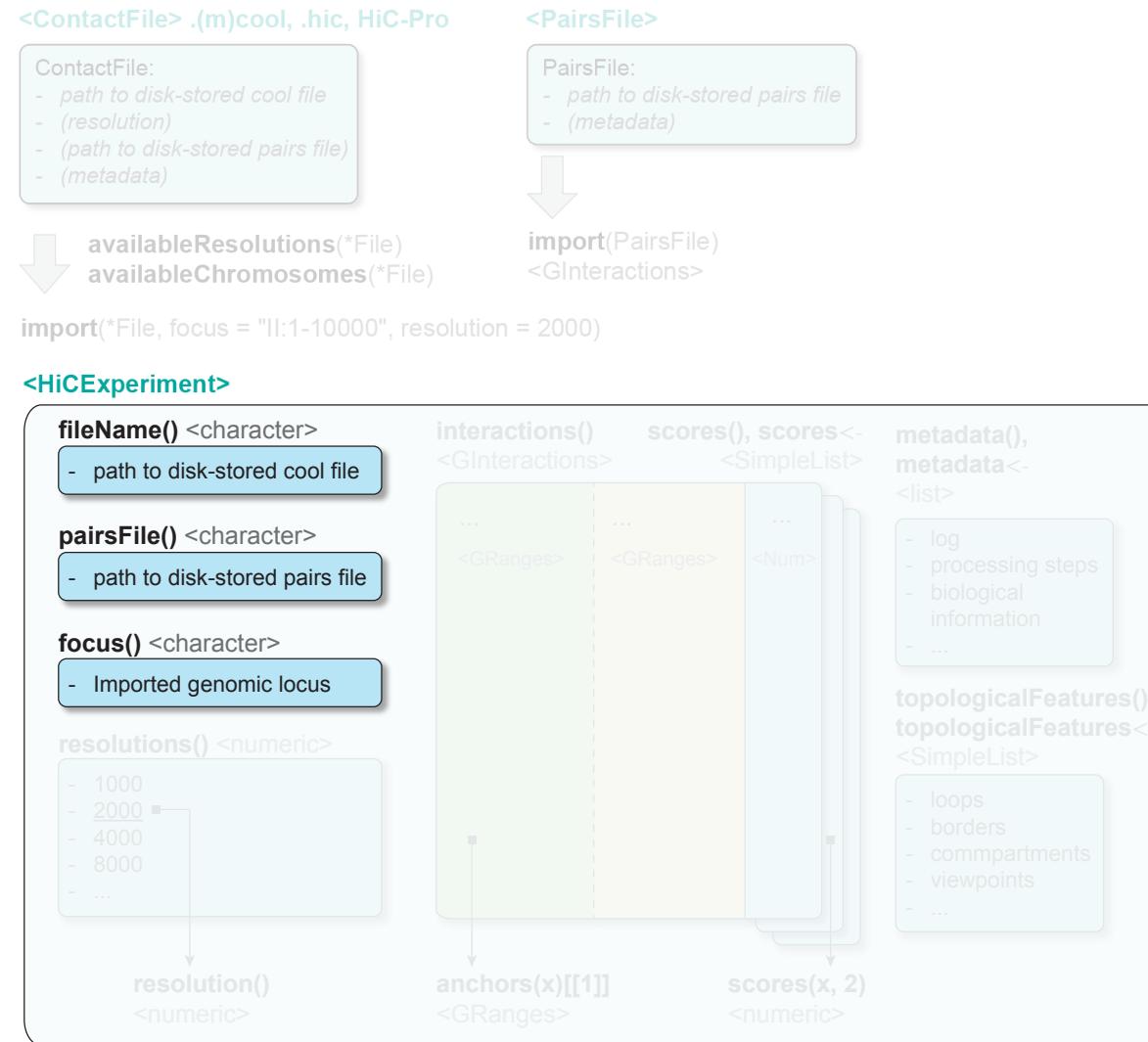
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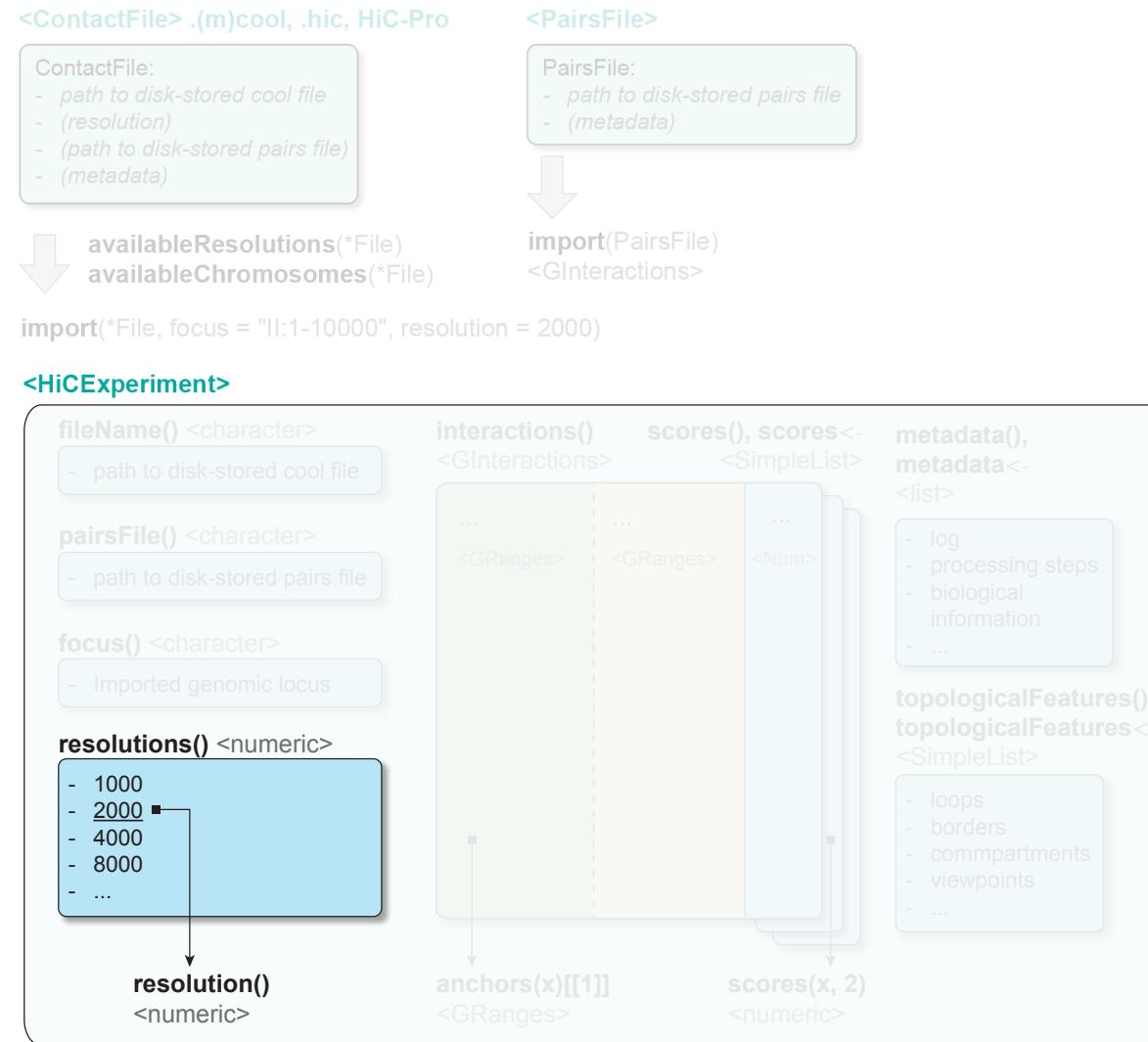
# HiCExperiment class



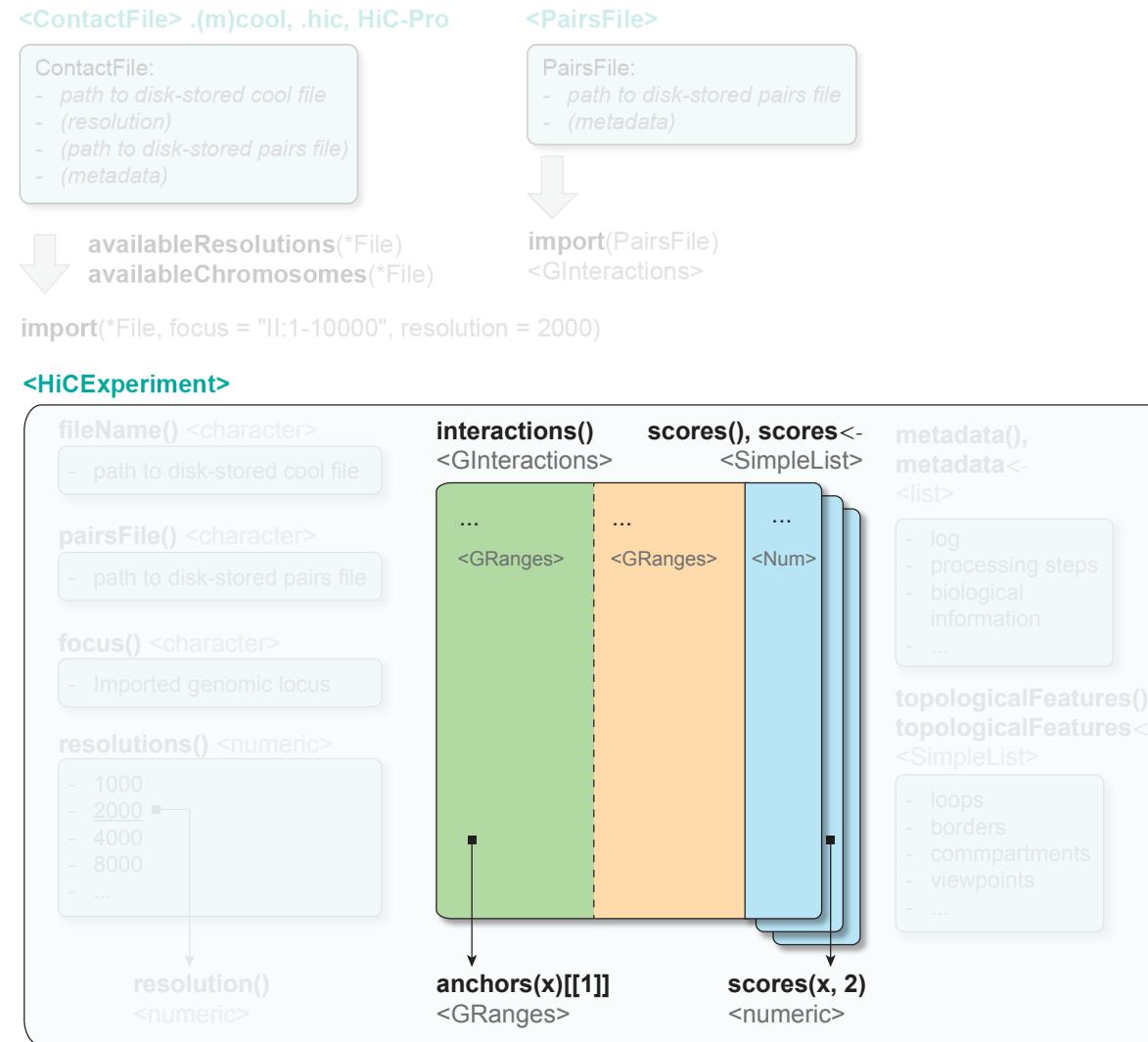
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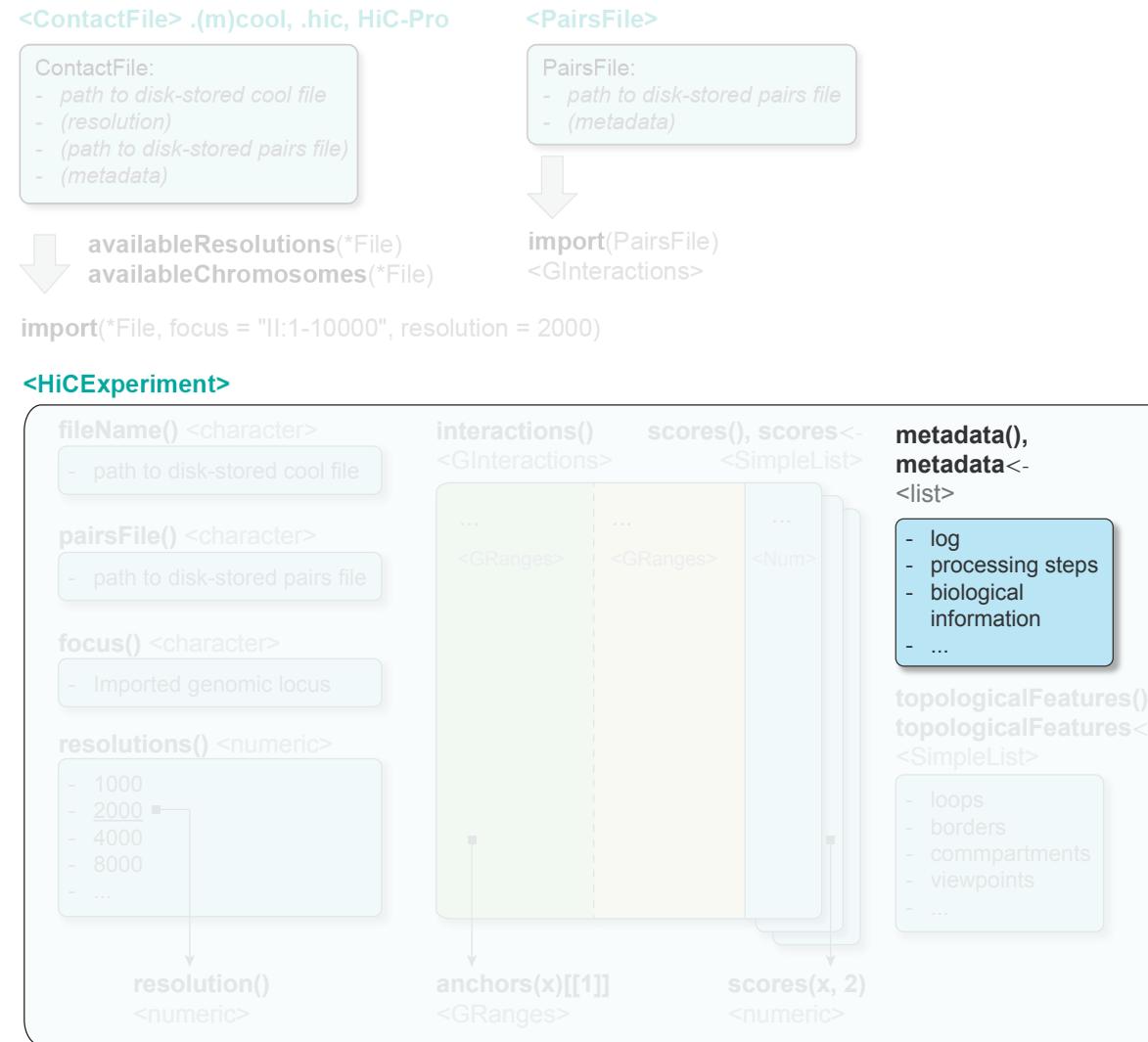
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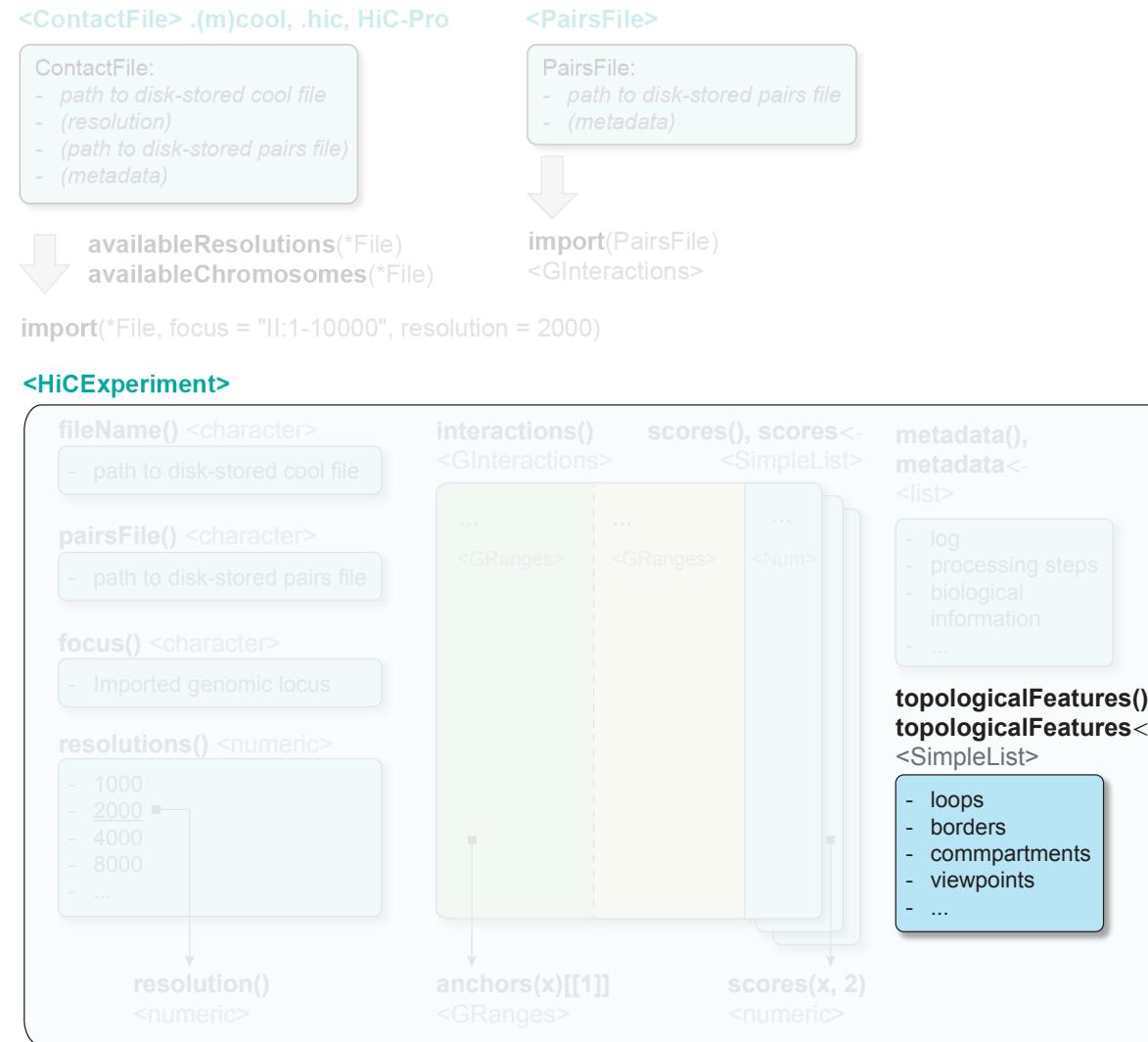
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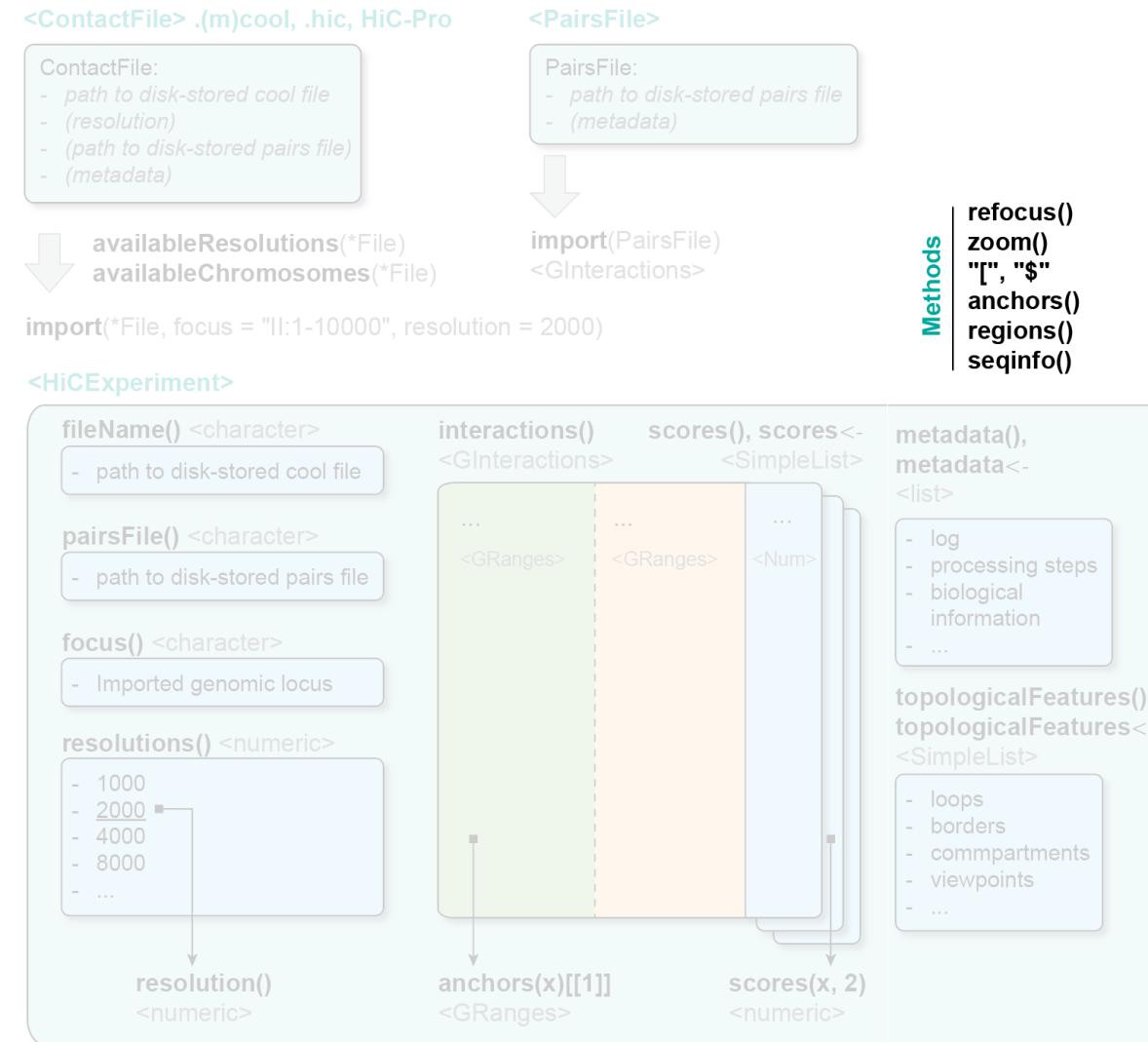
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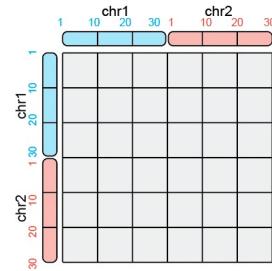


# Parsing Hi-C data in R

## Subsetting before importing

```
cool_file <- CoolFile("....mcool")
```

```
hic <- import(cool_file)
```

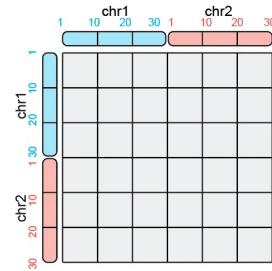


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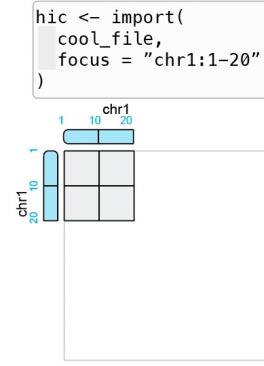
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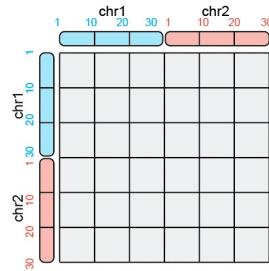
```
hic <- import(  
  cool_file,  
  focus = "chr1:1-20"  
)
```



# Parsing Hi-C data in R

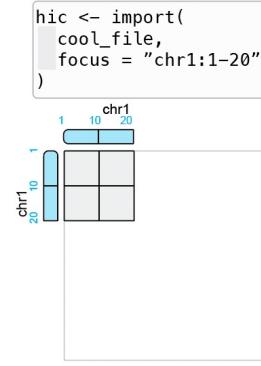
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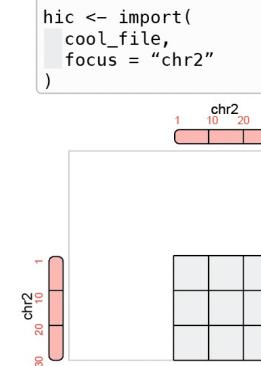


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```

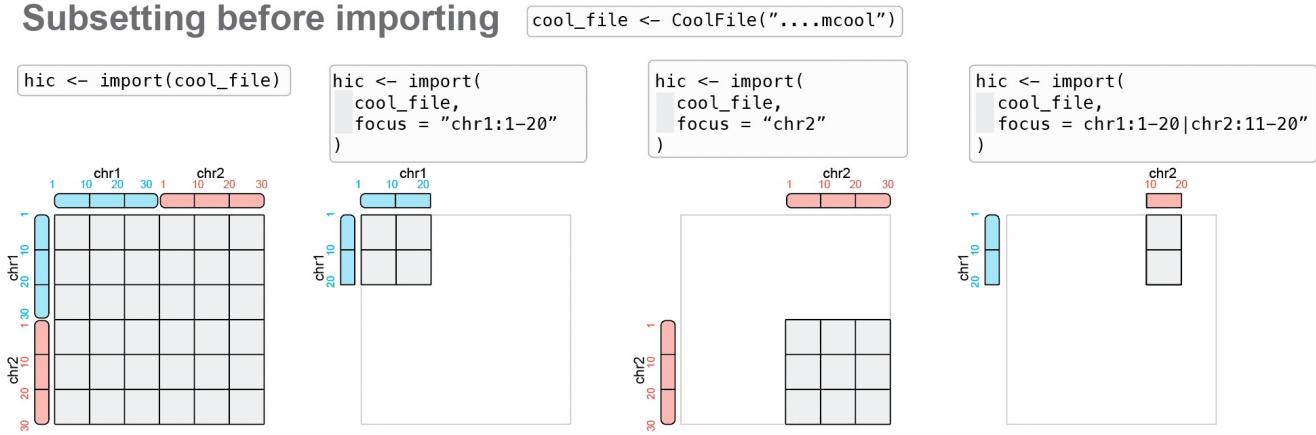


```
hic <- import(  
  cool_file,  
  focus = "chr2"  
)
```



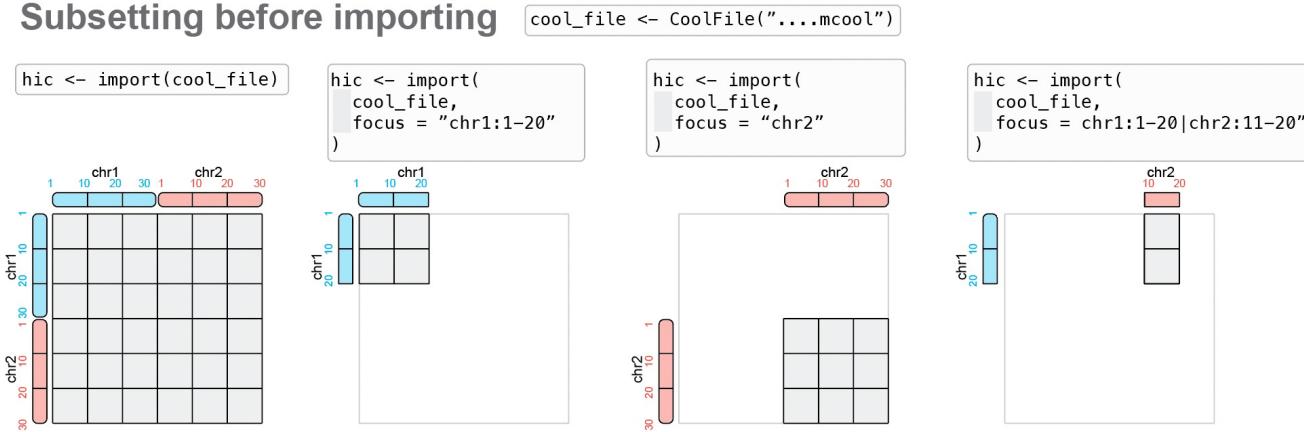
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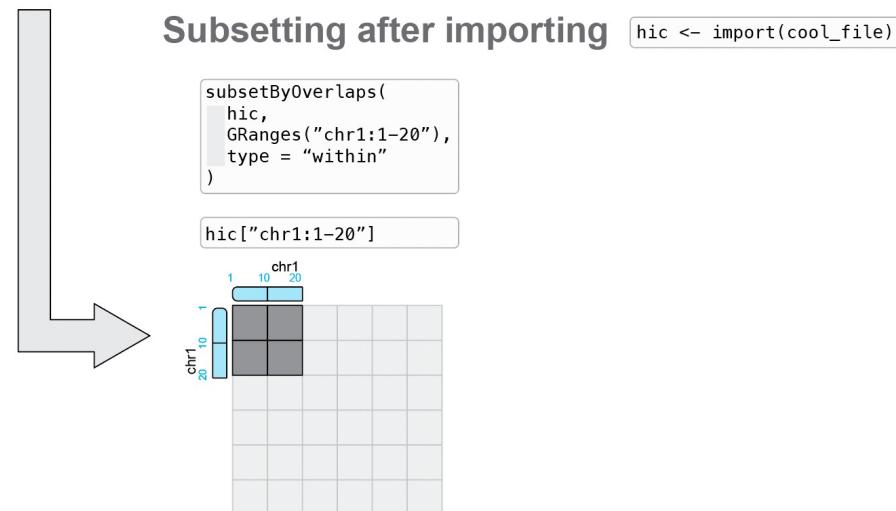


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## Subsetting before importing

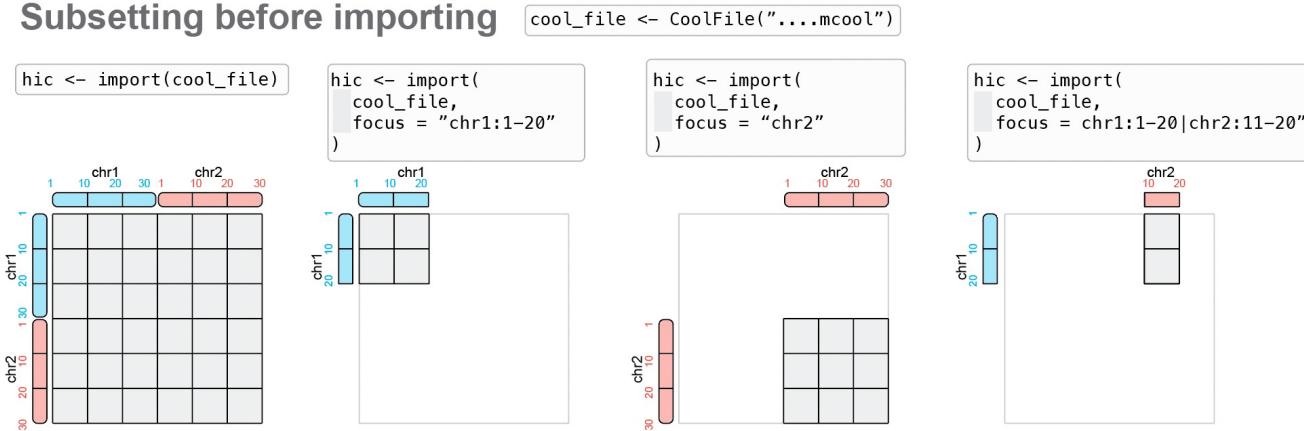


## Subsetting after importing

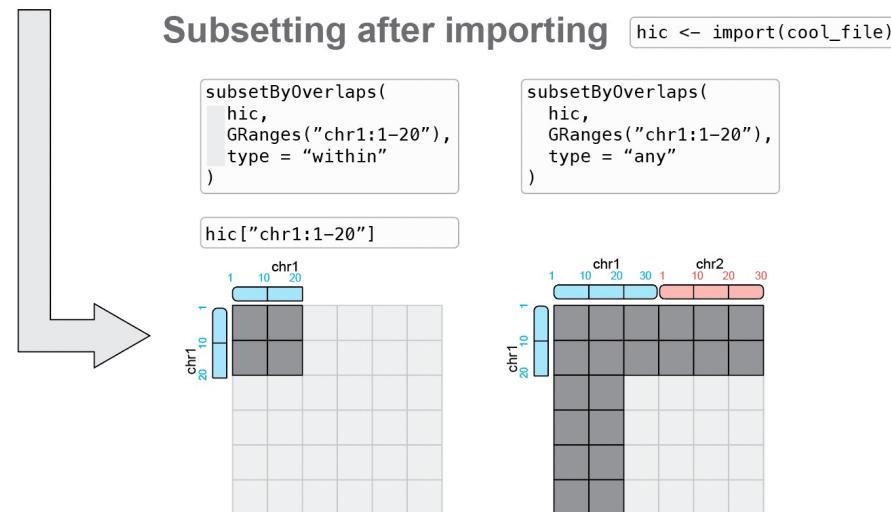


# Parsing Hi-C data in R

## Subsetting before importing

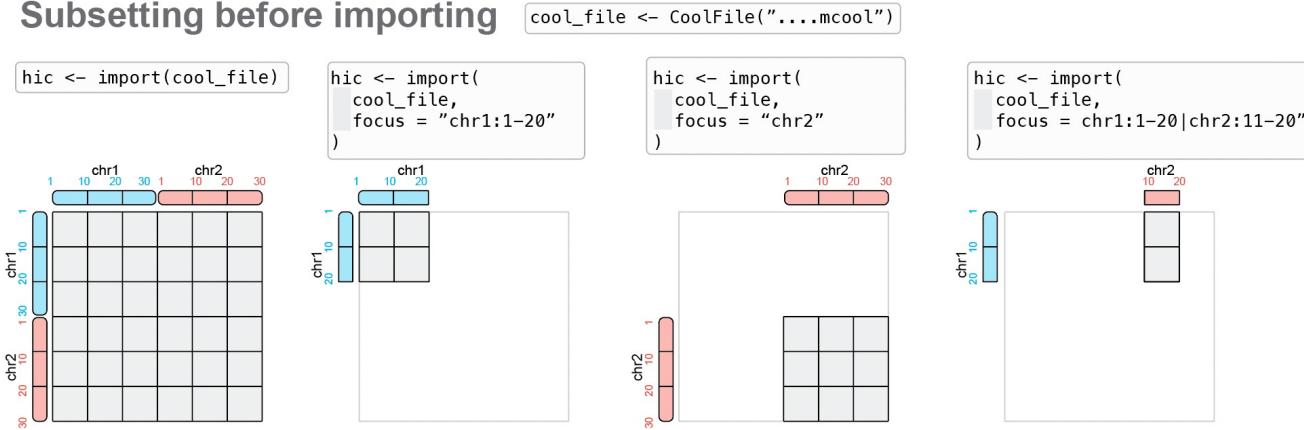


## Subsetting after importing

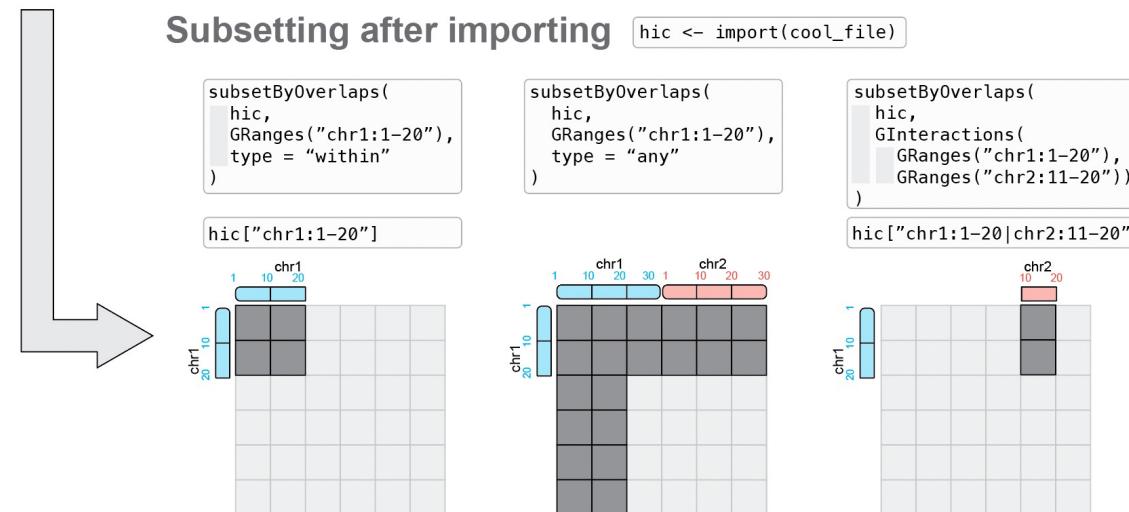


# Parsing Hi-C data in R

## Subsetting before importing



## Subsetting after importing



# Demonstration: Parsing Hi-C data in R

# Outline

- ❑ Overview of Chromosome Conformation Capture technical aspects
- ❑ Introduction to the OHCA ecosystem
- ❑ Importing Hi-C data with HiCExperiment
- ❑ Manipulating and visualizing Hi-C data with HiContacts**
- ❑ Inter-operability with existing Hi-C packages
- ❑ Wrapping-up

# Visualizing Hi-C data in R

- ❖ `HiContacts::plotMatrix()`: a generic method to plot contact map from (`Aggr`)`HiCExperiment`, `GInteractions` and `matrix` objects
  - Argument ``maxDistance = <int>`` : to plot a horizontal Hi-C map, up to a certain distance from the diagonal
  - Argument ``scale = c('linear', 'log10', 'exp0.2')`` : to rescale the counts
  - Argument ``limits = c(..., ...)`` : to clamp the color scale (re-scaled counts) to specific minimum/maximum values
  - Argument ``cmap = c(..., ..., ...)`` : to specify colors used to create a gradient color scale
  - Argument ``compare.to = <HiCExperiment>`` : to plot 2 different `HiCExperiment` objects on each side of the diagonal

# Demonstration: Visualizing Hi-C data in R

# Investigating Hi-C data in R (1)

## ❖ Arithmetic operations:

- `HiContacts::normalize()`: Normalize the contact matrix for coverage
- `HiContacts::detrend()`: Compute the observed/expected contact matrix
- `HiContacts::autocorrelate()`: Compute the auto-correlation matrix
- `HiContacts::despeckle()`: Smooth a contact matrix using a Gaussian blur
- `HiContacts::divide()`: Divide two `HiCExperiment` objects
- `HiContacts::merge()`: Merge multiple `HiCExperiment` objects together
- `HiContacts::aggregate()`: Extract “snippets” from a `HiCExperiment` object and compute average signal

# Demonstration: Investigating Hi-C data in R (1)

## Investigating Hi-C data in R (2)

### ❖ Genomic interactions analysis:

- `HiContacts::getPs()`: Compute the distance-dependent interaction frequency
- `HiContacts::v4C()`: Compute the interaction profile of a genomic locus with the rest of the genome
- `HiContacts::cisTransRatio()`: Compute the ratio of intra-chromosomal / inter-chromosomal interactions
- `HiContacts::scalogram()`: Compute the distance-dependent interaction frequency for sliding windows along the genome

# Demonstration: Investigating Hi-C data in R (2)

## Investigating Hi-C data in R (3)

### ❖ Annotation of topological features:

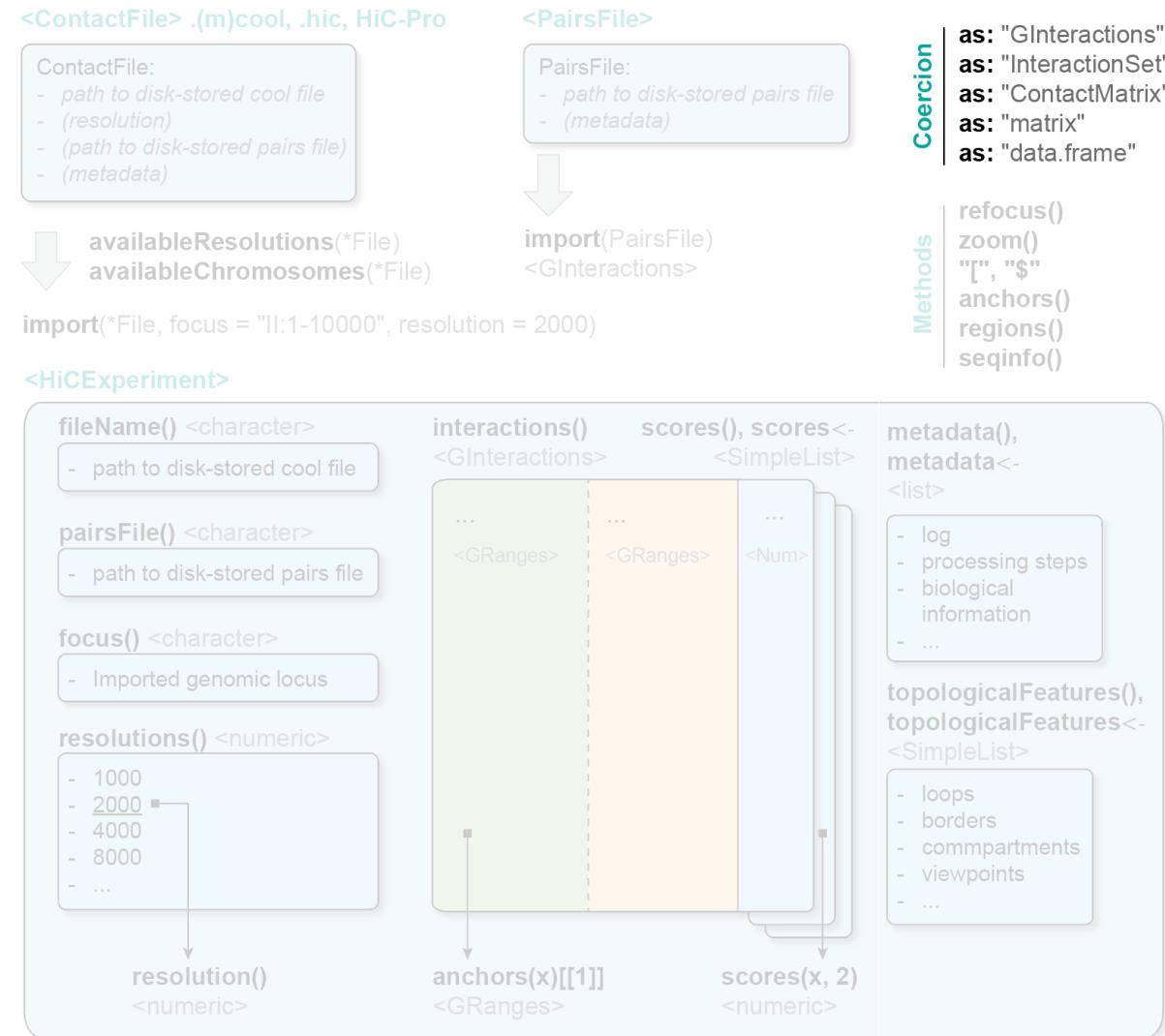
- `HiContacts::getCompartments()`: Compute and phase the eigenvector E1 from a Hi-C contact matrix, and extract A/B compartments
- `HiContacts::getDiamondInsulation()`: Compute the diamond insulation score along the diagonal of a Hi-C contact matrix, and extract significant borders
- `HiContacts::getLoops()`: Annotate focal contact enrichment (a.k.a. loops) using the computer vision-based [chromosight algorithm](#)

These functions implement standard methods used to annotate compartments, domains and chromatin loops, but more advanced approaches exist and are available in R.

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- ❑ Wrapping-up

# Coercing HiCExperiment objects



# Demonstration: Inter-operability with other packages

# Outline

- ❑ Overview of Chromosome Conformation Capture technical aspects
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- ❑ Inter-operability with existing Hi-C packages
- ❑ **Wrapping-up**

# Orchestrating Hi-C analysis with Bioconductor

