

GEF (Square Bin)

geneExp

Group

- bin10
 - Group
 - Optional
- bin20
 - Group
 - Optional
- bin50
 - Group
 - Optional
- bin100
 - Group
 - Optional
- bin200
 - Group
 - Optional
- bin500
 - Group
 - Optional

stat

Group Optional

gene

Dataset

attribute	
maxEI0	Maximum EI0 score
minEI0	Minimum EI0 score
cutoff	Threshold for filtering spots that will be used for computing EI0

compound	
gene	Gene name
MIDcount	MID count for the gene
EI0	The spatial pattern enrichment score (EI0) for the gene

attribute	
number	Number of non-zero spots in the dense matrix
minX	Minimum x coordinate in bin 1
lenX	Length of x
minY	Minimum y coordinate in bin 1
lenY	Length of y
maxMID	Maximum MID count in a spot
maxGene	Maximum gene type count in a spot
resolution	Pitch (nm) between neighbor spots

bin1

Group

compound 2D array (XxY)	
MIDcount	MID count in the spot. The spot coordinate can be identified from the row and column index of the 2D matrix plus the "minX" and "minY" specified in the attributes. Data type for "MIDcount" is dynamically changed for each sample.
genecount	Gene count in the spot. The spot coordinate can be identified from "Attributes" and the indexes of the 2D array.

bin10

Group

bin20

Group

bin50

Group

bin100

Group

bin200

Group

bin500

Group

wholeExpExon

Group Optional

bin1

Group

attribute	
maxExon	Maximum exon expression count in a spot when the bin size is 1
2D array (XxY)	
MIDCount	MID count in the spot. The spot coordinate can be identified from the row and column index of the 2D matrix plus the "minX" and "minY" specified in the attributes. Data type for "MIDcount" is dynamically changed for each sample.

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attribute

geftool_ver	geftool version
omics	Omics name
version	GEF format
gef_area	Tissue area
bin_type	Bin type

expression

Dataset

attribute	
minX	Minimum x coordinate in bin 1
minY	Minimum y coordinate in bin 1
maxX	Maximum x coordinate in bin 1
maxY	Maximum y coordinate in bin 1
maxExp	Maximum MID count in a spot when the bin size is 1. Data type for "maxExp" is dynamically changed for each sample
resolution	Physical pitch (nm) between neighbor spots

compound	
x	x coordinate in bin 1
y	y coordinate in bin 1
count	MID count at (x, y) when bin size is 1. Data type for "count" is consistent with "maxExp" in the "Attributes."

attribute	
maxExon	Max exon expression in bin 1

ID array	
count	Exon expression in bin1 at coordinate (x,y). Data type for "count" is dynamically changed for each sample.

compound	
gene	Gene name
offset	The starting row index in dataset "expression" for the gene
count	Row count

share same index

offset is the row index of "expression" dataset