1. Unsorted?
2. Nested (ragged arrays?)

GRanges

Gene 1
Exon 1
Exon 2
Gene 2
Ex 1
Ex 2

adata.var
adata.varranges

3. Range(..) index

Chr Start End

chr7
chr5

chr5 ...
chr7 ...

Ok)

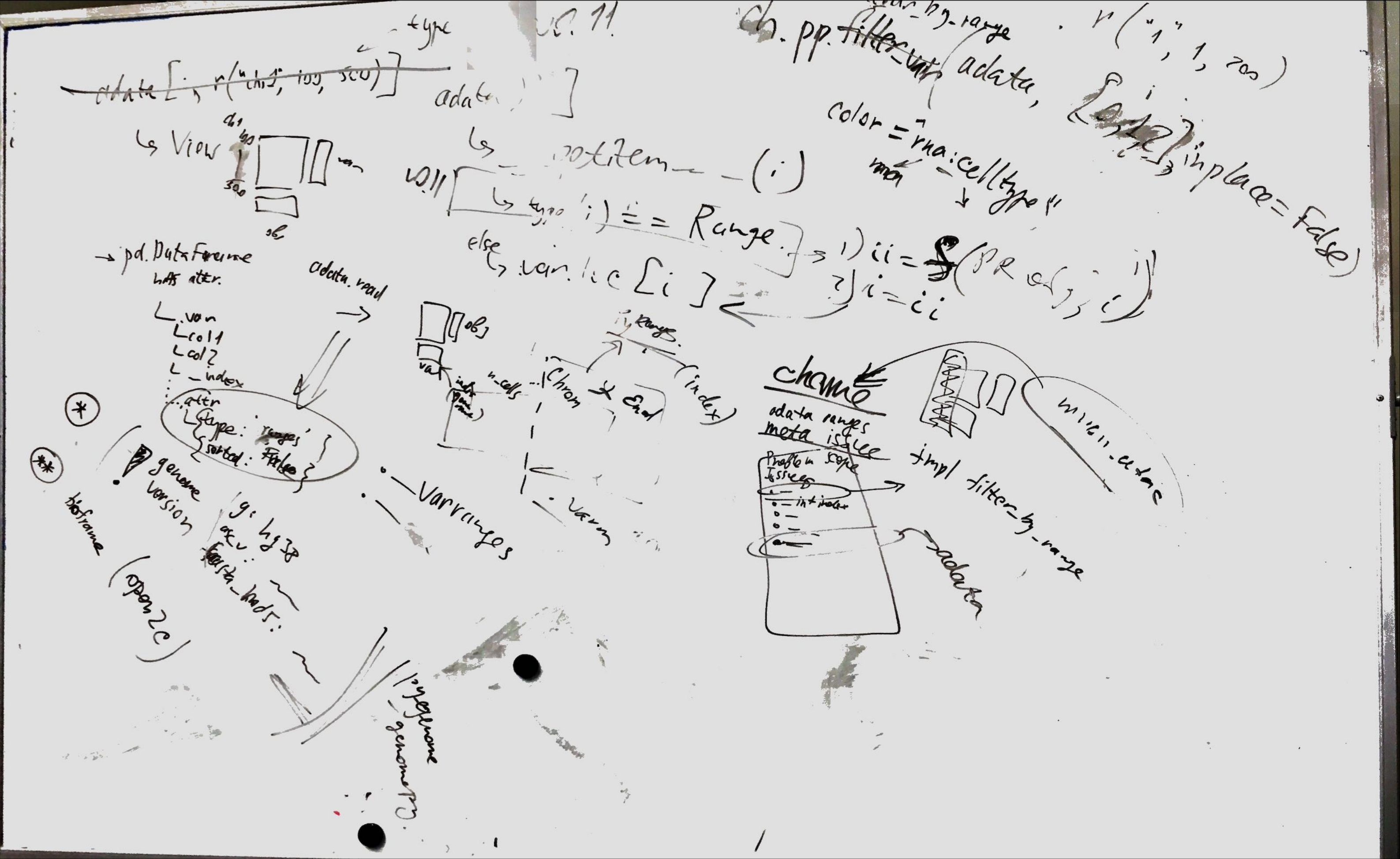
f(adata.var) ≠ f(PyRanges(adata.var))

f = return gene names
f = lambda df: df.index.values

	Chr	Start	End	Gene	
row 0	1	1	100	g4	1-300
	1	200	300	g4	
row 1	2	1	100	g8	1-500
	2	300	500	g8	

average RNA signal in exons

1 500



type
v0.11
adata[:, r("chr1", 100, 500)]
sc.pp.filter_by_range(adata, [...], inplace=False)
r("1", 1, 200)
color="rna:celltype"
View
var
obs
__getitem__(i)
type(i) == Range
else
.var.iloc[i]
pd.DataFrame
has attr.
.var
col1
col2
_index
attr
type: 'ranges'
sorted: False
adata.read
n_cells
Chrom
End
ranges
(index)
genome version
g: hg38
Varranges
chame
adata ranges
meta issue
Problem scope
Issues
int index
impl filter_by_range
adata
bioframe
(open2c)
pygenome
genome