

The R package *trioClasses* for definition of the class *SNPTrioExperiment*, an extension of *SummarizedExperiment*, for use in trio based analyses of genetic data.

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1 Classes

1.1 SnpMatrix, DataFrame, GRanges

The four key ingredients are the SNP matrix, the pedigree information as a *DataFrame*, position of the SNPs given by a *GRanges* object, and covariate data given as a *DataFrame*.

```
> sm
```

```
A SnpMatrix with 968 rows and 511 columns
Row names: subject1 ... subject968
Col names: chr14:54383433 ... chr14:54444750
```

```
> ped.DF
```

```
DataFrame with 968 rows and 6 columns
```

	famid	id	fid	mid	sex	dx
	<logical>	<character>	<logical>	<logical>	<logical>	<logical>
1	NA	subject1	NA	NA	NA	NA
2	NA	subject2	NA	NA	NA	NA
3	NA	subject3	NA	NA	NA	NA
4	NA	subject4	NA	NA	NA	NA
5	NA	subject5	NA	NA	NA	NA
6	NA	subject6	NA	NA	NA	NA
7	NA	subject7	NA	NA	NA	NA
8	NA	subject8	NA	NA	NA	NA
9	NA	subject9	NA	NA	NA	NA
...
960	NA	subject960	NA	NA	NA	NA
961	NA	subject961	NA	NA	NA	NA
962	NA	subject962	NA	NA	NA	NA
963	NA	subject963	NA	NA	NA	NA
964	NA	subject964	NA	NA	NA	NA
965	NA	subject965	NA	NA	NA	NA
966	NA	subject966	NA	NA	NA	NA
967	NA	subject967	NA	NA	NA	NA
968	NA	subject968	NA	NA	NA	NA

```
> gr
```

GRanges with 511 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
chr14:54383433	chr14	[1, 1]	*
chr14:54383470	chr14	[2, 2]	*
chr14:54383819	chr14	[3, 3]	*
chr14:54383945	chr14	[4, 4]	*
chr14:54384030	chr14	[5, 5]	*
chr14:54384232	chr14	[6, 6]	*
chr14:54384251	chr14	[7, 7]	*
chr14:54384291	chr14	[8, 8]	*
chr14:54384382	chr14	[9, 9]	*
...
chr14:54443495	chr14	[503, 503]	*
chr14:54443499	chr14	[504, 504]	*
chr14:54443514	chr14	[505, 505]	*
chr14:54443831	chr14	[506, 506]	*
chr14:54443880	chr14	[507, 507]	*
chr14:54444016	chr14	[508, 508]	*
chr14:54444124	chr14	[509, 509]	*
chr14:54444385	chr14	[510, 510]	*
chr14:54444750	chr14	[511, 511]	*

```
seqlengths:
chr14
NA
```

1.2 SummarizedExperiment

We combine three of the key ingredients when we create the SummarizedExperiment object.

```
> se <- SummarizedExperiment(assays = SimpleList(geno = t(sm)),
  colData = col.DF, rowData = gr)
```

1.3 SNP TrioExperiment

Now, we include the pedigree information as an object of class PedClass. We keep PedClass independent of SNP TrioExperiment for flexibility.

```
> ped <- PedClass(ped.DF)
> ste <- SNP TrioExperiment(se, pedigree = ped)
```

Here is the show method.

```
> ste

class: SNP TrioExperiment
dim: 511 968
exptData(0):
assays(1): geno
```

```

rownames(511): chr14:54383433 chr14:54383470 ...
chr14:54444385 chr14:54444750
rowData metadata column names(0):
colnames(968): subject1 subject2 ... subject967 subject968
colData names(1): id
pedigree(968): famid id fid mid sex dx

```

And now we verify that it is indeed an extension of SummarizedExperiment.

```
> getClass("SNPTrioExperiment")
```

```
Class "SNPTrioExperiment" [package "trioClasses"]
```

Slots:

Name:	pedigree	exptData
Class:	PedClass	SimpleList

Name:	rowData	colData
Class:	GenomicRangesORGRangesList	DataFrame

Name:	assays
Class:	Assays

```
Extends: "SummarizedExperiment"
```

1.4 PedClass

Now we investigate the pedigree slot of the SNPTrioExperiment object.

```
> class(pedigree(ste))
```

```

[1] "PedClass"
attr("package")
[1] "trioClasses"

```

```
> getClass("PedClass")
```

```
Class "PedClass" [package "trioClasses"]
```

Slots:

Name:	rownames	nrows	listData
Class:	characterORNULL	integer	list

Name:	elementType	elementMetadata	metadata
Class:	character	DataTableORNULL	list

Extends:

```

Class "DataFrame", directly
Class "DataTable", by class "DataFrame", distance 2
Class "SimpleList", by class "DataFrame", distance 2

```

```

Class "DataTableORNULL", by class "Dataframe", distance 3
Class "List", by class "Dataframe", distance 3
Class "Vector", by class "Dataframe", distance 4
Class "Annotated", by class "Dataframe", distance 5

```

```
> pedigree(ste)
```

```
PedClass with 968 rows and 6 columns
```

	famid	id	fid	mid	sex	dx
	<logical>	<character>	<logical>	<logical>	<logical>	<logical>
1	NA	subject1	NA	NA	NA	NA
2	NA	subject2	NA	NA	NA	NA
3	NA	subject3	NA	NA	NA	NA
4	NA	subject4	NA	NA	NA	NA
5	NA	subject5	NA	NA	NA	NA
6	NA	subject6	NA	NA	NA	NA
7	NA	subject7	NA	NA	NA	NA
8	NA	subject8	NA	NA	NA	NA
9	NA	subject9	NA	NA	NA	NA
...
960	NA	subject960	NA	NA	NA	NA
961	NA	subject961	NA	NA	NA	NA
962	NA	subject962	NA	NA	NA	NA
963	NA	subject963	NA	NA	NA	NA
964	NA	subject964	NA	NA	NA	NA
965	NA	subject965	NA	NA	NA	NA
966	NA	subject966	NA	NA	NA	NA
967	NA	subject967	NA	NA	NA	NA
968	NA	subject968	NA	NA	NA	NA

1.5 geno accessor

```
> class(geno(ste))
```

```

[1] "SnpMatrix"
attr(,"package")
[1] "snpStats"

```

```
> getClass("SnpMatrix")
```

```
Class "SnpMatrix" [package "snpStats"]
```

```
Slots:
```

```

Name:    .Data
Class: matrix

```

```
Extends:
```

```

Class "matrix", from data part
Class "array", by class "matrix", distance 2
Class "mMatrix", by class "matrix", distance 2
Class "structure", by class "matrix", distance 3

```

Class "vector", by class "matrix", distance 4, with explicit coerce

Known Subclasses: "XSnpmatrix"

```
> geno(ste)
```

A SnpMatrix with 968 rows and 511 columns
Row names: subject1 ... subject968
Col names: chr14:54383433 ... chr14:54444750

1.6 RowData

```
> rowData(ste)
```

GRanges with 511 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
chr14:54383433	chr14	[1, 1]	*
chr14:54383470	chr14	[2, 2]	*
chr14:54383819	chr14	[3, 3]	*
chr14:54383945	chr14	[4, 4]	*
chr14:54384030	chr14	[5, 5]	*
chr14:54384232	chr14	[6, 6]	*
chr14:54384251	chr14	[7, 7]	*
chr14:54384291	chr14	[8, 8]	*
chr14:54384382	chr14	[9, 9]	*
...
chr14:54443495	chr14	[503, 503]	*
chr14:54443499	chr14	[504, 504]	*
chr14:54443514	chr14	[505, 505]	*
chr14:54443831	chr14	[506, 506]	*
chr14:54443880	chr14	[507, 507]	*
chr14:54444016	chr14	[508, 508]	*
chr14:54444124	chr14	[509, 509]	*
chr14:54444385	chr14	[510, 510]	*
chr14:54444750	chr14	[511, 511]	*

seqlengths:
chr14
NA

2 Validity

3 Methods