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

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## 1 Packages & Data

```
> library("trioClasses")
> data("cleft.ts.pedigree")
> data("8q24-european-all.sm")
```

## 2 SummarizedExperiment

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

## 3 Pedigree

```
> ped <- PedClass(cleft.ts.pedigree)
```

## 4 FamilyExperiment

```
> (fe <- FamilyExperiment(se, pedigree = ped))

class: FamilyExperiment
dim: 8951 960
exptData(0):
assays(1): geno
rownames(8951): chr8:129296000 chr8:129296113 ...
  chr8:130354703 chr8:130354790
rowData metadata column names(0):
colnames(960): H_ME-DS10776_2-DS10776_2
  H_ME-DS10776_3-DS10776_3 ... H_ME-DS11313_3-DS11313_3
  H_ME-DS11313_1-DS11313_1
colData names(1): id
pedigree(4139): famid id fid mid sex dx
complete trios(320):
```

# 5  ScanTrio

The two implementations (R, C++) do not share a common method to deal with missing genotypes. So we remove all missingness for comparison.

```
> na.markers <- which(colSums(is.na(geno(fe))) > 0)
> (fe <- fe[-na.markers])

class: FamilyExperiment
dim: 4842 960
exptData(0):
assays(1): geno
rownames(4842): chr8:129296191 chr8:129296198 ...
  chr8:130354296 chr8:130354790
rowData metadata column names(0):
colnames(960): H_ME-DS10776_2-DS10776_2
  H_ME-DS10776_3-DS10776_3 ... H_ME-DS11313_3-DS11313_3
  H_ME-DS11313_1-DS11313_1
colData names(1): id
pedigree(4139): famid id fid mid sex dx
complete trios(320):

> wd <- 50000
> window <- GRanges(seqnames = seqnames(fe), ranges = IRanges(start = start(rowData(fe)),
    width = wd))
> (scan.trio <- ScanTrio(object = fe[MAF(fe) <= 0.01],
    window = window, block = range(rowData(fe))))

GRanges with 4842 ranges and 7 metadata columns:
        seqnames                    ranges strand  |          lr
          <Rle>                 <IRanges>  <Rle>  | <numeric>
    [1]     chr8 [129296191, 129346190]      *    |         1
    [2]     chr8 [129296198, 129346197]      *    |         1
    [3]     chr8 [129296209, 129346208]      *    |         1
    [4]     chr8 [129296289, 129346288]      *    |         1
    [5]     chr8 [129296343, 129346342]      *    |         1
    [6]     chr8 [129296732, 129346731]      *    |         1
    [7]     chr8 [129296739, 129346738]      *    |         1
    [8]     chr8 [129296848, 129346847]      *    |         1
    [9]     chr8 [129296944, 129346943]      *    |         1
    ...      ...                      ...    ... ...       ...
 [4834]     chr8 [130351706, 130401705]      *    |         1
 [4835]     chr8 [130351741, 130401740]      *    |         1
 [4836]     chr8 [130352210, 130402209]      *    |         1
 [4837]     chr8 [130352659, 130402658]      *    |         1
 [4838]     chr8 [130353414, 130403413]      *    |         1
 [4839]     chr8 [130353471, 130403470]      *    |         1
 [4840]     chr8 [130354182, 130404181]      *    |         1
 [4841]     chr8 [130354296, 130404295]      *    |         1
 [4842]     chr8 [130354790, 130404789]      *    |         1
          minor.in  major.in minor.out major.out mendel.in mendel.out
         <integer> <integer> <integer> <integer> <integer>  <integer>
```

```
[1]          189      205      3564      3750         0         0
[2]          189      205      3564      3750         0         0
[3]          189      205      3564      3750         0         0
[4]          189      204      3564      3751         0         0
[5]          191      207      3562      3748         0         0
[6]          192      209      3561      3746         0         0
[7]          192      208      3561      3747         0         0
[8]          191      208      3562      3747         0         0
[9]          190      208      3563      3747         0         0
...          ...      ...       ...       ...       ...       ...
[4834]         4       10      3749      3945         0         0
[4835]         4        9      3749      3946         0         0
[4836]         4        8      3749      3947         0         0
[4837]         4        7      3749      3948         0         0
[4838]         4        6      3749      3949         0         0
[4839]         3        6      3750      3949         0         0
[4840]         1        3      3752      3952         0         0
[4841]         1        2      3752      3953         0         0
[4842]         0        1      3753      3954         0         0
---
seqlengths:
 chr8
   NA
```

The following function creates the files needed to run scan-trio-cpp. The following command writes four files to the current working directory — 8q24.ped, 8q24.map, 8q24.blocks, 8q24.weights. Use these with scan-trios to compare. Please note which versions of trioClasses and scan-trios you are using.

```
> trioClasses:::make.files.for.cpp(fe, fileroot = "./8q24")
```