

# Run GENESPACE vignettes - Cotton genomes treated as tetraploids

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## 1. Global Parameters

```
baseDir <- "/Users/jlovell/Desktop/GENESPACE_data/results/"
rawAnnotationDir <- "/Users/jlovell/Desktop/GENESPACE_data"
mcscanDir <- "/Users/jlovell/Documents/comparative_genomics/programs/MCScanX"
nThreads <- 6
path2of <- "orthofinder" # since orthofinder is in the path via conda
```

## 2. Set parameters

**NOTE:** Wheat, Maize and Switchgrass WGD occurred after MRCA of all genomes below. Therefore, treat them as polyploid.

Since some ploidy > 1, run orthofinder again in syntenic blocks.

```
cottonSplit <- list(
  wd = file.path(baseDir, "cotton_split"),
  speciesIDs = "cotton",
  genomes = data.table(do.call("rbind", list(
    c(genome = "GbarbadenseA", version = "Gbarbadense", ploidy = 1),
    c("GdarwiniiA", "Gdarwinii", 1),
    c("GtomentosumA", "Gtomentosum", 1),
    c("GbarbadenseD", "Gbarbadense", 1),
    c("GdarwiniiD", "Gdarwinii", 1),
    c("GtomentosumD", "Gtomentosum", 1))))))

cottonParams <- list(
  pepString = "fa",
  orthofinderInBlk = T,
  blkSize = 10,
  nGaps = 10)
```

## 3 Initialize the cotton run with the above specified parameters

```
gparCotton2x <- with(cottonSplit, init_genespace(
  genomeIDs = genomes$genome,
```

```

versionIDs = genomes$version,
ploidy = genomes$ploidy,
speciesIDs = rep(speciesIDs, length(genomes$genome)),
orthofinderInBlk = TRUE,
pepString = "fa",
wd = wd,
nCores = nThreads,
path2orthofinder = path2of,
path2mcscanx = mcscanDir,
rawGenomeDir = rawAnnotationDir))

## set working directory to /Users/jlovell/Desktop/GENESPACE_data/results/cotton_split
##
## found raw gff files:
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gbarbadense/annotation/Gbarbadense.gff3.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gdarwinii/annotation/Gdarwinii.gff3.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gtomentosum/annotation/Gtomentosum.gff3.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gbarbadense/annotation/Gbarbadense.gff3.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gdarwinii/annotation/Gdarwinii.gff3.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gtomentosum/annotation/Gtomentosum.gff3.gz
##
## found raw peptide files:
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gbarbadense/annotation/Gbarbadense.fa.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gdarwinii/annotation/Gdarwinii.fa.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gtomentosum/annotation/Gtomentosum.fa.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gbarbadense/annotation/Gbarbadense.fa.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gdarwinii/annotation/Gdarwinii.fa.gz
## /Users/jlovell/Desktop/GENESPACE_data/cotton/Gtomentosum/annotation/Gtomentosum.fa.gz
##
##
## Can't find all parsed annotation files ... need to run parse_annotations, parse_ncbi or parse_phytoz
##
## GENESPACE run initialized:
## Initial orthofinder database generation method: default inside R
## Orthology graph method: inBlock

```

## 4 Parse the raw annotations.

Parse full annotations

```

parse_phytozome(gsParam = gparCotton2x)

## Parsing annotations: GbarbadenseA
## Reading gff ... found 74561 protein coding genes
## Reading peptide fasta ... found 74561 / 74561 total and unique entries
## Merging fa and gff found 74561 matching entires
## Parsing annotations: GdarwiniiA
## Reading gff ... found 78303 protein coding genes
## Reading peptide fasta ... found 78303 / 78303 total and unique entries
## Merging fa and gff found 78303 matching entires
## Parsing annotations: GtomentosumA
## Reading gff ... found 78338 protein coding genes
## Reading peptide fasta ... found 78338 / 78338 total and unique entries

```

```
## Merging fa and gff found 78338 matching entires
## Parsing annotations: GbarbadenseD
## Reading gff ... found 74561 protein coding genes
## Reading peptide fasta ... found 74561 / 74561 total and unique entries
## Merging fa and gff found 74561 matching entires
## Parsing annotations: GdarwiniiD
## Reading gff ... found 78303 protein coding genes
## Reading peptide fasta ... found 78303 / 78303 total and unique entries
## Merging fa and gff found 78303 matching entires
## Parsing annotations: GtomentosumD
## Reading gff ... found 78338 protein coding genes
## Reading peptide fasta ... found 78338 / 78338 total and unique entries
## Merging fa and gff found 78338 matching entires
```

Split into subgenomes

```
chk <- lapply(names(gparCotton2x$paths$gff[1:3]), function(i){
  g <- subset(fread(gparCotton2x$paths$gff[i]), grepl("^A", chr))
  p <- Biostrings::readAAStringSet(gparCotton2x$paths$peptide[i])[g$id]
  fwrite(g, file = gparCotton2x$paths$gff[i], sep = "\t", quote = F)
  Biostrings::writeXStringSet(p, filepath = gparCotton2x$paths$peptide[i])
})
chk <- lapply(names(gparCotton2x$paths$gff[4:6]), function(i){
  g <- subset(fread(gparCotton2x$paths$gff[i]), grepl("^D", chr))
  p <- Biostrings::readAAStringSet(gparCotton2x$paths$peptide[i])[g$id]
  fwrite(g, file = gparCotton2x$paths$gff[i], sep = "\t", quote = F)
  Biostrings::writeXStringSet(p, filepath = gparCotton2x$paths$peptide[i])
})
```

## 5 Get orthofinder results

```
gparCotton2x <- set_sytenyParams(gsParam = gparCotton2x)
gparCotton2x <- run_orthofinder(gsParam = gparCotton2x)
```

```
## Running 'default' genespace orthofinder method
## #####
## Cleaning out orthofinder directory and prepping run
## Calculating blast results and running OrthoFinder
## #####
## #####
##
##
## OrthoFinder version 2.5.4 Copyright (C) 2014 David Emms
##
## 2022-02-12 20:32:52 : Starting OrthoFinder 2.5.4
## 6 thread(s) for highly parallel tasks (BLAST searches etc.)
## 1 thread(s) for OrthoFinder algorithm
##
## Checking required programs are installed
## -----
## Test can run "mcl -h" - ok
## Test can run "fastme -i /Users/jlovell/Desktop/GENESPACE_data/results//cotton_split/orthofinder/Res
##
```

```

## Dividing up work for BLAST for parallel processing
## -----
## 2022-02-12 20:32:54 : Creating diamond database 1 of 6
## 2022-02-12 20:32:54 : Creating diamond database 2 of 6
## 2022-02-12 20:32:55 : Creating diamond database 3 of 6
## 2022-02-12 20:32:55 : Creating diamond database 4 of 6
## 2022-02-12 20:32:56 : Creating diamond database 5 of 6
## 2022-02-12 20:32:56 : Creating diamond database 6 of 6
##
## Running diamond all-versus-all
## -----
## Using 6 thread(s)
## 2022-02-12 20:32:56 : This may take some time....
## 2022-02-12 20:32:57 : Done 0 of 36
## 2022-02-12 20:54:28 : Done 10 of 36
## 2022-02-12 21:14:53 : Done 20 of 36
## 2022-02-12 21:25:55 : Done 30 of 36
## 2022-02-12 21:35:36 : Done all-versus-all sequence search
##
## Running OrthoFinder algorithm
## -----
## 2022-02-12 21:35:37 : Initial processing of each species
## 2022-02-12 21:36:17 : Initial processing of species 0 complete
## 2022-02-12 21:37:01 : Initial processing of species 1 complete
## 2022-02-12 21:37:44 : Initial processing of species 2 complete
## 2022-02-12 21:38:30 : Initial processing of species 3 complete
## 2022-02-12 21:39:13 : Initial processing of species 4 complete
## 2022-02-12 21:39:59 : Initial processing of species 5 complete
## 2022-02-12 21:40:19 : Connected putative homologues
## 2022-02-12 21:40:24 : Written final scores for species 0 to graph file
## 2022-02-12 21:40:30 : Written final scores for species 1 to graph file
## 2022-02-12 21:40:35 : Written final scores for species 2 to graph file
## 2022-02-12 21:40:41 : Written final scores for species 3 to graph file
## 2022-02-12 21:40:46 : Written final scores for species 4 to graph file
## 2022-02-12 21:40:52 : Written final scores for species 5 to graph file
## 2022-02-12 21:41:24 : Ran MCL
##
## Writing orthogroups to file
## -----
## OrthoFinder assigned 224499 genes (98.3% of total) to 36868 orthogroups. Fifty percent of all genes
##
## 2022-02-12 21:41:56 : Done orthogroups
##
## Analysing Orthogroups
## =====
##
## Calculating gene distances
## -----
## 2022-02-12 21:46:24 : Done
## 2022-02-12 21:46:27 : Done 0 of 29385
## 2022-02-12 21:46:32 : Done 1000 of 29385
## 2022-02-12 21:46:36 : Done 2000 of 29385
## 2022-02-12 21:46:40 : Done 3000 of 29385
## 2022-02-12 21:46:45 : Done 4000 of 29385

```

```

## 2022-02-12 21:46:49 : Done 5000 of 29385
## 2022-02-12 21:46:54 : Done 6000 of 29385
## 2022-02-12 21:46:58 : Done 7000 of 29385
## 2022-02-12 21:47:03 : Done 8000 of 29385
## 2022-02-12 21:47:07 : Done 9000 of 29385
## 2022-02-12 21:47:11 : Done 10000 of 29385
## 2022-02-12 21:47:16 : Done 11000 of 29385
## 2022-02-12 21:47:20 : Done 12000 of 29385
## 2022-02-12 21:47:24 : Done 13000 of 29385
## 2022-02-12 21:47:27 : Done 14000 of 29385
## 2022-02-12 21:47:31 : Done 15000 of 29385
## 2022-02-12 21:47:35 : Done 16000 of 29385
## 2022-02-12 21:47:39 : Done 17000 of 29385
## 2022-02-12 21:47:42 : Done 18000 of 29385
## 2022-02-12 21:47:46 : Done 19000 of 29385
## 2022-02-12 21:47:50 : Done 20000 of 29385
## 2022-02-12 21:47:54 : Done 21000 of 29385
## 2022-02-12 21:47:58 : Done 22000 of 29385
## 2022-02-12 21:48:02 : Done 23000 of 29385
## 2022-02-12 21:48:06 : Done 24000 of 29385
## 2022-02-12 21:48:09 : Done 25000 of 29385
## 2022-02-12 21:48:13 : Done 26000 of 29385
## 2022-02-12 21:48:17 : Done 27000 of 29385
## 2022-02-12 21:48:21 : Done 28000 of 29385
## 2022-02-12 21:48:25 : Done 29000 of 29385
##
## Inferring gene and species trees
## -----
##
## 23841 trees had all species present and will be used by STAG to infer the species tree
##
## Best outgroup(s) for species tree
## -----
## 2022-02-12 21:56:20 : Starting STRIDE
## 2022-02-12 21:56:26 : Done STRIDE
## Observed 225 well-supported, non-terminal duplications. 215 support the best root and 10 contradict
## Best outgroup for species tree:
##   GbarbadenseA, GtomentosumA, GdarwiniiA
##
## Reconciling gene trees and species tree
## -----
## Outgroup: GbarbadenseA, GtomentosumA, GdarwiniiA
## 2022-02-12 21:56:26 : Starting Recon and orthologues
## 2022-02-12 21:56:26 : Starting OF Orthologues
## 2022-02-12 21:56:26 : Done 0 of 29385
## 2022-02-12 21:56:35 : Done 1000 of 29385
## 2022-02-12 21:56:39 : Done 2000 of 29385
## 2022-02-12 21:56:44 : Done 3000 of 29385
## 2022-02-12 21:56:48 : Done 4000 of 29385
## 2022-02-12 21:56:51 : Done 5000 of 29385
## 2022-02-12 21:56:54 : Done 6000 of 29385
## 2022-02-12 21:56:56 : Done 7000 of 29385
## 2022-02-12 21:56:59 : Done 8000 of 29385
## 2022-02-12 21:57:02 : Done 9000 of 29385

```

```

## 2022-02-12 21:57:04 : Done 10000 of 29385
## 2022-02-12 21:57:07 : Done 11000 of 29385
## 2022-02-12 21:57:10 : Done 12000 of 29385
## 2022-02-12 21:57:12 : Done 13000 of 29385
## 2022-02-12 21:57:15 : Done 14000 of 29385
## 2022-02-12 21:57:18 : Done 15000 of 29385
## 2022-02-12 21:57:21 : Done 16000 of 29385
## 2022-02-12 21:57:24 : Done 17000 of 29385
## 2022-02-12 21:57:26 : Done 18000 of 29385
## 2022-02-12 21:57:29 : Done 19000 of 29385
## 2022-02-12 21:57:32 : Done 20000 of 29385
## 2022-02-12 21:57:34 : Done 21000 of 29385
## 2022-02-12 21:57:37 : Done 22000 of 29385
## 2022-02-12 21:57:40 : Done 23000 of 29385
## 2022-02-12 21:57:43 : Done 24000 of 29385
## 2022-02-12 21:57:45 : Done 25000 of 29385
## 2022-02-12 21:57:48 : Done 26000 of 29385
## 2022-02-12 21:57:50 : Done 27000 of 29385
## 2022-02-12 21:57:53 : Done 28000 of 29385
## 2022-02-12 21:57:55 : Done 29000 of 29385
## 2022-02-12 21:57:56 : Done 0f Orthologues
##
## Writing results files
## =====
## 2022-02-12 21:58:12 : Done orthologues
##
## Results:
##   /Users/jlovell/Desktop/GENESPACE_data/results/cotton_split/orthofinder/Results_Feb12/
##
## CITATION:
##   When publishing work that uses OrthoFinder please cite:
##   Emms D.M. & Kelly S. (2019), Genome Biology 20:238
##
##   If you use the species tree in your work then please also cite:
##   Emms D.M. & Kelly S. (2017), MBE 34(12): 3267-3278
##   Emms D.M. & Kelly S. (2018), bioRxiv https://doi.org/10.1101/267914

```

Also set the synteny parameters as default.

```

gparCotton2x <- set_syntenyParams(
  gsParam = gparCotton2x,
  blkSize = 10,
  nGaps = 10)

```

## 6 Build synteny data

```

gparCotton2x <- find_orthofinderResults(gsParam = gparCotton2x)
gparCotton2x <- synteny(gsParam = gparCotton2x, overwrite = T)

```

```

## Parsing the gff files ...
## Reading the gffs and adding orthofinder IDs ... Done!
## Found 40685 global OGs for 228316 genes
## QC-ing genome to ensure chromosomes/scaffolds are big enough...

```

```

##           Genome: n. chrs PASS/FAIL, n. genes PASS/FAIL, n. OGs PASS/FAIL
##   GbarbadenseA: 13/0, 34857/0, 32801/0
##   GbarbadenseD: 13/0, 37550/0, 34837/0
##   GdarwiniiA: 13/0, 38078/0, 35499/0
##   GdarwiniiD: 13/0, 39779/0, 36512/0
##   GtomentosumA: 13/0, 38045/0, 35346/0
##   GtomentosumD: 13/0, 40007/0, 36791/0
## All look good!
## Defining collinear orthogroup arrays ...
## Found the following counts of arrays / genome:
##   GbarbadenseA: 2706 genes in 1073 collinear arrays
##   GbarbadenseD: 3575 genes in 1320 collinear arrays
##   GdarwiniiA: 3240 genes in 1269 collinear arrays
##   GdarwiniiD: 4167 genes in 1476 collinear arrays
##   GtomentosumA: 3489 genes in 1343 collinear arrays
##   GtomentosumD: 4104 genes in 1496 collinear arrays
## Pulling synteny for 21 unique pairwise combinations of genomes
## Running 4 chunks of 6 combinations each:
## Chunk 1 / 4 (21:58:31) ... Done!
## Gtomento-Gtomento: 655357 (tot), 82369/13 (reg), 40003/13 (blk)
## Gtomento-Gdarwini: 652781 (tot), 81820/15 (reg), 34752/47 (blk)
## Gdarwini-Gdarwini: 658415 (tot), 87001/13 (reg), 39777/13 (blk)
## Gtomento-Gdarwini: 615716 (tot), 63465/29 (reg), 29640/134 (blk)
## Gtomento-Gtomento: 617153 (tot), 65309/27 (reg), 29704/142 (blk)
## Gdarwini-Gdarwini: 620975 (tot), 64577/28 (reg), 29746/128 (blk)
## Chunk 2 / 4 (22:00:17) ... Done!
## Gdarwini-Gtomento: 618627 (tot), 66367/27 (reg), 29655/139 (blk)
## Gtomento-Gbarbade: 629173 (tot), 75441/15 (reg), 33437/50 (blk)
## Gdarwini-Gbarbade: 631311 (tot), 78243/13 (reg), 34294/28 (blk)
## Gdarwini-Gdarwini: 616216 (tot), 68232/13 (reg), 38076/13 (blk)
## Gdarwini-Gtomento: 610865 (tot), 67599/13 (reg), 33055/45 (blk)
## Gtomento-Gtomento: 614195 (tot), 70569/13 (reg), 38043/13 (blk)
## Chunk 3 / 4 (22:01:46) ... Done!
## Gdarwini-Gbarbade: 599083 (tot), 60993/26 (reg), 29202/121 (blk)
## Gtomento-Gbarbade: 598784 (tot), 62876/26 (reg), 29151/142 (blk)
## Gbarbade-Gbarbade: 613444 (tot), 75470/13 (reg), 37544/13 (blk)
## Gtomento-Gbarbade: 594145 (tot), 60185/27 (reg), 28781/141 (blk)
## Gdarwini-Gbarbade: 597135 (tot), 60993/26 (reg), 28773/130 (blk)
## Gdarwini-Gbarbade: 583967 (tot), 62131/14 (reg), 32205/28 (blk)
## Chunk 4 / 4 (22:03:07) ... Done!
## Gtomento-Gbarbade: 583425 (tot), 63054/14 (reg), 31186/55 (blk)
## Gbarbade-Gbarbade: 579712 (tot), 58518/26 (reg), 28394/133 (blk)
## Gbarbade-Gbarbade: 564235 (tot), 60241/13 (reg), 34849/13 (blk)
## Defining synteny-constrained orthogroups ...
## Found 53524 synteny-split OGs for 228316 genes
## Running orthofinder by region ...
## genome combinat. : n. non-self genes, nOGs global/syntenic/inblk
## Gbarbade-Gbarbade: no non-self syn. regions
## Gdarwini-Gbarbade: 64009 genes, 29346 / 32864 / 32596
## Gdarwini-Gdarwini: no non-self syn. regions
## Gdarwini-Gtomento: 65953 genes, 30353 / 34252 / 33771
## Gdarwini-Gbarbade: 60002 genes, 28936 / 31965 / 31381
## Gtomento-Gbarbade: 62596 genes, 29155 / 32576 / 32142
## Gtomento-Gtomento: no non-self syn. regions

```

```

## Gtomento-Gbarbade: 60052 genes, 28930 / 31960 / 31342
## Gbarbade-Gbarbade: 58912 genes, 28365 / 31318 / 30756
## Gbarbade-Gbarbade: no non-self syn. regions
## Gdarwini-Gbarbade: 59333 genes, 28598 / 31588 / 31015
## Gdarwini-Gdarwini: 61026 genes, 29420 / 32523 / 31920
## Gdarwini-Gtomento: 60734 genes, 29245 / 32327 / 31715
## Gdarwini-Gbarbade: 67673 genes, 30881 / 34777 / 34409
## Gdarwini-Gdarwini: no non-self syn. regions
## Gtomento-Gbarbade: 59531 genes, 28614 / 31650 / 31101
## Gtomento-Gdarwini: 60865 genes, 29271 / 32377 / 31823
## Gtomento-Gtomento: 61153 genes, 29305 / 32471 / 31896
## Gtomento-Gbarbade: 66639 genes, 30810 / 34664 / 34127
## Gtomento-Gdarwini: 68703 genes, 31505 / 35646 / 35102
## Gtomento-Gtomento: no non-self syn. regions
## Combining synteny-constrained and inblock orthogroups ...
## syn OGs: 53524, inblk OGs: 92798, combined OGs: 51318
## Found the following counts of arrays / genome:
##   GbarbadenseA: 2949 genes in 1151 collinear arrays
##   GbarbadenseD: 3821 genes in 1391 collinear arrays
##   GdarwiniA: 3592 genes in 1392 collinear arrays
##   GdarwiniD: 4499 genes in 1580 collinear arrays
##   GtomentosumA: 3769 genes in 1431 collinear arrays
##   GtomentosumD: 4404 genes in 1585 collinear arrays
## Pulling synteny for 21 unique pairwise combinations of genomes
## Running 4 chunks of 6 combinations each:
## Chunk 1 / 4 (22:16:08) ... Done!
## Gtomento-Gtomento: 655357 (tot), 82405/13 (reg), 40003/13 (blk)
## Gtomento-Gdarwini: 652781 (tot), 82044/15 (reg), 34393/47 (blk)
## Gdarwini-Gdarwini: 658415 (tot), 87051/13 (reg), 39777/13 (blk)
## Gtomento-Gdarwini: 615716 (tot), 63683/28 (reg), 29313/133 (blk)
## Gtomento-Gtomento: 617153 (tot), 65566/27 (reg), 29437/144 (blk)
## Gdarwini-Gdarwini: 620975 (tot), 64655/28 (reg), 29456/128 (blk)
## Chunk 2 / 4 (22:17:48) ... Done!
## Gdarwini-Gtomento: 618627 (tot), 66475/27 (reg), 29371/139 (blk)
## Gtomento-Gbarbade: 629173 (tot), 75548/15 (reg), 33070/50 (blk)
## Gdarwini-Gbarbade: 631311 (tot), 78439/13 (reg), 33959/28 (blk)
## Gdarwini-Gdarwini: 616216 (tot), 68278/13 (reg), 38076/13 (blk)
## Gdarwini-Gtomento: 610865 (tot), 67643/13 (reg), 32670/45 (blk)
## Gtomento-Gtomento: 614195 (tot), 70629/13 (reg), 38043/13 (blk)
## Chunk 3 / 4 (22:19:19) ... Done!
## Gdarwini-Gbarbade: 599083 (tot), 61061/27 (reg), 28850/125 (blk)
## Gtomento-Gbarbade: 598784 (tot), 62956/26 (reg), 28890/142 (blk)
## Gbarbade-Gbarbade: 613444 (tot), 75556/13 (reg), 37544/13 (blk)
## Gtomento-Gbarbade: 594145 (tot), 60303/26 (reg), 28541/140 (blk)
## Gdarwini-Gbarbade: 597135 (tot), 61049/26 (reg), 28448/131 (blk)
## Gdarwini-Gbarbade: 583967 (tot), 62252/14 (reg), 31839/28 (blk)
## Chunk 4 / 4 (22:20:41) ... Done!
## Gtomento-Gbarbade: 583425 (tot), 63080/14 (reg), 30801/54 (blk)
## Gbarbade-Gbarbade: 579712 (tot), 58524/26 (reg), 28090/135 (blk)
## Gbarbade-Gbarbade: 564235 (tot), 60259/13 (reg), 34849/13 (blk)
## Found 51318 OGs across 228316 genes. gff3-like text file written to:
## /Users/jlovell/Desktop/GENESPACE_data/results//cotton_split/results/gffWithOgs.txt.gz
## Calculating syntenic block breakpoints ...
## Found 3016 blocks. Text file written to:

```



```
## /Users/jlovell/Desktop/GENESPACE_data/results//cotton_split/results/syntenicBlocks.txt.gz:
```

## 7 Print session info

```
save(gparCotton2x, file = file.path(baseDir, "gparCotton2x.rda"))
sessionInfo()
```

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] GENESPACE_0.9.3 data.table_1.14.2
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.8             compiler_4.1.2
## [3] restfulr_0.0.13        GenomeInfoDb_1.30.1
## [5] XVector_0.34.0         MatrixGenerics_1.6.0
## [7] R.methodsS3_1.8.1      bitops_1.0-7
## [9] R.utils_2.11.0         tools_4.1.2
## [11] zlibbioc_1.40.0        digest_0.6.29
## [13] lattice_0.20-45        evaluate_0.14
## [15] pkgconfig_2.0.3        rlang_1.0.0
## [17] Matrix_1.4-0           igraph_1.2.11
## [19] DelayedArray_0.20.0    cli_3.1.1
## [21] rstudioapi_0.13        yaml_2.2.2
## [23] parallel_4.1.2         xfun_0.29
## [25] fastmap_1.1.0          GenomeInfoDbData_1.2.7
## [27] rtracklayer_1.54.0     stringr_1.4.0
## [29] knitr_1.37             Biostrings_2.62.0
## [31] S4Vectors_0.32.3      IRanges_2.28.0
## [33] grid_4.1.2            stats4_4.1.2
## [35] Biobase_2.54.0         BiocParallel_1.28.3
## [37] XML_3.99-0.8           rmarkdown_2.11
## [39] magrittr_2.0.2         matrixStats_0.61.0
## [41] GenomicAlignments_1.30.0 Rsamtools_2.10.0
## [43] GenomicRanges_1.46.1  htmltools_0.5.2
## [45] BiocGenerics_0.40.0    SummarizedExperiment_1.24.0
## [47] stringi_1.7.6          RCurl_1.98-1.5
## [49] rjson_0.2.21           crayon_1.4.2
## [51] dbscan_1.1-10          BiocIO_1.4.0
## [53] R.oo_1.24.0
```