

# Run GENESPACE vignettes - Cotton genomes treated as tetraploids with an outgroup

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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_outgroup"),
  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),
    c("Tcacao", "Tcacao_v2.1", 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$ploidy,
  outgroup = "Tcacao",
  speciesIDs = rep(speciesIDs, length(genomes$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_outgroup
##
## 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
##   /Users/jlovell/Desktop/GENESPACE_data/cotton/Tcacao_v2.1/annotation/Tcacao_523_v2.1.gene.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
##   /Users/jlovell/Desktop/GENESPACE_data/cotton/Tcacao_v2.1/annotation/Tcacao_523_v2.1.protein_primary
##
## 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 entries
```

```
## 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
## Parsing annotations: Tcacao
## Reading gff ... found 27379 protein coding genes
## Reading peptide fasta ... found 27379 / 27379 total and unique entries
## Merging fa and gff found 27374 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

Also set the synteny parameters.

```
gparCotton2x <- set_sytenyParams(
  gsParam = gparCotton2x,
  blkSize = 10,
  nGaps = 10)
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
##
## 2022-02-22 17:49:38 : 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_outgroup/orthof
##
## Dividing up work for BLAST for parallel processing
## -----
## 2022-02-22 17:49:41 : Creating diamond database 1 of 7
## 2022-02-22 17:49:41 : Creating diamond database 2 of 7
## 2022-02-22 17:49:41 : Creating diamond database 3 of 7
## 2022-02-22 17:49:42 : Creating diamond database 4 of 7
## 2022-02-22 17:49:42 : Creating diamond database 5 of 7
## 2022-02-22 17:49:43 : Creating diamond database 6 of 7
## 2022-02-22 17:49:43 : Creating diamond database 7 of 7
##
## Running diamond all-versus-all
## -----
## Using 6 thread(s)
## 2022-02-22 17:49:43 : This may take some time....
## 2022-02-22 17:49:44 : Done 0 of 49
## 2022-02-22 18:12:59 : Done 10 of 49
## 2022-02-22 18:35:00 : Done 20 of 49
## 2022-02-22 18:46:52 : Done 30 of 49
## 2022-02-22 19:02:00 : Done 40 of 49
## 2022-02-22 19:12:48 : Done all-versus-all sequence search
##
## Running OrthoFinder algorithm
## -----
## 2022-02-22 19:12:48 : Initial processing of each species
## 2022-02-22 19:13:37 : Initial processing of species 0 complete
## 2022-02-22 19:14:29 : Initial processing of species 1 complete
## 2022-02-22 19:15:21 : Initial processing of species 2 complete
## 2022-02-22 19:16:15 : Initial processing of species 3 complete
## 2022-02-22 19:17:08 : Initial processing of species 4 complete
## 2022-02-22 19:18:02 : Initial processing of species 5 complete
## 2022-02-22 19:18:37 : Initial processing of species 6 complete
## 2022-02-22 19:19:05 : Connected putative homologues
## 2022-02-22 19:19:11 : Written final scores for species 0 to graph file
## 2022-02-22 19:19:18 : Written final scores for species 1 to graph file
## 2022-02-22 19:19:24 : Written final scores for species 2 to graph file
## 2022-02-22 19:19:32 : Written final scores for species 3 to graph file
## 2022-02-22 19:19:38 : Written final scores for species 4 to graph file
## 2022-02-22 19:19:45 : Written final scores for species 5 to graph file
## 2022-02-22 19:19:50 : Written final scores for species 6 to graph file

```

```

## 2022-02-22 19:20:31 : Ran MCL
##
## Writing orthogroups to file
## -----
## OrthoFinder assigned 248403 genes (97.2% of total) to 34961 orthogroups. Fifty percent of all genes
##
## 2022-02-22 19:21:02 : Done orthogroups
##
## Analysing Orthogroups
## =====
##
## Calculating gene distances
## -----
## 2022-02-22 19:27:02 : Done
## 2022-02-22 19:27:06 : Done 0 of 27941
## 2022-02-22 19:27:11 : Done 1000 of 27941
## 2022-02-22 19:27:15 : Done 2000 of 27941
## 2022-02-22 19:27:18 : Done 3000 of 27941
## 2022-02-22 19:27:22 : Done 4000 of 27941
## 2022-02-22 19:27:26 : Done 5000 of 27941
## 2022-02-22 19:27:30 : Done 6000 of 27941
## 2022-02-22 19:27:35 : Done 7000 of 27941
## 2022-02-22 19:27:39 : Done 8000 of 27941
## 2022-02-22 19:27:43 : Done 9000 of 27941
## 2022-02-22 19:27:47 : Done 10000 of 27941
## 2022-02-22 19:27:52 : Done 11000 of 27941
## 2022-02-22 19:27:56 : Done 12000 of 27941
## 2022-02-22 19:28:00 : Done 13000 of 27941
## 2022-02-22 19:28:04 : Done 14000 of 27941
## 2022-02-22 19:28:08 : Done 15000 of 27941
## 2022-02-22 19:28:13 : Done 16000 of 27941
## 2022-02-22 19:28:17 : Done 17000 of 27941
## 2022-02-22 19:28:21 : Done 18000 of 27941
## 2022-02-22 19:28:26 : Done 19000 of 27941
## 2022-02-22 19:28:30 : Done 20000 of 27941
## 2022-02-22 19:28:34 : Done 21000 of 27941
## 2022-02-22 19:28:38 : Done 22000 of 27941
## 2022-02-22 19:28:43 : Done 23000 of 27941
## 2022-02-22 19:28:47 : Done 24000 of 27941
## 2022-02-22 19:28:51 : Done 25000 of 27941
## 2022-02-22 19:28:55 : Done 26000 of 27941
## 2022-02-22 19:29:00 : Done 27000 of 27941
##
## Inferring gene and species trees
## -----
##
## 16170 trees had all species present and will be used by STAG to infer the species tree
##
## Best outgroup(s) for species tree
## -----
## 2022-02-22 19:34:23 : Starting STRIDE
## 2022-02-22 19:34:32 : Done STRIDE
## Observed 1612 well-supported, non-terminal duplications. 1612 support the best root and 0 contradic
## Best outgroup for species tree:

```

```

##      Tcacao
##
## Reconciling gene trees and species tree
## -----
## Outgroup: Tcacao
## 2022-02-22 19:34:32 : Starting Recon and orthologues
## 2022-02-22 19:34:32 : Starting OF Orthologues
## 2022-02-22 19:34:33 : Done 0 of 27941
## 2022-02-22 19:34:45 : Done 1000 of 27941
## 2022-02-22 19:34:53 : Done 2000 of 27941
## 2022-02-22 19:34:59 : Done 3000 of 27941
## 2022-02-22 19:35:04 : Done 4000 of 27941
## 2022-02-22 19:35:10 : Done 5000 of 27941
## 2022-02-22 19:35:14 : Done 6000 of 27941
## 2022-02-22 19:35:19 : Done 7000 of 27941
## 2022-02-22 19:35:23 : Done 8000 of 27941
## 2022-02-22 19:35:27 : Done 9000 of 27941
## 2022-02-22 19:35:31 : Done 10000 of 27941
## 2022-02-22 19:35:35 : Done 11000 of 27941
## 2022-02-22 19:35:39 : Done 12000 of 27941
## 2022-02-22 19:35:43 : Done 13000 of 27941
## 2022-02-22 19:35:47 : Done 14000 of 27941
## 2022-02-22 19:35:51 : Done 15000 of 27941
## 2022-02-22 19:35:55 : Done 16000 of 27941
## 2022-02-22 19:35:59 : Done 17000 of 27941
## 2022-02-22 19:36:03 : Done 18000 of 27941
## 2022-02-22 19:36:07 : Done 19000 of 27941
## 2022-02-22 19:36:10 : Done 20000 of 27941
## 2022-02-22 19:36:14 : Done 21000 of 27941
## 2022-02-22 19:36:17 : Done 22000 of 27941
## 2022-02-22 19:36:21 : Done 23000 of 27941
## 2022-02-22 19:36:25 : Done 24000 of 27941
## 2022-02-22 19:36:29 : Done 25000 of 27941
## 2022-02-22 19:36:32 : Done 26000 of 27941
## 2022-02-22 19:36:35 : Done 27000 of 27941
## 2022-02-22 19:36:37 : Done OF Orthologues
##
## Writing results files
## =====
## 2022-02-22 19:36:53 : Done orthologues
##
## Results:
##      /Users/jlovell/Desktop/GENESPACE_data/results/cotton_split_outgroup/orthofinder/Results_Feb22/
##
## 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

```

## 6 Build syntenic data

```
gparCotton2x <- find_orthofinderResults(gsParam = gparCotton2x)
gparCotton2x <- syntenic(gsParam = gparCotton2x, overwrite = T)

## Parsing the gff files ...
## Reading the gffs and adding orthofinder IDs ... Done!
## Found 38652 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, 32279/0
##           GbarbadenseD: 13/0, 37550/0, 34279/0
##           GdarwiniA: 13/0, 38078/0, 34912/0
##           GdarwiniD: 13/0, 39779/0, 35896/0
##           GtomentosumA: 13/0, 38045/0, 34779/0
##           GtomentosumD: 13/0, 40007/0, 36211/0
## All look good!
## Defining collinear orthogroup arrays ...
## Found the following counts of arrays / genome:
##           GbarbadenseA: 3310 genes in 1259 collinear arrays
##           GbarbadenseD: 4172 genes in 1475 collinear arrays
##           GdarwiniA: 3877 genes in 1450 collinear arrays
##           GdarwiniD: 4807 genes in 1633 collinear arrays
##           GtomentosumA: 4108 genes in 1517 collinear arrays
##           GtomentosumD: 4701 genes in 1640 collinear arrays
## Pulling syntenic for 21 unique pairwise combinations of genomes
## Running 4 chunks of up to 6 combinations each:
## Chunk 1 / 4 (19:37:21) ... Done!
## Gtomento-Gdarwini: 652781 (tot), 81938/15 (reg), 33589/47 (blk)
## Gtomento-Gdarwini: 615716 (tot), 63365/29 (reg), 28718/134 (blk)
## Gtomento-Gtomento: 617153 (tot), 65404/27 (reg), 28819/142 (blk)
## Gdarwini-Gdarwini: 620975 (tot), 64555/26 (reg), 28837/127 (blk)
## Gdarwini-Gtomento: 618627 (tot), 66494/27 (reg), 28764/138 (blk)
## Gtomento-Gbarbade: 629173 (tot), 75416/15 (reg), 32357/46 (blk)
## Chunk 2 / 4 (19:40:06) ... Done!
## Gdarwini-Gbarbade: 631311 (tot), 78635/13 (reg), 33287/28 (blk)
## Gdarwini-Gtomento: 610865 (tot), 67734/13 (reg), 32118/43 (blk)
## Gdarwini-Gbarbade: 599083 (tot), 60916/26 (reg), 28231/122 (blk)
## Gtomento-Gbarbade: 598784 (tot), 62946/26 (reg), 28358/138 (blk)
## Gtomento-Gbarbade: 594145 (tot), 60156/27 (reg), 27870/141 (blk)
## Gdarwini-Gbarbade: 597135 (tot), 61061/26 (reg), 27836/130 (blk)
## Chunk 3 / 4 (19:42:25) ... Done!
## Gdarwini-Gbarbade: 583967 (tot), 62305/14 (reg), 31188/28 (blk)
## Gtomento-Gbarbade: 583425 (tot), 63122/14 (reg), 30224/53 (blk)
## Gbarbade-Gbarbade: 579712 (tot), 58555/26 (reg), 27511/130 (blk)
## Gtomento-Gtomento: 655357 (tot), 82437/13 (reg), 40003/13 (blk)
## Gdarwini-Gdarwini: 658415 (tot), 87045/13 (reg), 39777/13 (blk)
## Gdarwini-Gdarwini: 616216 (tot), 68304/13 (reg), 38076/13 (blk)
## Chunk 4 / 4 (19:43:41) ... Done!
## Gtomento-Gtomento: 614195 (tot), 70455/13 (reg), 38043/13 (blk)
## Gbarbade-Gbarbade: 613444 (tot), 75628/13 (reg), 37544/13 (blk)
## Gbarbade-Gbarbade: 564235 (tot), 60275/13 (reg), 34849/13 (blk)
## Defining syntenic-constrained orthogroups ...
```

```

## Found 52849 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: 63149 genes, 27558 / 32384 / 32090
## Gdarwini-Gdarwini: no non-self syn. regions
## Gdarwini-Gtomento: 65060 genes, 28517 / 33771 / 33251
## Gdarwini-Gbarbade: 59129 genes, 26998 / 31337 / 30751
## Gtomento-Gbarbade: 61747 genes, 27343 / 32084 / 31632
## Gtomento-Gtomento: no non-self syn. regions
## Gtomento-Gbarbade: 59201 genes, 27020 / 31371 / 30739
## Gbarbade-Gbarbade: 58081 genes, 26476 / 30711 / 30156
## Gbarbade-Gbarbade: no non-self syn. regions
## Gdarwini-Gbarbade: 58467 genes, 26705 / 30975 / 30402
## Gdarwini-Gdarwini: 60118 genes, 27483 / 31893 / 31279
## Gdarwini-Gtomento: 59860 genes, 27334 / 31742 / 31090
## Gdarwini-Gbarbade: 66749 genes, 28998 / 34291 / 33894
## Gdarwini-Gdarwini: no non-self syn. regions
## Gtomento-Gbarbade: 58675 genes, 26728 / 31061 / 30485
## Gtomento-Gdarwini: 59976 genes, 27339 / 31786 / 31179
## Gtomento-Gtomento: 60292 genes, 27411 / 31914 / 31271
## Gtomento-Gbarbade: 65753 genes, 28922 / 34176 / 33606
## Gtomento-Gdarwini: 67776 genes, 29601 / 35175 / 34567
## Gtomento-Gtomento: no non-self syn. regions
## Combining synteny-constrained and inblock orthogroups ...
## syn OGs: 52849, inblk OGs: 91431, combined OGs: 50622
## Found the following counts of arrays / genome:
##   GbarbadenseA: 3520 genes in 1328 collinear arrays
##   GbarbadenseD: 4375 genes in 1525 collinear arrays
##   GdarwiniA: 4180 genes in 1558 collinear arrays
##   GdarwiniD: 5092 genes in 1723 collinear arrays
##   GtomentosumA: 4346 genes in 1588 collinear arrays
##   GtomentosumD: 4964 genes in 1716 collinear arrays
## Pulling synteny for 21 unique pairwise combinations of genomes
## Running 4 chunks of up to 6 combinations each:
## Chunk 1 / 4 (19:58:59) ... Done!
## Gtomento-Gdarwini: 652781 (tot), 81803/15 (reg), 33279/47 (blk)
## Gtomento-Gdarwini: 615716 (tot), 63753/28 (reg), 28451/132 (blk)
## Gtomento-Gtomento: 617153 (tot), 65474/27 (reg), 28635/143 (blk)
## Gdarwini-Gdarwini: 620975 (tot), 64731/28 (reg), 28604/128 (blk)
## Gdarwini-Gtomento: 618627 (tot), 66367/27 (reg), 28484/137 (blk)
## Gtomento-Gbarbade: 629173 (tot), 75342/15 (reg), 32126/46 (blk)
## Chunk 2 / 4 (20:01:34) ... Done!
## Gdarwini-Gbarbade: 631311 (tot), 78337/13 (reg), 32947/28 (blk)
## Gdarwini-Gtomento: 610865 (tot), 67695/13 (reg), 31850/43 (blk)
## Gdarwini-Gbarbade: 599083 (tot), 61289/27 (reg), 28046/125 (blk)
## Gtomento-Gbarbade: 598784 (tot), 62995/26 (reg), 28140/137 (blk)
## Gtomento-Gbarbade: 594145 (tot), 60299/26 (reg), 27683/140 (blk)
## Gdarwini-Gbarbade: 597135 (tot), 61071/26 (reg), 27636/131 (blk)
## Chunk 3 / 4 (20:03:51) ... Done!
## Gdarwini-Gbarbade: 583967 (tot), 62338/14 (reg), 30942/28 (blk)
## Gtomento-Gbarbade: 583425 (tot), 63120/14 (reg), 29994/53 (blk)
## Gbarbade-Gbarbade: 579712 (tot), 58528/26 (reg), 27291/131 (blk)
## Gtomento-Gtomento: 655357 (tot), 82489/13 (reg), 40003/13 (blk)

```



```
## Gdarwini-Gdarwini: 658415 (tot), 87229/13 (reg), 39777/13 (blk)
## Gdarwini-Gdarwini: 616216 (tot), 68362/13 (reg), 38076/13 (blk)
## Chunk 4 / 4 (20:05:17) ... Done!
## Gtomento-Gtomento: 614195 (tot), 70511/13 (reg), 38043/13 (blk)
## Gbarbade-Gbarbade: 613444 (tot), 75686/13 (reg), 37544/13 (blk)
## Gbarbade-Gbarbade: 564235 (tot), 60331/13 (reg), 34849/13 (blk)
## Found 50622 OGs across 228316 genes. gff3-like text file written to:
## /Users/jlovell/Desktop/GENESPACE_data/results//cotton_split_outgroup/results/gffWithOgs.txt.gz
## Calculating syntenic block breakpoints ...
## Found 2976 blocks. Text file written to:
## /Users/jlovell/Desktop/GENESPACE_data/results//cotton_split_outgroup/results/syntenicBlocks.txt.gz:
```

## 7 Print session info

```
gparCotton2x_outgroup <- gparCotton2x
save(gparCotton2x_outgroup, file = file.path(baseDir, "gparCotton2x_outgroup.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	