setwd("C:/Users/HP/OneDrive/Desktop/mapping\_example-main")

> library(devtools)

Loading required package: usethis

Warning messages:

1: package ‘devtools’ was built under R version 4.3.2

2: package ‘usethis’ was built under R version 4.3.2

> library(mappoly)

=====================================================

MAPpoly Package [Version 0.3.32023-01-05 20:10:02 UTC]

More information: https://github.com/mmollina/MAPpoly

=====================================================

Warning message:

package ‘mappoly’ was built under R version 4.3.2

> library(qtlpoly)

Warning message:

package ‘qtlpoly’ was built under R version 4.3.2

> library(viewpoly)

Warning message:

package ‘viewpoly’ was built under R version 4.3.2

> dat = read\_geno\_csv(file="C:/Users/HP/OneDrive/Desktop/mapping\_example-main/data/BExMG\_subset\_with\_contaminants\_2075mrks.csv",

+ ploidy = 4, filter.non.conforming = F)

Reading the following data:

Ploidy level: 4

No. individuals: 169

No. markers: 2075

No. informative markers: 2075 (100%)

...

Done with reading.

> library(polymapR)

Attaching package: ‘polymapR’

The following object is masked from ‘package:mappoly’:

compare\_maps

Warning message:

package ‘polymapR’ was built under R version 4.3.2

> polymapR\_dosage\_matrix=export\_data\_to\_polymapR(dat)

> PCA\_progeny(polymapR\_dosage\_matrix)

> contaminants = c("X16009\_N001", "X16009\_N010","SW","X16009\_N005","X16009\_N006","X16009\_N009")

> screened\_data <- screen\_for\_duplicate\_individuals(dosage\_matrix = ALL\_dosages,

+ cutoff = 0.95,

+ plot\_cor = T)

Combining F1\_060 & F1\_081 into F1\_060

Combining F1\_046 & F1\_085 into F1\_046

Combining F1\_032 & F1\_100 into F1\_032

Combining F1\_032 & F1\_114 into F1\_032

Combining F1\_079 & F1\_101 into F1\_079

Combining F1\_106 & F1\_113 into F1\_106

Combining F1\_112 & F1\_199 into F1\_112

#### 7 individuals removed:

\_ \_ \_ \_

[1,] "F1\_081" "F1\_085" "F1\_100" "F1\_114"

[2,] "F1\_101" "F1\_113" "F1\_199" ""

|\_ |\_ |\_ |\_ |

|:------|:------|:------|:------|

|F1\_081 |F1\_085 |F1\_100 |F1\_114 |

|F1\_101 |F1\_113 |F1\_199 | |

Warning message:

In screen\_for\_duplicate\_individuals(dosage\_matrix = ALL\_dosages, :

Multiple duplicates of single genotype identified at this threshold. Attempting to merge...

> duplicates = c("X16035\_N028.1", "X16035\_N029.1","X16400\_N023","X16400\_N038","X16405\_N113","X16400\_N006")

> remove = c(contaminants,duplicates)

> genotype\_data = read.csv("C:/Users/HP/OneDrive/Desktop/mapping\_example-main/data/BExMG\_subset\_with\_contaminants\_2075mrks.csv")

> genotype\_data\_after\_QC=genotype\_data[,which(!colnames(genotype\_data)%in%remove)]

> write.csv(genotype\_data\_after\_QC,"C:/Users/HP/OneDrive/Desktop/mapping\_example-main/data/BExMG\_subset\_with\_contaminants\_2075mrks\_afterQC.csv", row.names = F)

> library(mappoly)

> dat = read\_geno\_csv(file="C:/Users/HP/OneDrive/Desktop/mapping\_example-main/data/BExMG\_subset\_with\_contaminants\_2075mrks\_afterQC.csv", ploidy = 4, filter.non.conforming = T)

Reading the following data:

Ploidy level: 4

No. individuals: 157

No. markers: 2075

No. informative markers: 2075 (100%)

...

Done with reading.

Filtering non-conforming markers.

...

Done with filtering.

> dat = filter\_missing(input.data = dat, type = "marker",

+ filter.thres = 0.10, inter = F)

> ## Filtering dataset by individual

> dat = filter\_missing(input.data = dat, type = "individual",

+ filter.thres = 0.10, inter = F)

> dat

This is an object of class 'mappoly.data'

Ploidy level: 4

No. individuals: 157

No. markers: 2074

Missing data: 1.35%

Redundant markers: 0.05%

This dataset contains chromosome information.

----------

No. of markers per dosage combination in both parents:

P1 P2 freq

0 1 182

0 2 52

0 3 15

1 0 168

1 1 215

1 2 102

1 3 52

1 4 12

2 0 48

2 1 113

2 2 116

2 3 108

2 4 52

3 0 11

3 1 50

3 2 115

3 3 223

3 4 203

4 1 5

4 2 52

4 3 180

> pval.bonf = 0.05/dat$n.mrk

> mrks.chi.filt = filter\_segregation(dat, chisq.pval.thres = pval.bonf, inter = F)

> seq.init = make\_seq\_mappoly(mrks.chi.filt)

> seq.init

This is an object of class 'mappoly.sequence'

------------------------

Parameters not estimated

------------------------

Ploidy level: 4

No. individuals: 157

No. markers: 2062

----------

No. markers per sequence:

chrom No.mrk

1 267

2 432

3 234

4 263

5 234

6 325

7 307

----------

No. of markers per dosage in both parents:

dP1 dP2 freq

0 1 182

0 2 52

0 3 14

1 0 168

1 1 213

1 2 102

1 3 51

1 4 12

2 0 48

2 1 113

2 2 116

2 3 108

2 4 52

3 0 11

3 1 46

3 2 115

3 3 221

3 4 202

4 1 4

4 2 52

4 3 180

> plot(seq.init)

> all.rf.pairwise = est\_pairwise\_rf(input.seq = seq.init, ncpus = 7)

INFO: Using 7 CPUs for calculation.

INFO: Done with 2124891 pairs of markers

INFO: Calculation took: 819.25 seconds

> mat = rf\_list\_to\_matrix(all.rf.pairwise)

INFO: Going singlemode. Using one CPU.

> mat = rf\_list\_to\_matrix(all.rf.pairwise)

INFO: Going singlemode. Using one CPU.

> plot(mat)

> mat = rf\_list\_to\_matrix(all.rf.pairwise)

INFO: Going singlemode. Using one CPU.

> mat = rf\_list\_to\_matrix(all.rf.pairwise)

INFO: Going singlemode. Using one CPU.

> plot(mat)

> plot(mat)

> grs = group\_mappoly(input.mat = mat,

+ expected.groups = 7,

+ comp.mat = TRUE,

+ inter = F)

> grs

This is an object of class 'mappoly.group'

------------------------------------------

Criteria used to assign markers to groups:

- Number of markers: 2062

- Number of linkage groups: 7

- Number of markers per linkage groups:

group n.mrk

1 275

2 448

3 229

4 292

5 263

6 236

7 319

------------------------------------------

1 2 3 7 4 5 6 NoChr

1 266 0 6 0 1 0 2 0

2 1 431 1 6 1 1 7 0

3 0 1 226 2 0 0 0 0

4 0 0 1 291 0 0 0 0

5 0 0 0 1 261 0 1 0

6 0 0 0 4 0 232 0 0

7 0 0 0 3 0 1 315 0

------------------------------------------

> grs = group\_mappoly(input.mat = mat,

+ expected.groups = 7,

+ comp.mat = TRUE,

+ inter = F)

> grs

This is an object of class 'mappoly.group'

------------------------------------------

Criteria used to assign markers to groups:

- Number of markers: 2062

- Number of linkage groups: 7

- Number of markers per linkage groups:

group n.mrk

1 275

2 448

3 229

4 292

5 263

6 236

7 319

------------------------------------------

1 2 3 7 4 5 6 NoChr

1 266 0 6 0 1 0 2 0

2 1 431 1 6 1 1 7 0

3 0 1 226 2 0 0 0 0

4 0 0 1 291 0 0 0 0

5 0 0 0 1 261 0 1 0

6 0 0 0 4 0 232 0 0

7 0 0 0 3 0 1 315 0

------------------------------------------

> grs = group\_mappoly(input.mat = mat,

+ expected.groups = 7,

+ comp.mat = TRUE,

+ inter = F)

> grs

This is an object of class 'mappoly.group'

------------------------------------------

Criteria used to assign markers to groups:

- Number of markers: 2062

- Number of linkage groups: 7

- Number of markers per linkage groups:

group n.mrk

1 275

2 448

3 229

4 292

5 263

6 236

7 319

------------------------------------------

1 2 3 7 4 5 6 NoChr

1 266 0 6 0 1 0 2 0

2 1 431 1 6 1 1 7 0

3 0 1 226 2 0 0 0 0

4 0 0 1 291 0 0 0 0

5 0 0 0 1 261 0 1 0

6 0 0 0 4 0 232 0 0

7 0 0 0 3 0 1 315 0

------------------------------------------

> grs = group\_mappoly(input.mat = mat,

+ expected.groups = 7,

+ comp.mat = TRUE,

+ inter = F)

> grs

This is an object of class 'mappoly.group'

------------------------------------------

Criteria used to assign markers to groups:

- Number of markers: 2062

- Number of linkage groups: 7

- Number of markers per linkage groups:

group n.mrk

1 275

2 448

3 229

4 292

5 263

6 236

7 319

------------------------------------------

1 2 3 7 4 5 6 NoChr

1 266 0 6 0 1 0 2 0

2 1 431 1 6 1 1 7 0

3 0 1 226 2 0 0 0 0

4 0 0 1 291 0 0 0 0

5 0 0 0 1 261 0 1 0

6 0 0 0 4 0 232 0 0

7 0 0 0 3 0 1 315 0

------------------------------------------

> plot(grs)

> LGS.inter=vector("list", 7)

> for(j in 1:7){

+ temp1 = make\_seq\_mappoly(grs, j, genomic.info=1)

+ tpt = make\_pairs\_mappoly(all.rf.pairwise, input.seq = temp1)

+ temp2 = rf\_snp\_filter(input.twopt = tpt, diagnostic.plot = FALSE)

+ tpt2 = make\_pairs\_mappoly(tpt, input.seq = temp2)

+ LGS.inter[[as.numeric(names(table(temp2$chrom))[which.max(table(temp2$chrom))])]] = list(seq = temp2, tpt = tpt2)

+ }

> LGS.inter=vector("list", 7)

> for(j in 1:7){

+ temp1 = make\_seq\_mappoly(grs, j, genomic.info=1)

+ tpt = make\_pairs\_mappoly(all.rf.pairwise, input.seq = temp1)

+ temp2 = rf\_snp\_filter(input.twopt = tpt, diagnostic.plot = FALSE)

+ tpt2 = make\_pairs\_mappoly(tpt, input.seq = temp2)

+ LGS.inter[[as.numeric(names(table(temp2$chrom))[which.max(table(temp2$chrom))])]] = list(seq = temp2, tpt = tpt2)

+ }

> LGS.genomic = vector("list", 7)

> for (i in 1:7){

+ tempseq1 = make\_seq\_mappoly(dat, arg = paste0("seq",i), genomic.info = 1)

+ mrks = intersect(tempseq1$seq.mrk.names, seq.init$seq.mrk.names)

+ tempseq = make\_seq\_mappoly(dat, arg = mrks)

+ temptpt = make\_pairs\_mappoly(all.rf.pairwise, input.seq = tempseq)

+ rffilt = rf\_snp\_filter(input.twopt = temptpt, diagnostic.plot = FALSE)

+ temptpt2 = make\_pairs\_mappoly(temptpt, input.seq = rffilt)

+ LGS.genomic[[as.numeric(unique(rffilt$chrom))]] = list(seq = rffilt, tpt = temptpt2)

+ }

> LGS.upgma=vector("list", 7)

> for(j in 1:7){

+ temp1 = make\_seq\_mappoly(grs, j)

+ tpt = make\_pairs\_mappoly(all.rf.pairwise, input.seq = temp1)

+ temp2 = rf\_snp\_filter(input.twopt = tpt, diagnostic.plot = FALSE)

+ tpt2 = make\_pairs\_mappoly(tpt, input.seq = temp2)

+ LGS.upgma[[as.numeric(names(table(temp2$chrom))[which.max(table(temp2$chrom))])]] = list(seq = temp2, tpt = tpt2)

+ }

> comp = data.frame(UPGMA\_Genomic = unlist(lapply(LGS.inter, function(x) length(x$seq$seq.num))),

+ Genomic = unlist(lapply(LGS.genomic, function(x) length(x$seq$seq.num))),

+ UPGMA = unlist(lapply(LGS.upgma, function(x) length(x$seq$seq.num))))

> comp

UPGMA\_Genomic Genomic UPGMA

1 253 253 264

2 410 412 427

3 214 222 218

4 250 252 250

5 223 222 224

6 299 308 304

7 279 294 279

> LGS<-LGS.inter

> single\_chrom <- est\_rf\_hmm\_sequential(input.seq = LGS[[1]]$seq,

+ start.set = 3,

+ thres.twopt = 10,

+ thres.hmm = 50,

+ extend.tail = 30,

+ twopt = LGS[[1]]$tpt,

+ verbose = TRUE,

+ phase.number.limit = 20,

+ sub.map.size.diff.limit = 5)

Number of markers: 253

══════════════════════════════════════════════════════════════════ Initial sequence ══

3 markers...

• Trying sequence: 1 2 3 :

4 phase(s): . . . .

• Trying sequence: 2 3 4 :

3 phase(s): . . .

════════════════════════════════════════════════════════ Done with initial sequence ══

Making 'reestimate.single.ph.configuration = TRUE' to use map expansion

4 /5 :(2%) 6 : 2 ph (1/2) -- tail: 3 •||| •••• ||•| ••••

5 /6 :(2.4%) 7 : 1 ph (1/1) -- tail: 4 ••|• •|||

6 /7 :(2.8%) 9 : 1 ph (1/1) -- tail: 5 |||| |||•

7 /8 :(3.2%) 10 : 1 ph (1/1) -- tail: 6 |||| |||•

8 /9 :(3.6%) 11 : 1 ph (1/1) -- tail: 7 |||| ||••

9 /10 :(4%) 12 : 1 ph (1/1) -- tail: 8 |||| |||•

10 /11 :(4.3%) 14 : 4 ph (1/4) -- tail: 9 ••|| ••|| ... ••|| •|•|

11 /12 :(4.7%) 16 : 1 ph (1/1) -- tail: 10 •••• •••|

12 /13 :(5.1%) 17 : 1 ph (1/1) -- tail: 11 •••• ••||

13 /14 :(5.5%) 18 : 1 ph (1/1) -- tail: 12 ••|• •••|

14 /15 :(5.9%) 20 : 4 ph (1/4) -- tail: 13 •••| •••• ... ••|• ••••

15 /16 :(6.3%) 21 : 1 ph (1/1) -- tail: 14 ••|• •••|

16 /17 :(6.7%) 22 : 1 ph (1/1) -- tail: 15 ••|• •••|

17 /18 :(7.1%) 23 : 2 ph (1/2) -- tail: 16 |||| ||•| |||| |||•

18 /19 :(7.5%) 24 : 1 ph (1/1) -- tail: 17 ••|• •••|

19 /20 :(7.9%) 26 : 1 ph (1/1) -- tail: 18 •••• •••|

20 /21 :(8.3%) 28 : 2 ph (1/2) -- tail: 19 •••• •|•| •••• |••|

21 /22 :(8.7%) 29 : 1 ph (1/1) -- tail: 20 •••• |•••

22 /23 :(9.1%) 30 : 4 ph (1/4) -- tail: 21 •••| |••| ... ••|• |••|

23 /24 :(9.5%) 31 : 2 ph (1/2) -- tail: 22 •••| |•|• |••• |•|•

24 /25 :(9.9%) 32 : 1 ph (1/1) -- tail: 23 |||• ||••

25 /26 :(10.3%) 34 : 1 ph (1/1) -- tail: 24 |||• |||•

26 /27 :(10.7%) 35 : 1 ph (1/1) -- tail: 25 •••• •••|

27 /28 :(11.1%) 36 : 1 ph (1/1) -- tail: 26 |||• |||•

28 /29 :(11.5%) 37 : 1 ph (1/1) -- tail: 27 •••| •••|

29 /30 :(11.9%) 38 : 2 ph (1/2) -- tail: 28 |||| |•|| |||| ||•|

30 /31 :(12.3%) 39 : 1 ph (1/1) -- tail: 29 |||• |||•

31 /32 :(12.6%) 40 : 1 ph (1/1) -- tail: 30 |||| |••|

32 /33 :(13%) 41 : 1 ph (1/1) -- tail: 30 •••• •||•

33 /34 :(13.4%) 42 : 1 ph (1/1) -- tail: 30 |••• |•••

34 /35 :(13.8%) 44 : 1 ph (1/1) -- tail: 30 •••• •||•

35 /36 :(14.2%) 45 : 1 ph (1/1) -- tail: 30 ||•| ||||

36 /37 :(14.6%) 46 : 1 ph (1/1) -- tail: 30 ••|| •••|

37 /38 :(15%) 48 : 1 ph (1/1) -- tail: 30 ||•| ||||

38 /39 :(15.4%) 50 : 1 ph (1/1) -- tail: 30 |||| |••|

39 /40 :(15.8%) 51 : 1 ph (1/1) -- tail: 30 •||| •|||

40 /41 :(16.2%) 52 : 1 ph (1/1) -- tail: 30 •••| •••|

41 /42 :(16.6%) 53 : 1 ph (1/1) -- tail: 30 ||•| ||||

42 /43 :(17%) 54 : 1 ph (1/1) -- tail: 30 •••• |••|

43 /44 :(17.4%) 55 : 3 ph (1/3) -- tail: 30 ||•• ••|• ... ||•• •|••

44 /45 :(17.8%) 56 : 1 ph (1/1) -- tail: 30 ||•| |•||

45 /46 :(18.2%) 57 : 1 ph (1/1) -- tail: 30 ••|| •|••

46 /47 :(18.6%) 58 : 1 ph (1/1) -- tail: 30 |||• |||•

47 /48 :(19%) 59 : 1 ph (1/1) -- tail: 30 |||| |||•

48 /49 :(19.4%) 60 : 1 ph (1/1) -- tail: 30 |||| |||•

49 /50 :(19.8%) 62 : 1 ph (1/1) -- tail: 30 ••|| •••|

50 /51 :(20.2%) 63 : 1 ph (1/1) -- tail: 30 |||• ||||

51 /52 :(20.6%) 64 : 1 ph (1/1) -- tail: 30 ||•| ||||

52 /53 :(20.9%) 65 : 1 ph (1/1) -- tail: 30 |||| ||•|

53 /54 :(21.3%) 66 : 1 ph (1/1) -- tail: 30 •••• ••|•

54 /55 :(21.7%) 67 : 9 ph (1/9) -- tail: 30 •||• •||• ... •||• |•|•

55 /56 :(22.1%) 68 : 1 ph (1/1) -- tail: 30 •••• •••|

56 /57 :(22.5%) 69 : 2 ph (1/2) -- tail: 30 •|•| |||| |••| ||||

57 /58 :(22.9%) 70 : 2 ph (1/2) -- tail: 30 |•|| ••|• ||•| ••|•

58 /59 :(23.3%) 71 : 1 ph (1/1) -- tail: 30 •••| ••||

59 /60 :(23.7%) 72 : 1 ph (1/1) -- tail: 30 •••| ••|•

60 /61 :(24.1%) 73 : 1 ph (1/1) -- tail: 30 •••| ••|•

61 /62 :(24.5%) 74 : 1 ph (1/1) -- tail: 30 •••• •••|

62 /63 :(24.9%) 75 : 1 ph (1/1) -- tail: 30 |||| |||•

63 /64 :(25.3%) 76 : 1 ph (1/1) -- tail: 30 •••• ••|•

64 /65 :(25.7%) 77 : 1 ph (1/1) -- tail: 30 •••| ••||

65 /66 :(26.1%) 78 : 1 ph (1/1) -- tail: 30 •••| ••||

66 /67 :(26.5%) 79 : 1 ph (1/1) -- tail: 30 |•|• ||••

67 /68 :(26.9%) 80 : 1 ph (1/1) -- tail: 30 •|•| ||||

68 /69 :(27.3%) 81 : 1 ph (1/1) -- tail: 30 •||• ••••

69 /70 :(27.7%) 84 : 1 ph (1/1) -- tail: 30 ••|• ••••

70 /71 :(28.1%) 85 : 1 ph (1/1) -- tail: 30 •••| ••••

71 /72 :(28.5%) 86 : 2 ph (1/2) -- tail: 30 ••|• ||•• |••• ||••

72 /73 :(28.9%) 87 : 1 ph (1/1) -- tail: 30 •••| ••||

73 /74 :(29.2%) 88 : 1 ph (1/1) -- tail: 30 •||| ••||

74 /75 :(29.6%) 89 : 1 ph (1/1) -- tail: 30 ••|• ••••

75 /76 :(30%) 90 : 1 ph (1/1) -- tail: 30 |||| ||•|

76 /77 :(30.4%) 92 : 1 ph (1/1) -- tail: 31 •|•| ••••

77 /78 :(30.8%) 93 : 1 ph (1/1) -- tail: 32 ••|• ••••

78 /79 :(31.2%) 94 : 1 ph (1/1) -- tail: 33 ||•| ••||

79 /80 :(31.6%) 95 : 3 ph (1/3) -- tail: 34 •••| ••|• ... ••|• ••|•

80 /81 :(32%) 96 : 4 ph (1/4) -- tail: 35 •||| |||• ... |•|| |||•

81 /82 :(32.4%) 97 : 1 ph (1/1) -- tail: 36 |••• •••|

82 /83 :(32.8%) 98 : 1 ph (1/1) -- tail: 37 •••• ••|•

83 /84 :(33.2%) 99 : 1 ph (1/1) -- tail: 38 |||| ||•|

84 /85 :(33.6%) 100: 1 ph (1/1) -- tail: 39 |••• •••|

85 /86 :(34%) 101: 1 ph (1/1) -- tail: 40 ••|• ••••

86 /87 :(34.4%) 102: 1 ph (1/1) -- tail: 41 |••• •••|

87 /88 :(34.8%) 103: 1 ph (1/1) -- tail: 42 ••|• ••••

88 /89 :(35.2%) 104: 1 ph (1/1) -- tail: 43 •||| |||•

89 /90 :(35.6%) 105: 1 ph (1/1) -- tail: 44 •••• ••|•

90 /91 :(36%) 106: 1 ph (1/1) -- tail: 45 ||•| ||||

91 /92 :(36.4%) 107: 1 ph (1/1) -- tail: 46 |•|• ||||

92 /93 :(36.8%) 108: 1 ph (1/1) -- tail: 47 •••• •••|

93 /94 :(37.2%) 109: 1 ph (1/1) -- tail: 48 •••• •••|

94 /95 :(37.5%) 110: 1 ph (1/1) -- tail: 49 ||•| ||||

95 /96 :(37.9%) 111: 1 ph (1/1) -- tail: 50 |•|• |||•

96 /97 :(38.3%) 112: 1 ph (1/1) -- tail: 51 •||| ••||

97 /98 :(38.7%) 113: 1 ph (1/1) -- tail: 52 •||| ••||

98 /99 :(39.1%) 114: 1 ph (1/1) -- tail: 53 •|•| ••••

99 /100:(39.5%) 115: 1 ph (1/1) -- tail: 54 •||| ••||

100/101:(39.9%) 116: 1 ph (1/1) -- tail: 55 •||| ••||

101/102:(40.3%) 117: 1 ph (1/1) -- tail: 56 |••• ||••

102/103:(40.7%) 118: 1 ph (1/1) -- tail: 57 ||•| ||||

103/104:(41.1%) 119: 1 ph (1/1) -- tail: 58 |••• ||••

104/105:(41.5%) 120: 4 ph (1/4) -- tail: 59 |||| •||| ... |||| |•||

105/106:(41.9%) 121: 1 ph (1/1) -- tail: 33 ||•| ||||

106/107:(42.3%) 122: 2 ph (1/2) -- tail: 34 |••• •|•• |••• |•••

107/108:(42.7%) 123: 1 ph (1/1) -- tail: 35 •||| •|||

108/109:(43.1%) 124: 4 ph (1/4) -- tail: 36 •••| •|•• ... ••|• •|••

109/110:(43.5%) 125: 1 ph (1/1) -- tail: 30 •||| •|||

110/111:(43.9%) 126: 3 ph (1/3) -- tail: 30 |•|| ||•• ... ||•| ||••

111/112:(44.3%) 127: 1 ph (1/1) -- tail: 30 •••| •|••

112/113:(44.7%) 128: 1 ph (1/1) -- tail: 30 |•|• |•••

113/114:(45.1%) 129: 1 ph (1/1) -- tail: 30 •||| •|||

114/115:(45.5%) 130: 1 ph (1/1) -- tail: 30 •••| •|••

115/116:(45.8%) 131: 1 ph (1/1) -- tail: 30 |••• |•••

116/117:(46.2%) 132: 1 ph (1/1) -- tail: 30 |••| |•••

117/118:(46.6%) 133: 1 ph (1/1) -- tail: 30 |•|| ||••

118/119:(47%) 134: 1 ph (1/1) -- tail: 30 •||• •|||

119/120:(47.4%) 135: 1 ph (1/1) -- tail: 30 •||• •|||

120/121:(47.8%) 136: 1 ph (1/1) -- tail: 30 •||• •|||

121/122:(48.2%) 137: 1 ph (1/1) -- tail: 30 •••• •|••

122/123:(48.6%) 138: 1 ph (1/1) -- tail: 30 |••| ||••

123/124:(49%) 139: 1 ph (1/1) -- tail: 30 |••| |•••

124/125:(49.4%) 140: 1 ph (1/1) -- tail: 30 •||• ||||

125/126:(49.8%) 141: 1 ph (1/1) -- tail: 30 •||• ||||

126/127:(50.2%) 142: 1 ph (1/1) -- tail: 31 |••| •|••

127/128:(50.6%) 143: 1 ph (1/1) -- tail: 32 ||•| ||||

128/129:(51%) 144: 1 ph (1/1) -- tail: 33 |••| ||••

129/130:(51.4%) 145: 1 ph (1/1) -- tail: 34 •|•• •|||

130/131:(51.8%) 146: 1 ph (1/1) -- tail: 35 •|•• ••||

131/132:(52.2%) 147: 1 ph (1/1) -- tail: 36 •||• |•||

132/133:(52.6%) 148: 1 ph (1/1) -- tail: 37 •||• ••||

133/134:(53%) 149: 1 ph (1/1) -- tail: 38 •••• •|••

134/135:(53.4%) 150: 6 ph (1/6) -- tail: 39 •||| ••|| ... •||| |••|

135/136:(53.8%) 151: 1 ph (1/1) -- tail: 30 •||| |•|•

136/137:(54.2%) 152: 1 ph (1/1) -- tail: 30 |••• •|•|

137/138:(54.5%) 153: 1 ph (1/1) -- tail: 30 |•|• ||•|

138/139:(54.9%) 154: 1 ph (1/1) -- tail: 30 ••|• ||•|

139/140:(55.3%) 155: 1 ph (1/1) -- tail: 30 ••|• ||•|

140/141:(55.7%) 156: 1 ph (1/1) -- tail: 30 |••• •|•|

141/142:(56.1%) 157: 1 ph (1/1) -- tail: 30 •||| |•|•

142/143:(56.5%) 158: 1 ph (1/1) -- tail: 30 |••• •|•|

143/144:(56.9%) 159: 1 ph (1/1) -- tail: 30 |•|• ||•|

144/145:(57.3%) 160: 1 ph (1/1) -- tail: 30 |••• •|•|

145/146:(57.7%) 161: 1 ph (1/1) -- tail: 30 •|•• ••••

146/147:(58.1%) 162: 2 ph (1/2) -- tail: 30 •••| ••|• •|•• ••|•

147/148:(58.5%) 163: 1 ph (1/1) -- tail: 30 |||• ||•|

148/149:(58.9%) 164: 1 ph (1/1) -- tail: 30 •||| |•|•

149/150:(59.3%) 165: 1 ph (1/1) -- tail: 30 •||| |•|•

150/151:(59.7%) 166: 1 ph (1/1) -- tail: 30 |••• •|•|

151/152:(60.1%) 167: 1 ph (1/1) -- tail: 30 |•|• •|•|

152/153:(60.5%) 168: 1 ph (1/1) -- tail: 30 •|•• ••••

153/154:(60.9%) 169: 1 ph (1/1) -- tail: 30 •||| |•|•

154/155:(61.3%) 170: 1 ph (1/1) -- tail: 30 |•|• ||•|

155/156:(61.7%) 171: 1 ph (1/1) -- tail: 30 |••• •|•|

156/157:(62.1%) 172: 1 ph (1/1) -- tail: 30 ••|• ••••

157/158:(62.5%) 173: 1 ph (1/1) -- tail: 30 |•|• ||•|

158/159:(62.8%) 174: 1 ph (1/1) -- tail: 30 •||| |•|•

159/160:(63.2%) 175: 1 ph (1/1) -- tail: 30 •|•| ••|•

160/161:(63.6%) 176: 1 ph (1/1) -- tail: 30 •|•| ••|•

161/162:(64%) 177: 1 ph (1/1) -- tail: 30 •||| |•|•

162/163:(64.4%) 178: 1 ph (1/1) -- tail: 30 •||| |•|•

163/164:(64.8%) 179: 1 ph (1/1) -- tail: 30 •••• •|•|

164/165:(65.2%) 180: 1 ph (1/1) -- tail: 31 •••• •|•|

165/166:(65.6%) 181: 1 ph (1/1) -- tail: 32 |••• •|•|

166/167:(66%) 182: 1 ph (1/1) -- tail: 33 |•|• ||•|

167/168:(66.4%) 183: 1 ph (1/1) -- tail: 34 |••• •|•|

168/169:(66.8%) 184: 1 ph (1/1) -- tail: 35 •||| |•|•

169/170:(67.2%) 185: 1 ph (1/1) -- tail: 36 •|•| ••|•

170/171:(67.6%) 186: 1 ph (1/1) -- tail: 37 •|•| ••|•

171/172:(68%) 187: 1 ph (1/1) -- tail: 38 •||| |•|•

172/173:(68.4%) 188: 1 ph (1/1) -- tail: 39 •||| ||||

173/174:(68.8%) 189: 1 ph (1/1) -- tail: 40 •••| ••|•

174/175:(69.2%) 190: 1 ph (1/1) -- tail: 41 •••| ••|•

175/176:(69.6%) 191: 1 ph (1/1) -- tail: 42 |||• ||•|

176/177:(70%) 192: 2 ph (1/2) -- tail: 43 •••• ••|• •••• |•••

177/178:(70.4%) 193: 1 ph (1/1) -- tail: 44 |||• •|•|

178/179:(70.8%) 194: 1 ph (1/1) -- tail: 45 •••• |•••

179/180:(71.1%) 195: 2 ph (1/2) -- tail: 46 ••|| |•|• •|•| |•|•

180/181:(71.5%) 196: 1 ph (1/1) -- tail: 47 ••|| |•|•

181/182:(71.9%) 197: 1 ph (1/1) -- tail: 48 |||| ||•|

182/183:(72.3%) 198: 1 ph (1/1) -- tail: 49 |||| ||•|

183/184:(72.7%) 199: 1 ph (1/1) -- tail: 50 ••|• |•|•

184/185:(73.1%) 200: 1 ph (1/1) -- tail: 51 •••• ••|•

185/186:(73.5%) 201: 1 ph (1/1) -- tail: 52 ••|| |•|•

186/187:(73.9%) 202: 1 ph (1/1) -- tail: 53 |||| ||•|

187/188:(74.3%) 203: 1 ph (1/1) -- tail: 54 •••• ••|•

188/189:(74.7%) 204: 1 ph (1/1) -- tail: 55 •••• |•|•

189/190:(75.1%) 205: 1 ph (1/1) -- tail: 56 |||• •|•|

190/191:(75.5%) 206: 1 ph (1/1) -- tail: 57 ••|• |•|•

191/192:(75.9%) 207: 1 ph (1/1) -- tail: 58 ••|| |•|•

192/193:(76.3%) 208: 1 ph (1/1) -- tail: 59 •••• ••|•

193/194:(76.7%) 209: 1 ph (1/1) -- tail: 60 ••|• ••••

194/195:(77.1%) 210: 1 ph (1/1) -- tail: 61 ||•| •|•|

195/196:(77.5%) 211: 1 ph (1/1) -- tail: 62 |||• ||||

196/197:(77.9%) 212: 1 ph (1/1) -- tail: 63 •••| |•|•

197/198:(78.3%) 213: 1 ph (1/1) -- tail: 64 |||• •|||

198/199:(78.7%) 214: 1 ph (1/1) -- tail: 65 ••|• |•|•

199/200:(79.1%) 215: 1 ph (1/1) -- tail: 66 |||• ||||

200/201:(79.4%) 216: 1 ph (1/1) -- tail: 67 |||| ||•|

201/202:(79.8%) 217: 1 ph (1/1) -- tail: 68 |||• ||||

202/203:(80.2%) 218: 1 ph (1/1) -- tail: 69 ||•• •|•|

203/204:(80.6%) 219: 1 ph (1/1) -- tail: 70 ••|• ••••

204/205:(81%) 220: 1 ph (1/1) -- tail: 71 ||•• •|•|

205/206:(81.4%) 221: 1 ph (1/1) -- tail: 72 ••|| |•|•

206/207:(81.8%) 222: 1 ph (1/1) -- tail: 73 ••|| |•|•

207/208:(82.2%) 223: 1 ph (1/1) -- tail: 74 •••| ••|•

208/209:(82.6%) 224: 1 ph (1/1) -- tail: 75 •••| ••|•

209/210:(83%) 225: 1 ph (1/1) -- tail: 76 ••|| |•|•

210/211:(83.4%) 226: 1 ph (1/1) -- tail: 77 ••|• |•••

211/212:(83.8%) 227: 1 ph (1/1) -- tail: 78 ••|• |•|•

212/213:(84.2%) 228: 1 ph (1/1) -- tail: 79 ||•| •|•|

213/214:(84.6%) 229: 1 ph (1/1) -- tail: 80 ••|• |•••

214/215:(85%) 230: 1 ph (1/1) -- tail: 81 ••|• |•|•

215/216:(85.4%) 231: 1 ph (1/1) -- tail: 82 ••|• |•|•

216/217:(85.8%) 232: 1 ph (1/1) -- tail: 83 ||•| •|||

217/218:(86.2%) 233: 1 ph (1/1) -- tail: 84 ||•| •|•|

218/219:(86.6%) 234: 1 ph (1/1) -- tail: 85 ••|• ••••

219/220:(87%) 235: 1 ph (1/1) -- tail: 86 |||| •|||

220/221:(87.4%) 236: 1 ph (1/1) -- tail: 87 ||•| ||||

221/222:(87.7%) 237: 1 ph (1/1) -- tail: 88 |||| ||•|

222/223:(88.1%) 238: 1 ph (1/1) -- tail: 89 •••• ••|•

223/224:(88.5%) 239: 1 ph (1/1) -- tail: 90 |||| •|||

224/225:(88.9%) 240: 1 ph (1/1) -- tail: 91 ||•| ||||

225/226:(89.3%) 241: 1 ph (1/1) -- tail: 92 |||| ||•|

226/227:(89.7%) 242: 2 ph (1/2) -- tail: 93 ||•| •••| ||•| •|••

227/228:(90.1%) 243: 1 ph (1/1) -- tail: 55 |||| ||•|

228/229:(90.5%) 244: 1 ph (1/1) -- tail: 56 ||•• •••|

229/230:(90.9%) 245: 1 ph (1/1) -- tail: 57 ••|• ••••

230/231:(91.3%) 246: 1 ph (1/1) -- tail: 58 ||•• •••|

231/232:(91.7%) 248: 2 ph (1/2) -- tail: 59 |||| |•|| |||| |||•

232/233:(92.1%) 249: 1 ph (1/1) -- tail: 60 •||| |||•

233/234:(92.5%) 250: 1 ph (1/1) -- tail: 30 ••|• ••••

234/235:(92.9%) 251: 1 ph (1/1) -- tail: 30 |||| |||•

235/236:(93.3%) 252: 3 ph (1/3) -- tail: 30 ••|| ••|• ... •|•| ••|•

236/237:(93.7%) 253: 1 ph (1/1) -- tail: 30 ••|• ••••

237/238:(94.1%) 254: 1 ph (1/1) -- tail: 30 ••|| |||•

238/239:(94.5%) 255: 1 ph (1/1) -- tail: 30 ||•• •••|

239/240:(94.9%) 256: 1 ph (1/1) -- tail: 30 •••• |•••

240/241:(95.3%) 257: 1 ph (1/1) -- tail: 30 ||•| ||||

241/242:(95.7%) 258: 2 ph (1/2) -- tail: 30 |•|| ||•| |||• ||•|

242/243:(96%) 259: 2 ph (1/2) -- tail: 30 •||| |||• |•|| |||•

243/244:(96.4%) 260: 1 ph (1/1) -- tail: 30 ••|| |||•

244/245:(96.8%) 261: 1 ph (1/1) -- tail: 30 |||| |•||

245/246:(97.2%) 262: 1 ph (1/1) -- tail: 30 ||•• •••|

246/247:(97.6%) 263: 1 ph (1/1) -- tail: 30 ||•• •••|

247/248:(98%) 264: 1 ph (1/1) -- tail: 30 |•|| |||•

248/249:(98.4%) 265: 2 ph (1/2) -- tail: 30 ||•• •|•| ||•• |••|

249/250:(98.8%) 266: 1 ph (1/1) -- tail: 30 |||| |•||

250/251:(99.2%) 267: 1 ph (1/1) -- tail: 30 •••| |||•

251/252:(99.6%) 268: 1 ph (1/1) -- tail: 30 ||•• •••|

252/253:(100%) 269: 1 ph (1/1) -- tail: 30 ||•• •••|

════════════════════════════════════════ Reestimating final recombination fractions ══

Markers in the initial sequence: 253

Mapped markers : 252 (99.6%)

══════════════════════════════════════════════════════════════════════════════════════

> plot(single\_chrom)

> phasing\_and\_hmm\_rf <- function(X){

+ fl <- paste0("output\_map\_ch\_", unique(X$seq$chrom), ".txt")

+ sink(fl)

+ map <- est\_rf\_hmm\_sequential(input.seq = X$seq,

+ start.set = 3,

+ thres.twopt = 10,

+ thres.hmm = 50,

+ extend.tail = 30,

+ twopt = X$tpt,

+ verbose = TRUE,

+ phase.number.limit = 20,

+ sub.map.size.diff.limit = 5)

+ sink()

+ return(map)

+ }

> my.error.func<-function(X){

+ x<-est\_full\_hmm\_with\_global\_error(input.map = X,

+ error = 0.05,

+ tol = 10e-4,

+ verbose = FALSE)

+ return(x)

+ }

> ptm <- proc.time()

> cl <- parallel::makeCluster(7)

> parallel::clusterEvalQ(cl, require(mappoly))

[[1]]

[1] TRUE

[[2]]

[1] TRUE

[[3]]

[1] TRUE

[[4]]

[1] TRUE

[[5]]

[1] TRUE

[[6]]

[1] TRUE

[[7]]

[1] TRUE