

GeneratedFigures

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Collect inferred models

Here, we extract the inferred model and regimes and add them as columns to the testData_t4 data.table.
Manual execution.

Evaluate the 7 binary criterions on the inferred models

```
if(file.exists("../data-raw/ResultsTestData_t4/TestResultData_t4.RData")) {
  load("../data-raw/ResultsTestData_t4/TestResultData_t4.RData")
} else {
  testResultData <- NULL
}

testResultDataBhatt <- rbindlist(
  lapply(1:nrow(testData_t4), function(i) {

    resultFile <- paste0("../data-raw/ResultsTestData_t4/FinalResult_MixedGaussian_testData_t4_id_",
                          i)

    if(file.exists(resultFile)) {
      cat("Loading ", resultFile, "\n")
      load(resultFile)
      bestFitAIC <- RetrieveBestFitAIC(fitMappings)
      trueFromTestData <- RetrieveTrueFromTestData(testData_t4, i)

      bhatt <- bhattacharyya(trueFromTestData$tree, trueFromTestData$trueModel,
                               bestFitAIC$tree, bestFitAIC$inferredModel)

      cat("Bhatt: ", bhatt, "\n")
      data.table(i = i,
                 treeType=testData_t4[i, treeType],
                 treeSize=testData_t4[i, treeSize],
                 numClusters = testData_t4[i, numClusters],
                 crit = factor(c("Bhattacharyya dist.")),
                 tpr = NA,
                 fpr = NA,
                 AIC_Final = AIC(bestFitAIC$inferredModel),
                 AIC_True = AIC(trueFromTestData$trueModel),
                 inferred.x0 = bestFitAIC$inferredModel$X0[[1]],
                 inferred.y0 = bestFitAIC$inferredModel$X0[[2]],
                 true.x0 = trueFromTestData$trueModel$X0[[1]],
                 true.y0 = trueFromTestData$trueModel$X0[[2]],
                 value = bhatt
    }
  })
}
```

```

        )
    } else {
      NULL
    }

  })
}

if(!is.null(testResultData)) {
  testResultData <- rbindlist(list(testResultData, testResultDataNew), fill = TRUE)
} else {
  testResultData <- testResultDataNew
}

testResultData[, crit2:=factor(crit, levels = c("Cluster",
                                                 "BM process",
                                                 "OU process",
                                                 "Uncorrelated traits",
                                                 "Correlated traits",
                                                 "NonDiagonal H",
                                                 "Asymmetric H",
                                                 "Bhattacharyya dist."))]

load("../data-raw/ResultsTestData_t4/TestResultData_t4.RData")
testResultData[, numClusters2:=paste0(numClusters, " regimes")]
testResultData[, treeType2:=factor(paste0(treeType, " tree"), levels=c("ultrametric tree", "non-ultrametric tree"))]
ggplot(testResultData[testSize == "N=80" & !(crit2 %in% c("BM process", "Uncorrelated traits"))]) +
  geom_abline(slope = 1, intercept = 0, linetype = 2, size = 0.2, color="red") +
  geom_label(aes(label = i, x = fpr, y = tpr,
                 #size = 0.5*apply(cbind((0.2+1-tpr), (0.2+fpr)), 1, max),
                 color = 0.5*apply(cbind((0.2+1-tpr), (0.2+fpr)), 1, max),
                 fill = AIC_Final<AIC_True ),
                 size = 2,
                 position = position_jitter(width=0.05, height = 0.05),
                 label.padding = unit(0.1, "lines"), fontface = "bold") +
  xlab("False positive rate") + ylab("True positive rate") +
  scale_color_continuous(low="green", high="red") +
  scale_fill_manual(values = c("TRUE"="white", "FALSE"="black")) +
  #scale_size_continuous(range = c(1.5, 3)) +
  scale_x_continuous(breaks=c(0, 0.25, 0.5, 0.75, 1)) +
  scale_y_continuous(breaks=c(0, 0.25, 0.5, 0.75, 1)) +
  facet_grid(numClusters2*treeType2~crit2) +
  theme_bw() +
  theme(legend.position = "none")

ggplot(testResultData[testSize == "N=159" & !(crit2 %in% c("BM process", "Uncorrelated traits"))]) +
  geom_abline(slope = 1, intercept = 0, linetype = 2, size = 0.2, color="red") +
  geom_label(aes(label = i, x = fpr, y = tpr,
                 #size = 0.5*apply(cbind((0.2+1-tpr), (0.2+fpr)), 1, max),
                 color = 0.5*apply(cbind((0.2+1-tpr), (0.2+fpr)), 1, max),
                 fill = AIC_Final<AIC_True ),
                 size = 2,
                 position = position_jitter(width=0.05, height = 0.05),
                 label.padding = unit(0.1, "lines"), fontface = "bold") +

```

```

xlab("False positive rate") + ylab("True positive rate") +
scale_color_continuous(low="green", high="red") +
scale_fill_manual(values = c("TRUE"="white", "FALSE"="black")) +
#scale_size_continuous(range = c(1.5, 3)) +
scale_x_continuous(breaks=c(0, 0.25, 0.5, 0.75, 1)) +
scale_y_continuous(breaks=c(0, 0.25, 0.5, 0.75, 1)) +
facet_grid(numClusters2*treeType2~crit2) +
theme_bw() +
theme(legend.position = "none")

ids <- testData_t4[1:256, list(id = min(.I), .N), keyby=list(treeType, treeSize, numClusters)][, sort(i

for(id in ids) {
  print(data.table(
    id = id,
    type = testData_t4$treeType[[id]],
    size = testData_t4$treeSize[[id]],
    numRegimes = testData_t4$numClusters[[id]]))
  tree <- testData_t4$treeWithRegimes[[id]]
  print(PCMTreeDtNodeRegimes(tree)[endNode <= PCMTreeNumTips(tree), .N, keyby=regime])
}

##      id      type size numRegimes
## 1: 1 ultrametric N=80          2
## regime N
## 1: 1 52
## 2: 2 28
##      id      type size numRegimes
## 1: 33 ultrametric N=80          3
## regime N
## 1: 1 31
## 2: 2 21
## 3: 3 28
##      id      type size numRegimes
## 1: 65 non-ultrametric N=80          2
## regime N
## 1: 1 52
## 2: 2 28
##      id      type size numRegimes
## 1: 97 non-ultrametric N=80          3
## regime N
## 1: 1 24
## 2: 2 29
## 3: 3 27
##      id      type size numRegimes
## 1: 129 ultrametric N=159          2
## regime N
## 1: 1 128
## 2: 2 31
##      id      type size numRegimes
## 1: 161 ultrametric N=159          5
## regime N
## 1: 1 24
## 2: 2 54

```

```

## 3:      3 28
## 4:      4 31
## 5:      5 22
##           id          type   size numRegimes
## 1: 193 non-ultrametric N=159              2
##   regime   N
## 1:      1 117
## 2:      2 42
##           id          type   size numRegimes
## 1: 225 non-ultrametric N=159              5
##   regime   N
## 1:      1 46
## 2:      2 28
## 3:      3 23
## 4:      4 38
## 5:      5 24
ids <- testData_t4[1:256, list(id = min(.I), .N), keyby=list(treeType, treeSize)][, sort(id)]

dtNumAllPartitions <- rbindlist(lapply(ids, function(id) {
  data.table(
    id = id,
    type = testData_t4$treeType[[id]],
    size = testData_t4$treeSize[[id]],
    P18 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 18), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)],
    P19 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 19), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)],
    P20 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 20), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)],
    P21 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 21), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)],
    P22 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 22), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)],
    P23 = data.table(a=sapply(PCMTreeListAllPartitions(
      testData_t4$tree[[id]], 23), length) + 1)[
      , .N, keyby=a][, sum(N*6^a)]
  )
}))
```

`save(dtNumAllPartitions, file = "dtNumAllPartitions.RData")`

```

load("dtNumAllPartitions.RData")
dtNumAllPartitions
```

	id	type	size	P18	P19	P20	P21	P22
## 1:	1	ultrametric	N=80	24054	17358	1050	582	114
## 2:	65	non-ultrametric	N=80	5550	4902	4254	3822	2922
## 3:	129	ultrametric	N=159	85719534	20672574	3862086	3862086	688110
## 4:	193	non-ultrametric	N=159	203397990	89043666	56089842	10719654	3108858

```

##      P23
## 1:    78
## 2: 2238
## 3: 62718
## 4: 547278

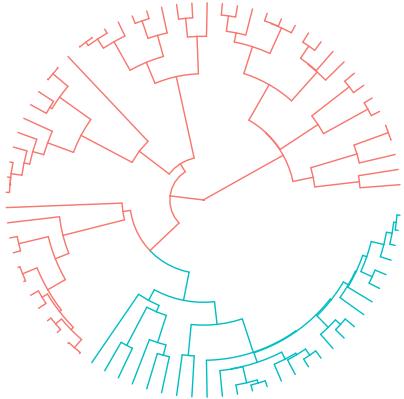
ids <- testData_t4[, list(id = min(.I), .N), keyby=list(treeType, treeSize, numClusters)][, sort(id)]

plList <- lapply(ids, function(id) {
  PCMTreePlot(testData_t4$treeWithRegimes[[id]], layout="fan", open.angle=2, size=.25) +
    ggtitle(paste0(LETTERS[match(id, ids)], ".",
                  testData_t4$treeType[[id]], " / ",
                  testData_t4$treeSize[[id]], " / ",
                  testData_t4$numClusters[[id]], " regimes"))
})

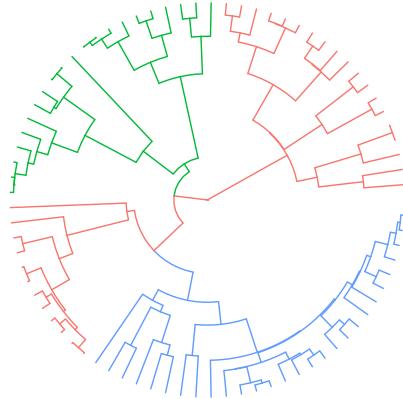
cowplot:::plot_grid(plotlist = plList[1:4], nrow = 2, ncol=2)

```

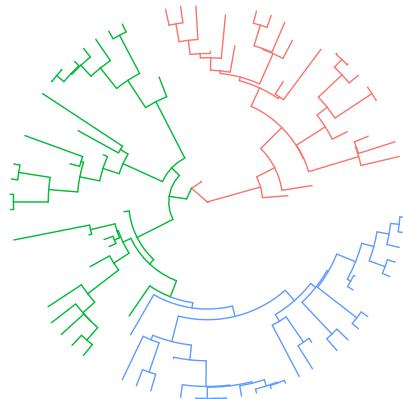
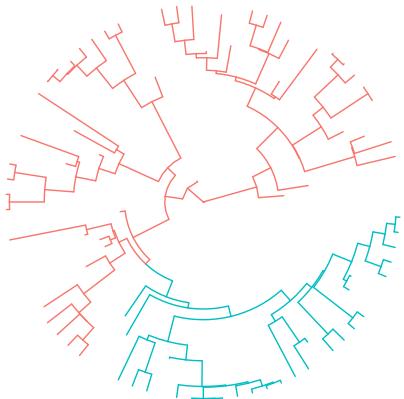
A. ultrametric / N=80 / 2 regimes



B. ultrametric / N=80 / 3 regimes



C. non-ultrametric / N=80 / 2 regimes D. non-ultrametric / N=80 / 3 regimes

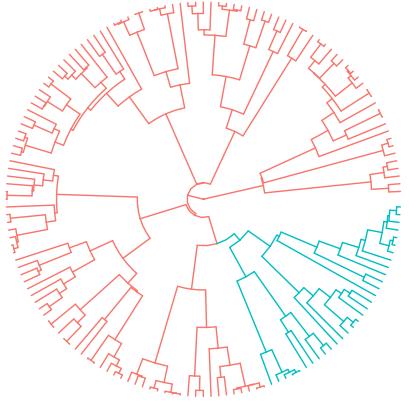


```

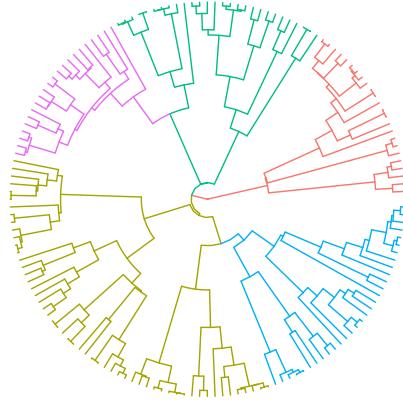
cowplot:::plot_grid(plotlist = plList[5:8], nrow = 2, ncol=2)

```

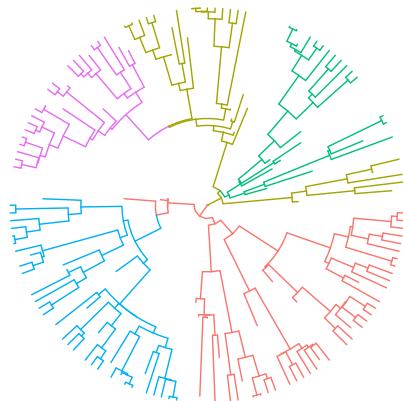
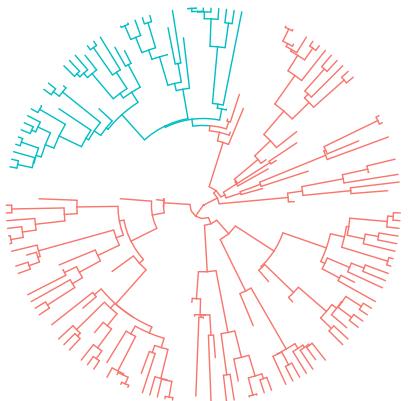
E. ultrametric / N=159 / 2 regimes



F. ultrametric / N=159 / 5 regimes

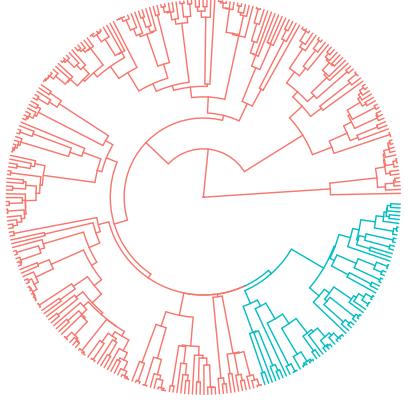


G. non-ultrametric / N=159 / 2 regim H. non-ultrametric / N=159 / 5 regi

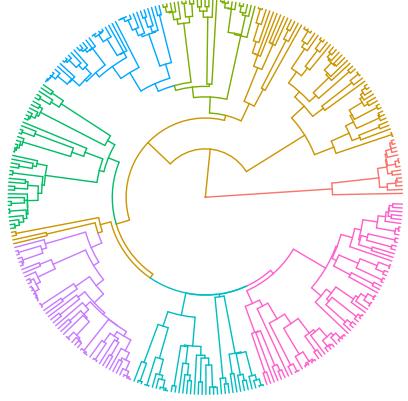


```
cowplot:::plot_grid(plotlist = plList[9:12], nrow = 2, ncol=2)
```

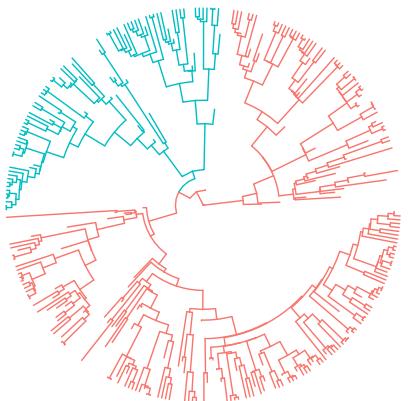
I. ultrametric / N=318 / 2 regimes



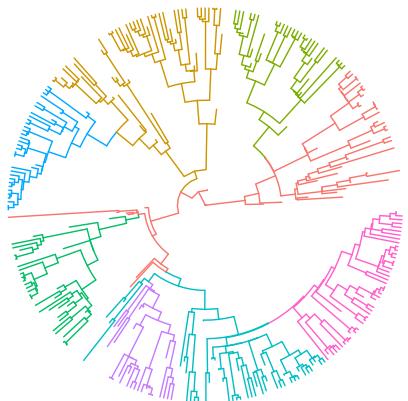
J. ultrametric / N=318 / 8 regimes



K. non-ultrametric / N=318 / 2 regimes

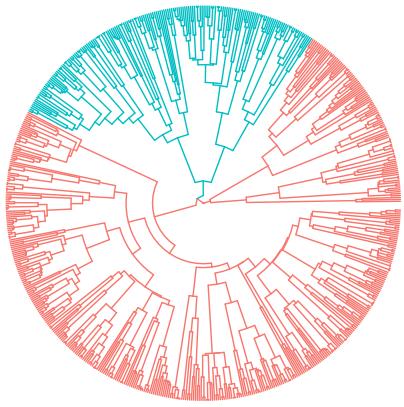


L. non-ultrametric / N=318 / 8 regimes

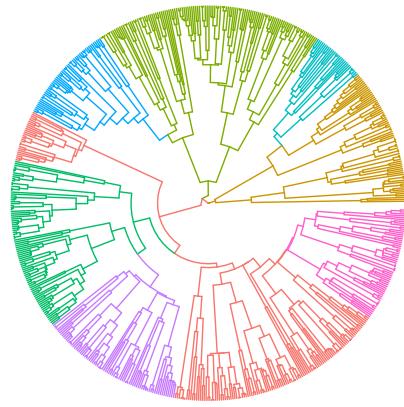


```
cowplot:::plot_grid(plotlist = plList[13:16], nrow = 2, ncol=2)
```

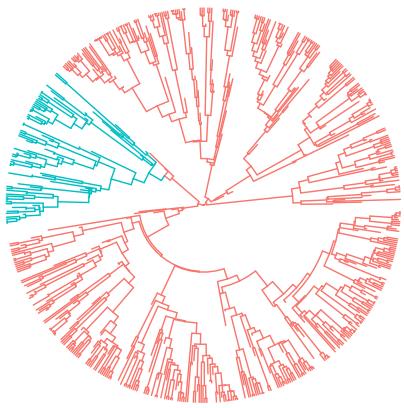
M. ultrametric / N=638 / 2 regimes



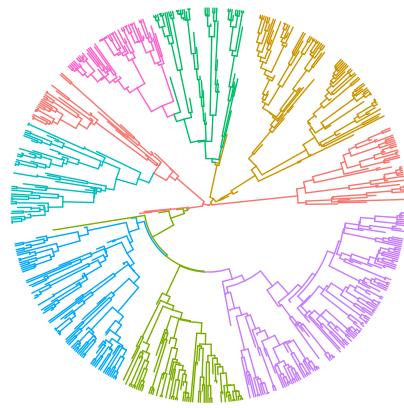
N. ultrametric / N=638 / 8 regimes

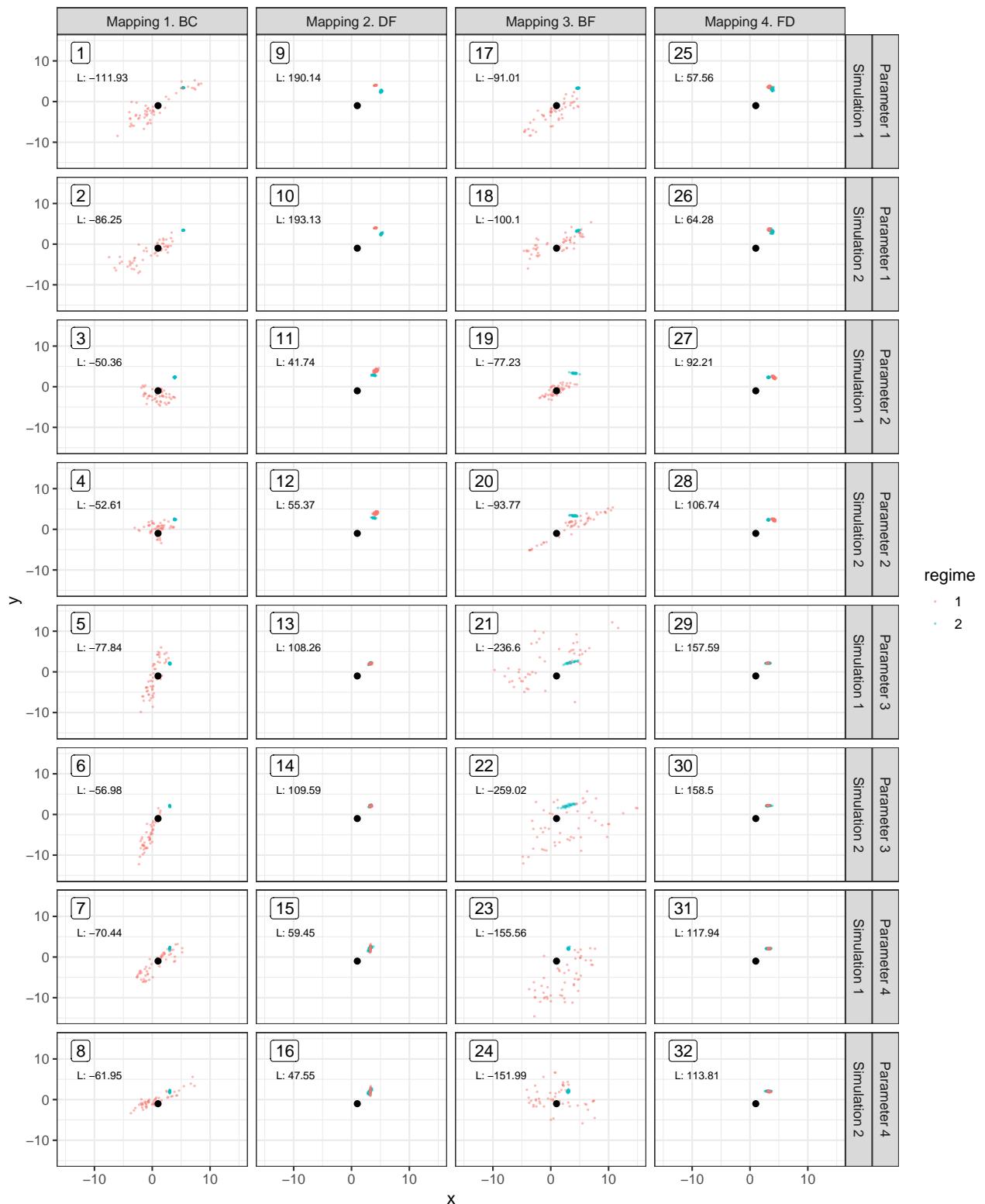


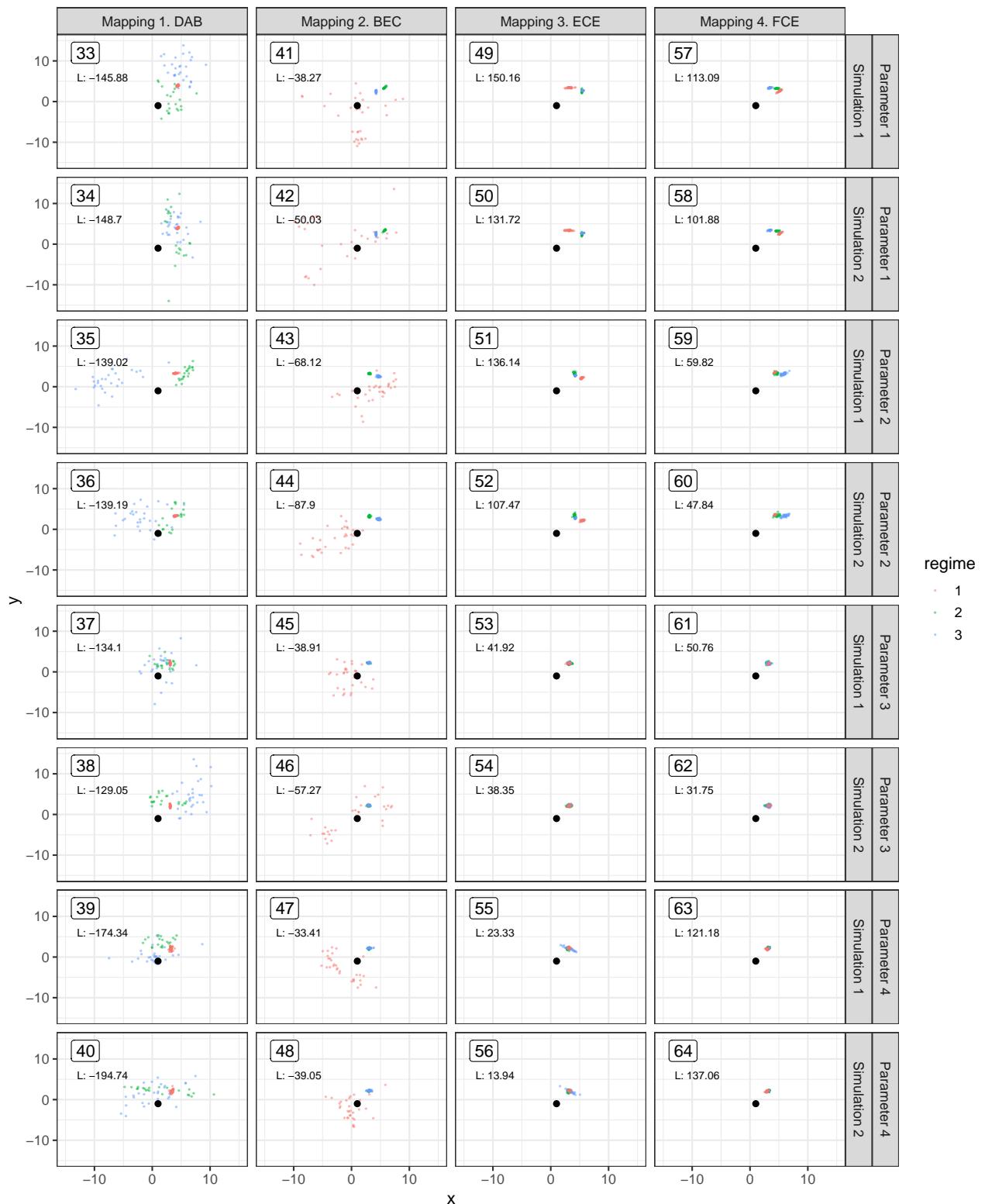
O. non-ultrametric / N=638 / 2 regim

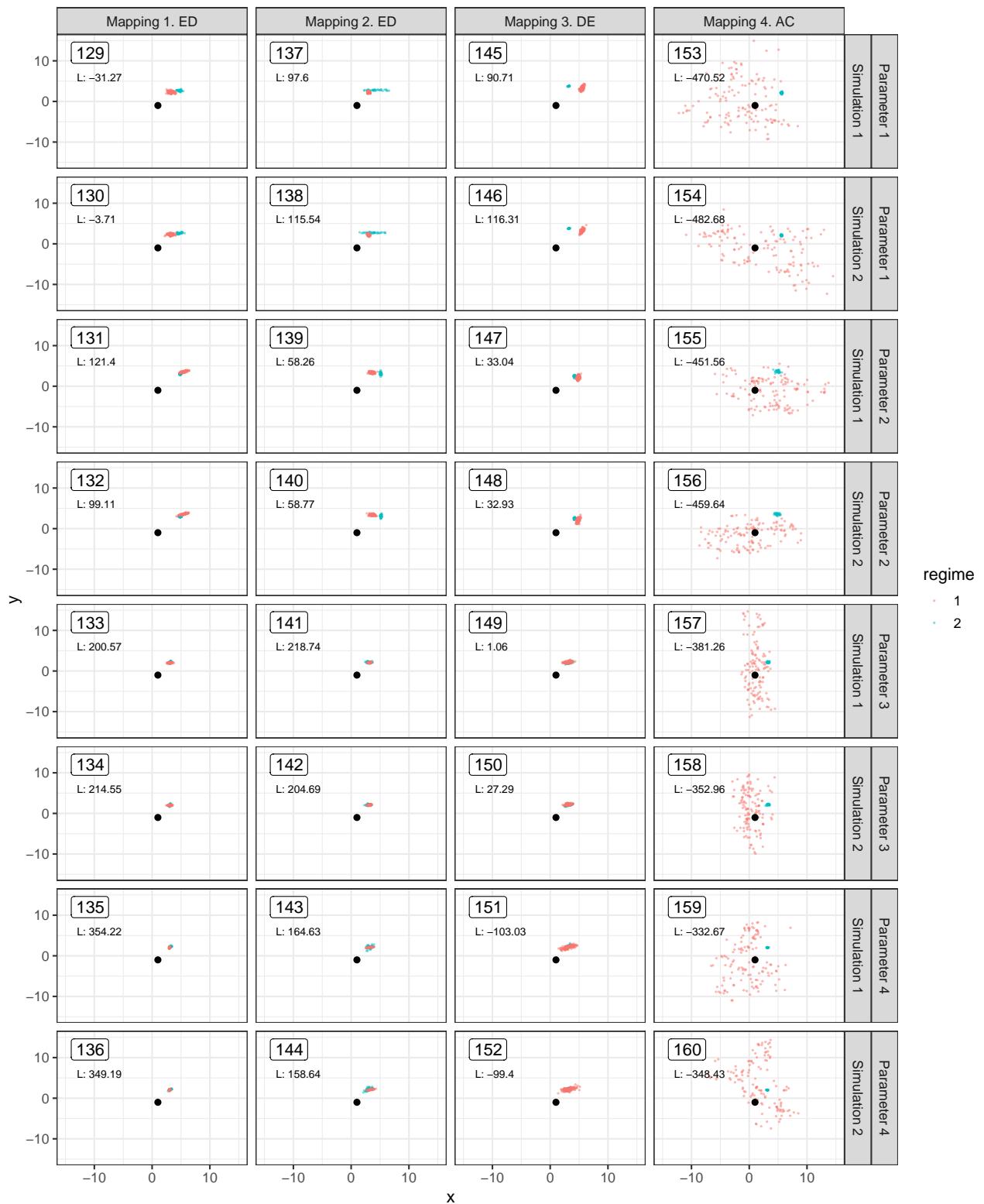


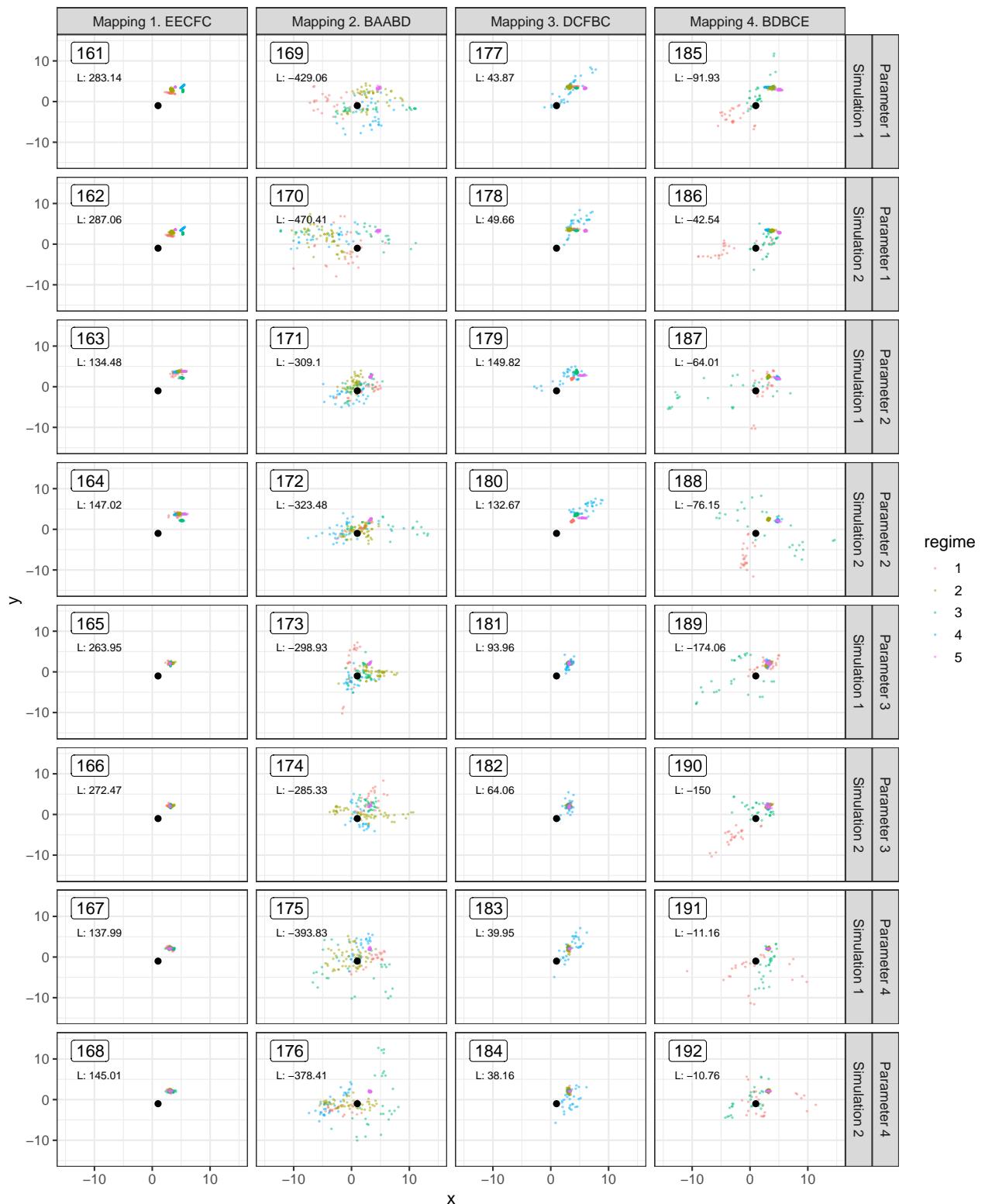
P. non-ultrametric / N=638 / 8 regim

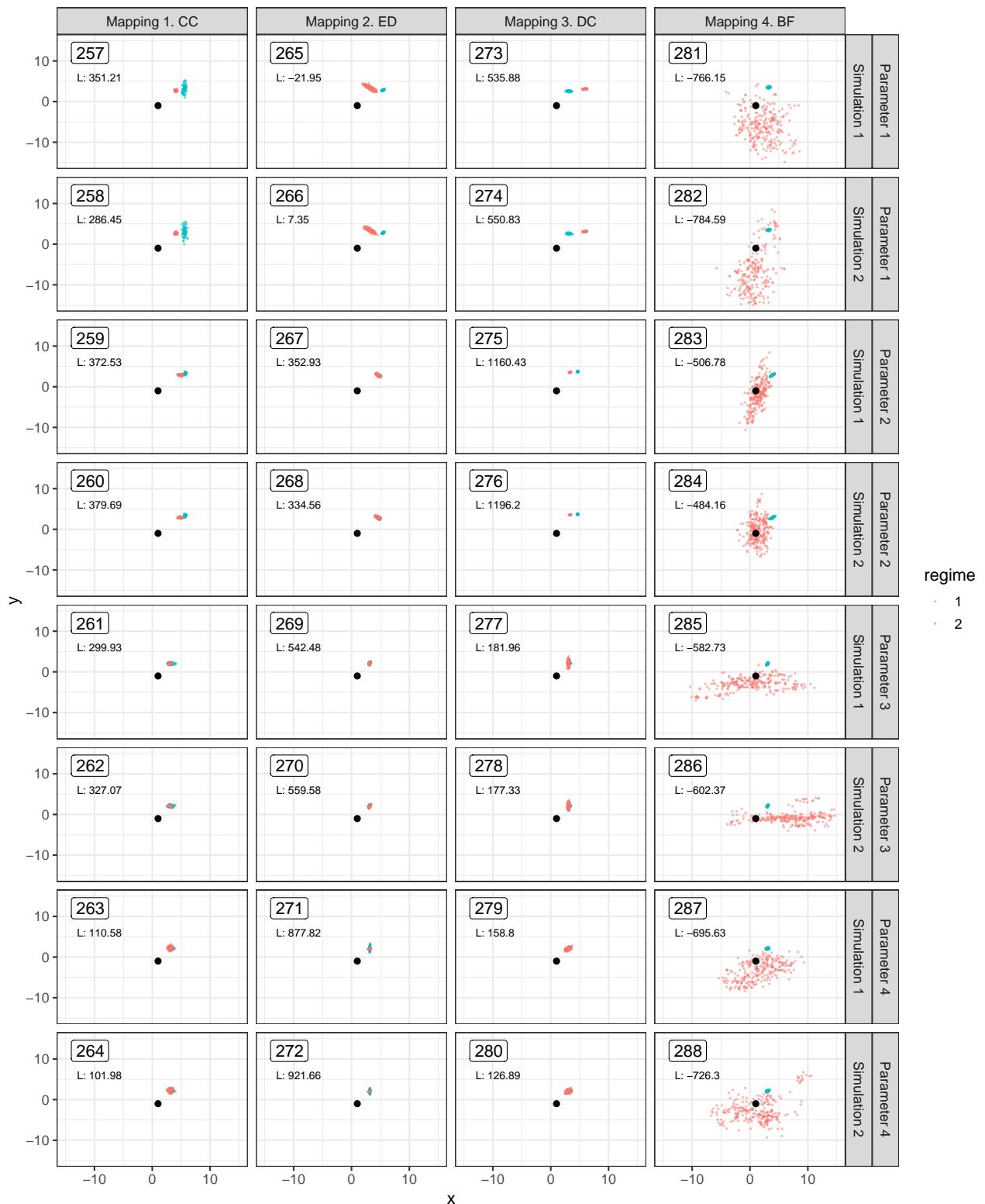


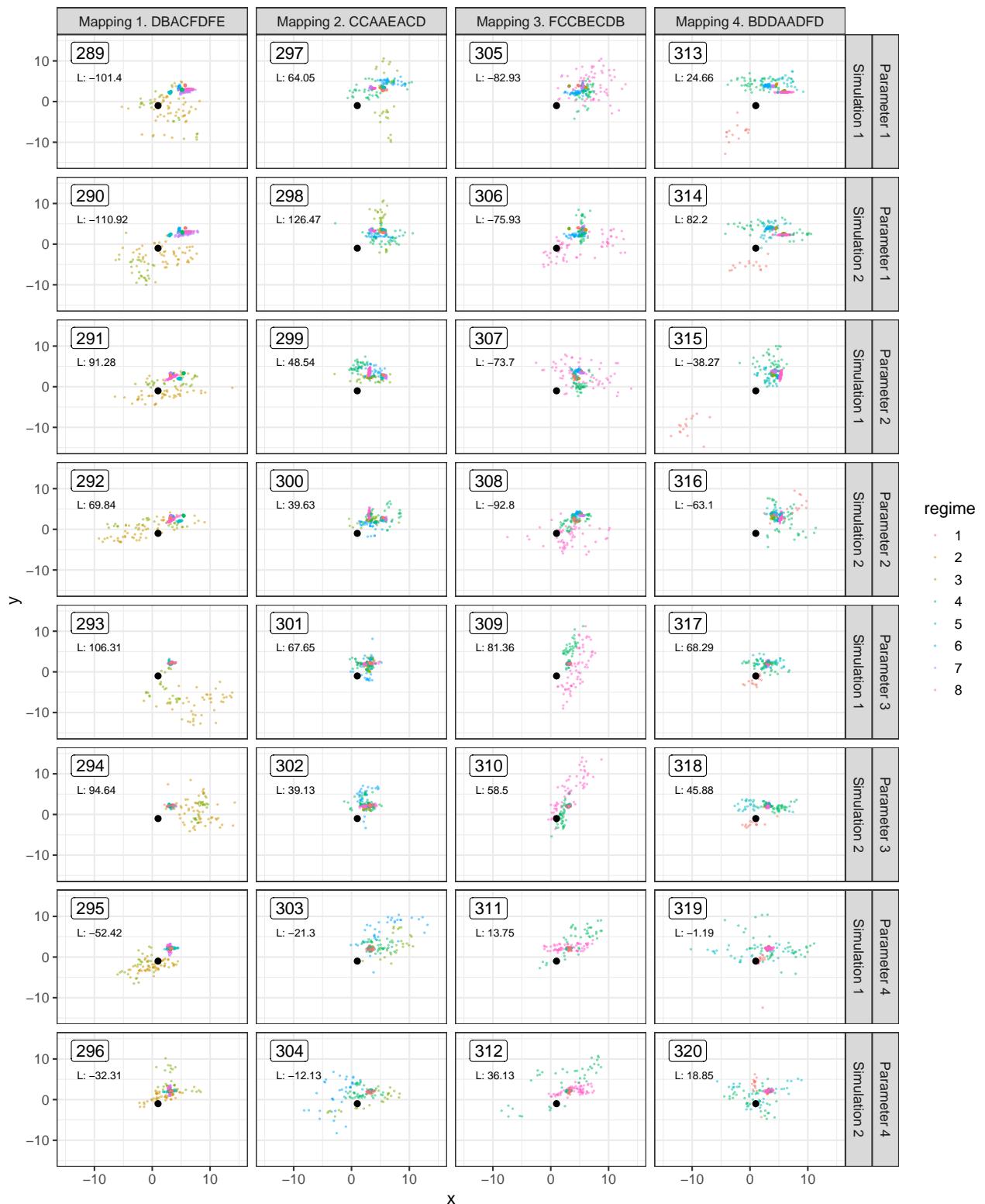


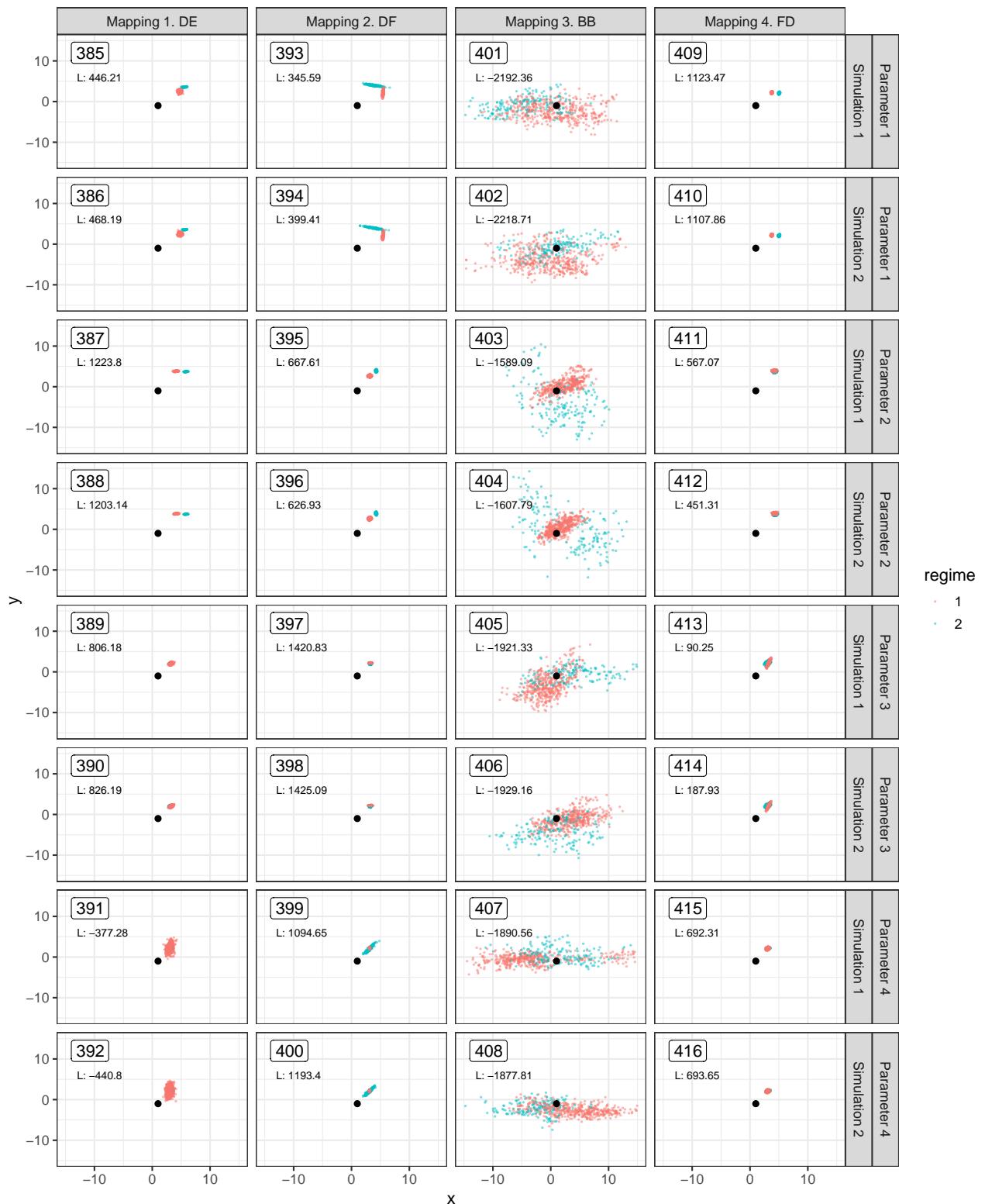


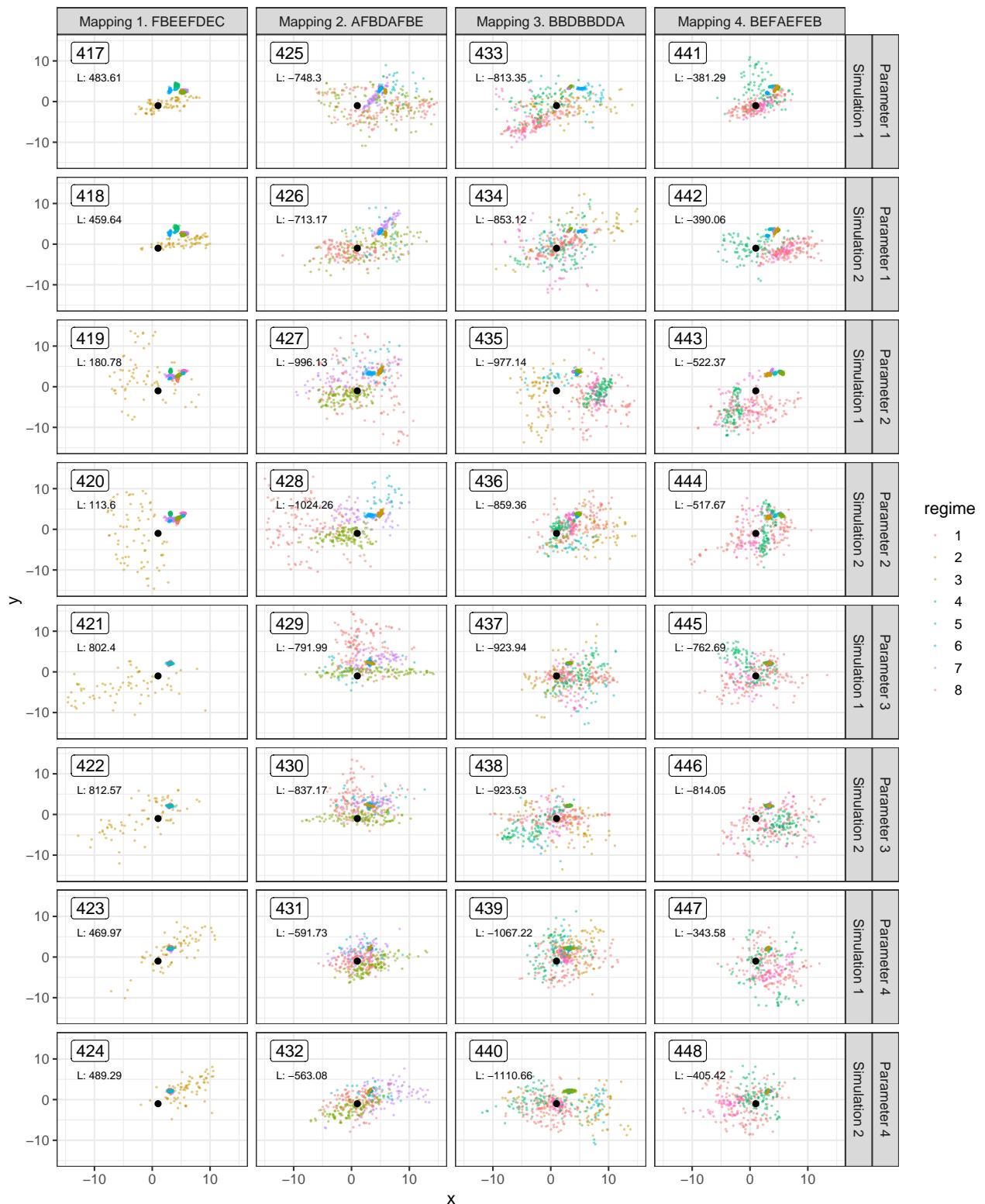


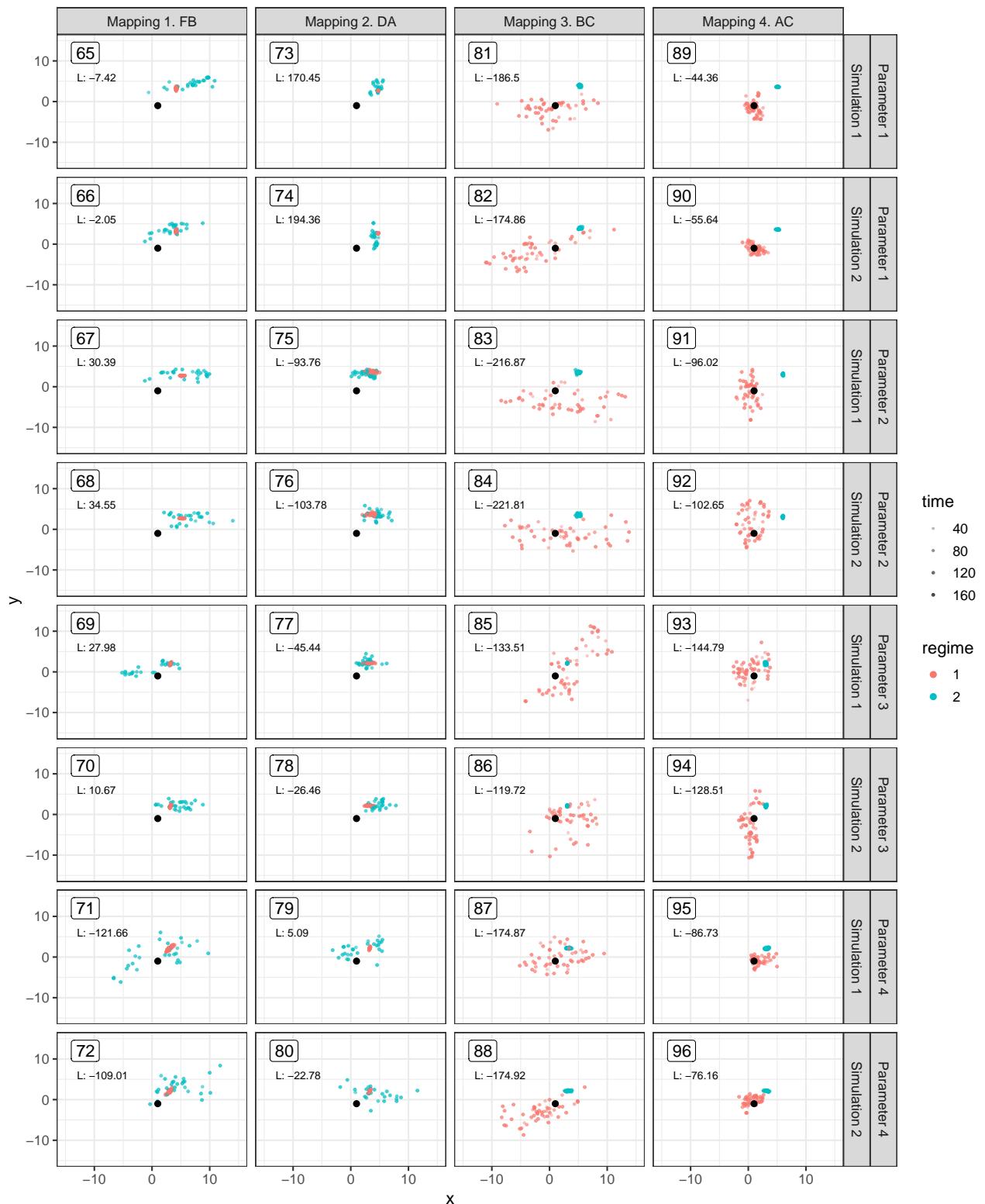




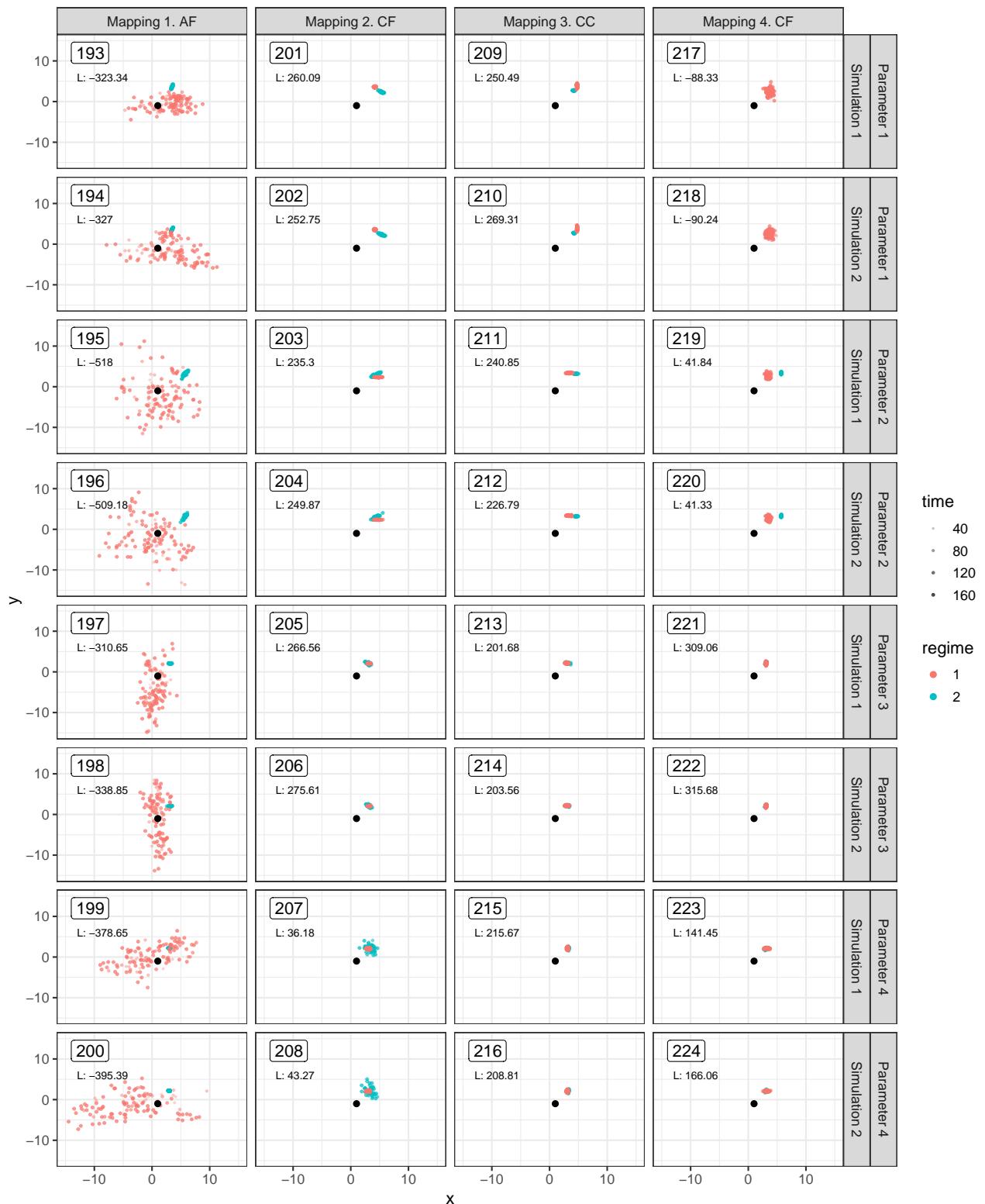


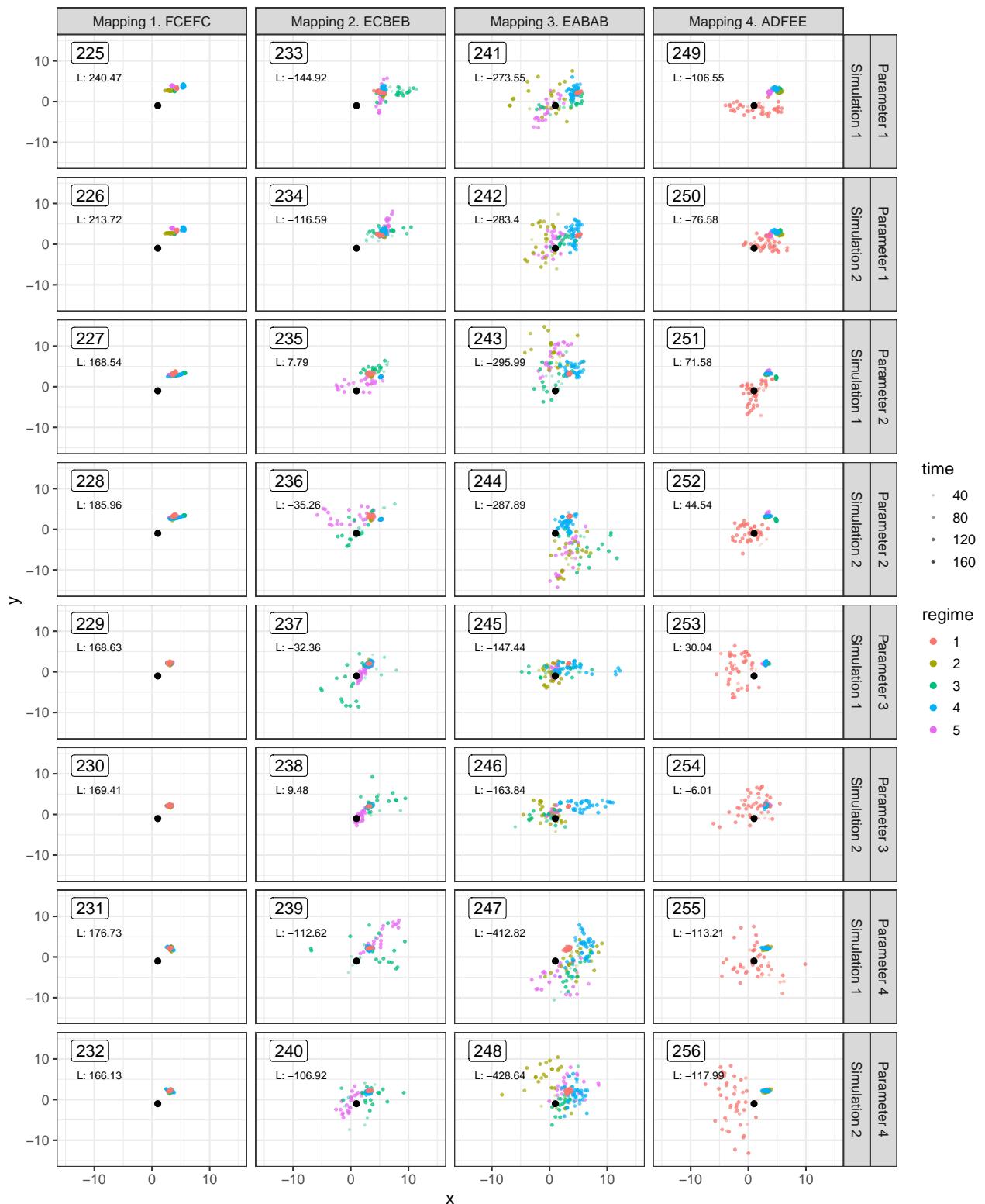


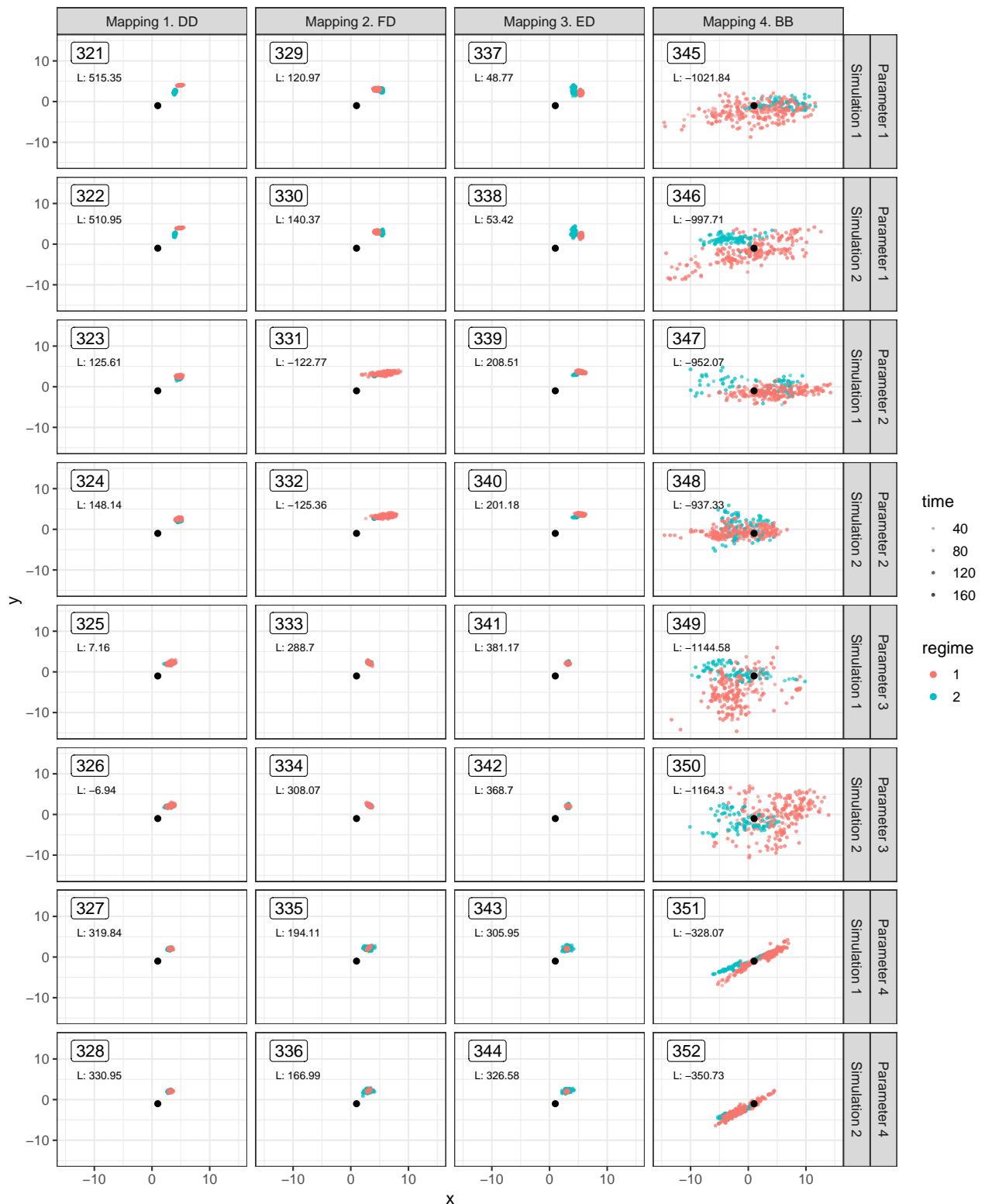


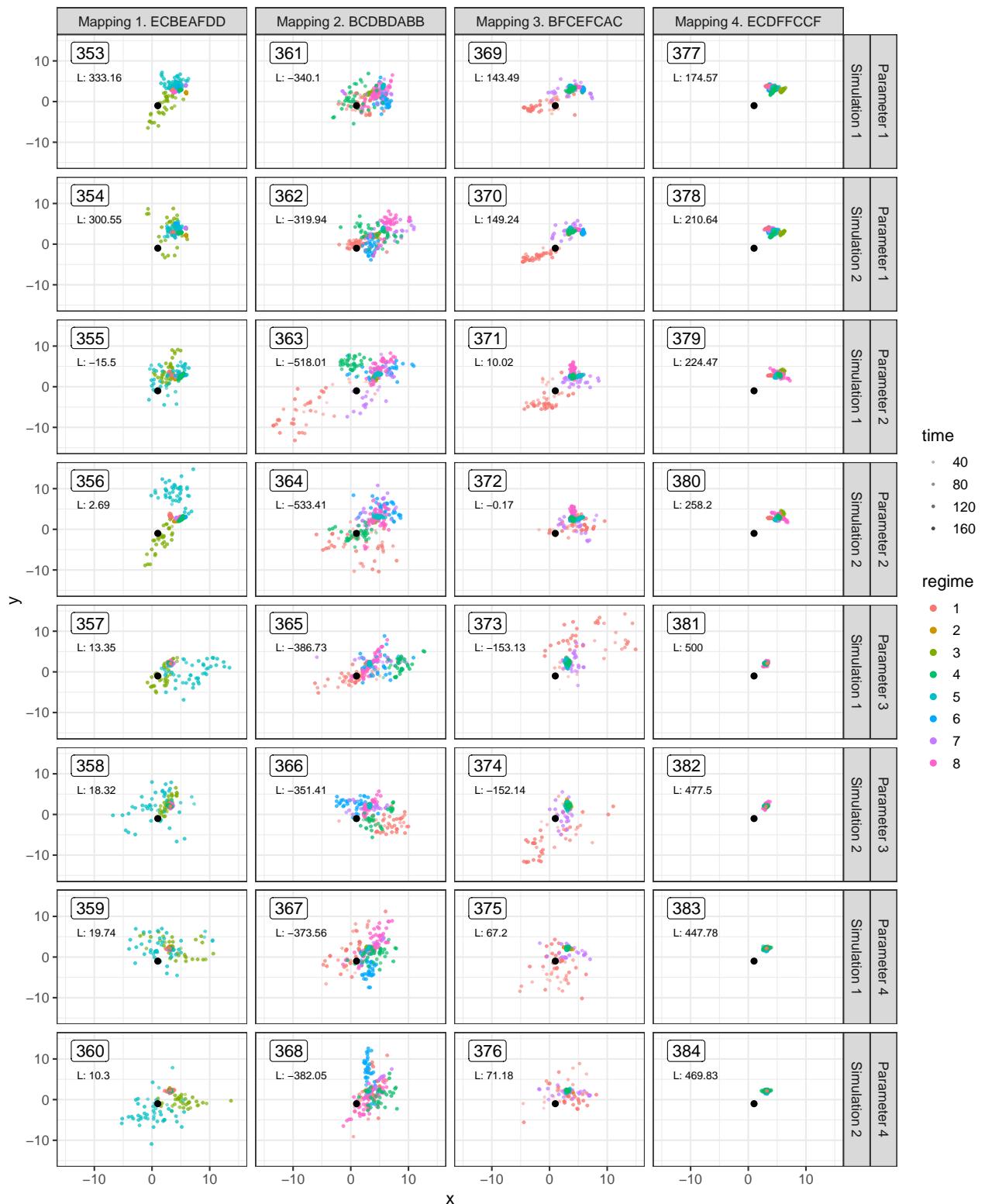


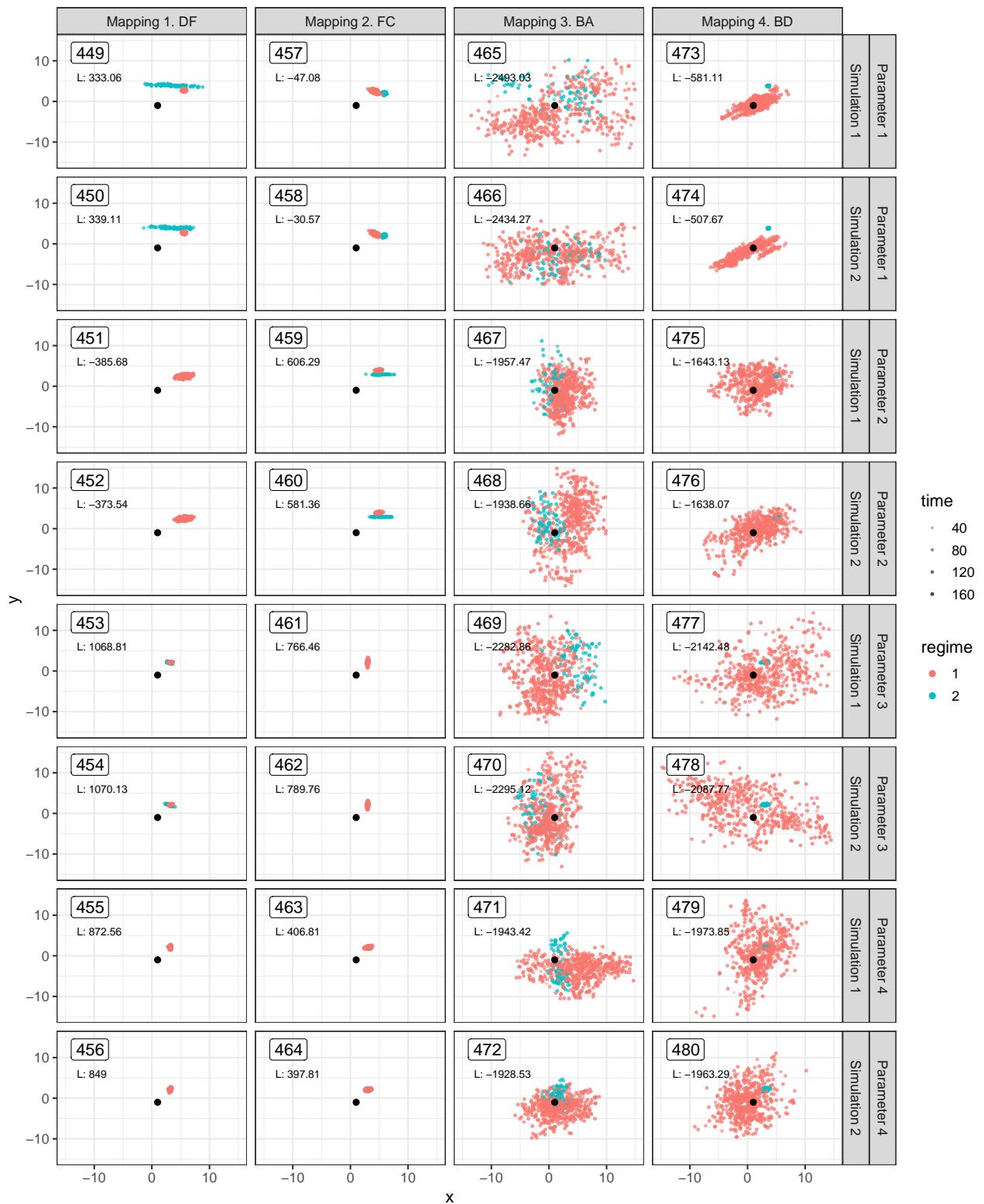


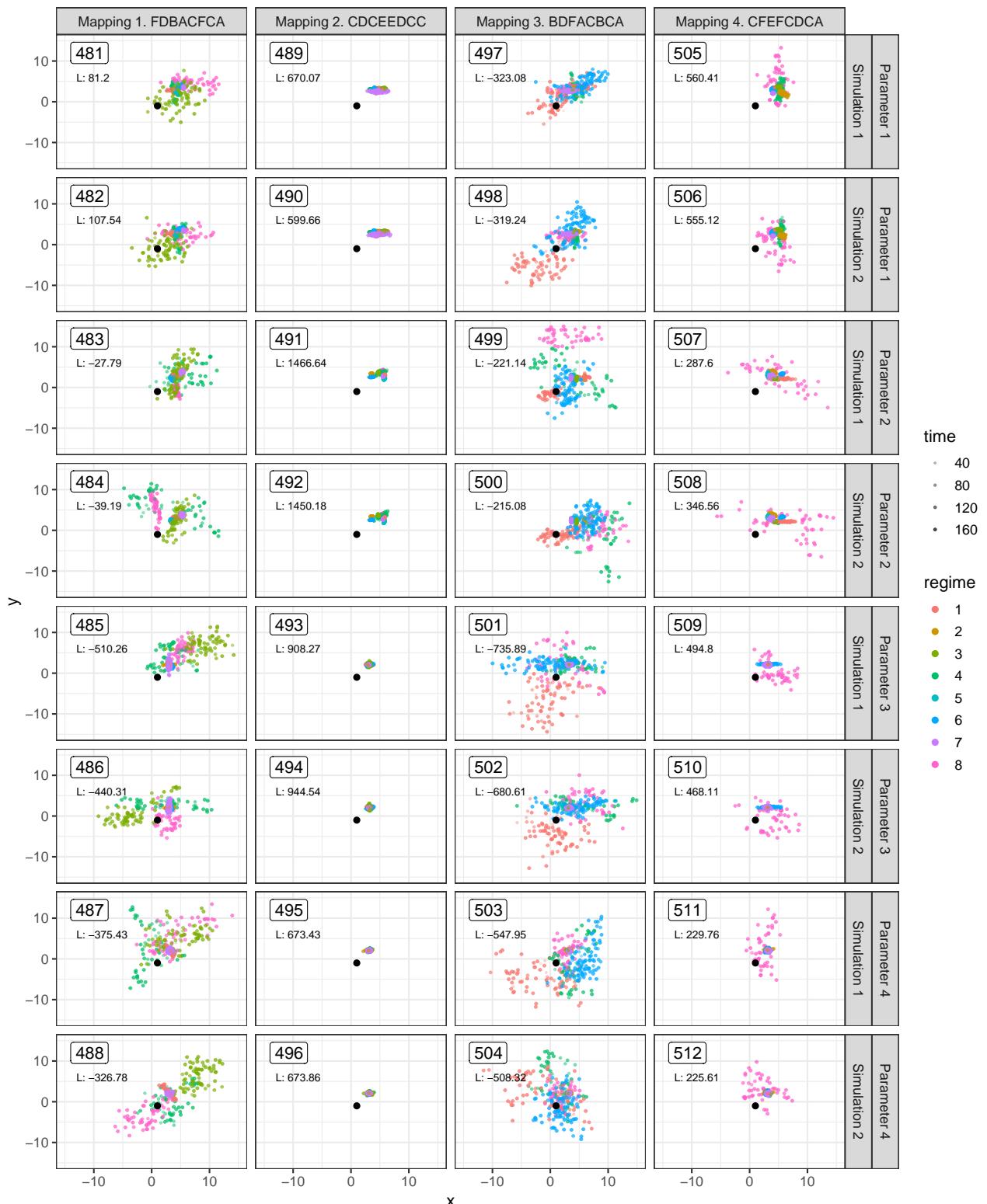












```

load("../data-raw/ResultsTestData_t4/TestResultData_t4.RData")
summaryTable <- testResultData[, {
  maskTests <- !is.na(fpr) & !is.na(tpr)
  numTests <- sum(maskTests)
  list(
    numTests = numTests,
    maskTests = maskTests
  )
}]
  
```

```

`#tests`=numTests,
`Better AIC` = sum(AIC_Final[maskTests] - AIC_True[maskTests] <= 0)/numTests,
fpr=sum(fpr[maskTests])/numTests,
#`SE(fpr)`=sd(fpr[maskTests])/sqrt(numTests),
tpr=sum(tpr[maskTests])/numTests#,
#`SE(tpr)`=sd(tpr[maskTests])/sqrt(numTests)
)
},
keyby=list(Crit.=crit2, N=factor(treeSize, levels=c("N=80", "N=159", "N=318", "N=638"), labels=c(80, 159,
`#regimes`=as.integer(numClusters),
`Tree-type`=factor(treeType, levels=c("ultrametric", "non-ultrametric")))] [Crit. %in% c("Clustered", "Unclustered")]
print.xtable(xtable(summaryTable), comment=FALSE, include.rownames = FALSE)

```