R Code for HostSwitch paper (Trivellone, Araujo, Panassiti, 2021). Includes the three examples of application of HostSwitch simulation using real data described in the Usage scenarios section.

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Scenario 1: Cephaloleia-Zingeriberales (wildlife ecology)

## Code showed for Scenario 1 only.

```
# MODEL SETTINGS
simulations = seq(100, 200, by = 50)  # set the iterations (n_sim) you want to compare
# in the results. Here we compare 100, 150 and 200
# iterations
df = parli$Cephaloleia

# get the column names for Cephaloleia placida
namesCp = colnames(df)[grep("Cp", colnames(df))]
# get the column names for Cephaloleia belti
namesCb = colnames(df)[grep("Cb", colnames(df))]

# creates all possible combinations between namesCp
# and namesCb
Combs = data.frame(expand.grid(a = namesCp, b = namesCb))

# prepares the dataframe to save results of
# comparisons (p-values, one for each estimated
# parameter - j, s, d).
testResult = data.frame(expand.grid(combs = apply(Combs,
    1, function(x) paste(x, collapse = "_")), simulations = simulations))
testResult = data.frame(apply(testResult, 2, as.character))
testResult = transform(testResult, group = do.call(rbind,
    strsplit(combs, "_", fixed = TRUE)), stringsAsFactors = F)
testResult$simulations = as.numeric(testResult$simulations)
testResult$p.value.j = NA
testResult$p.value.s = NA
testResult$p.value.d = NA

# prepare list for simHostSwitch results
simResult <- vector("list", length(simulations))
simResult <- sapply(paste("n_sim_", simulations, sep = ""),
    function(x) NULL)  # assign names

# Prepare 8 HostSwitch objects using the columns of
# Cephaloleia dataset loop for simulations
for (i in 1:length(simulations)) {

    df["n_sim", ] = rep(simulations[i], length(df["n_sim",
        ]))  # overwrite number simulations

    simResult[[i]] = lapply(colnames(df), function(x) simHostSwitch(data = df,
        column = x))
    names(simResult[[i]]) = colnames(df)
}

# Perform 16 pairwise comparisons for 3 parameters
# using t test in testHostSwitch function
for (i in 1:nrow(testResult)) {

    Nsim = which(paste("n_sim_", testResult$simulations[i],
        sep = "") == names(simResult))  # get simulation -> list id
    Ngroup1 = which(testResult$group.1[i] == names(simResult[[Nsim]]))
    Ngroup2 = which(testResult$group.2[i] == names(simResult[[Nsim]]))

    # jump
    simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
        simResult[[Nsim]][[Ngroup2]], "j", "t", plot = F)
    testResult$p.value.j[i] = simTestResult$p.value
    # survive
    simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
        simResult[[Nsim]][[Ngroup2]], "s", "t", plot = F)
    testResult$p.value.s[i] = simTestResult$p.value
    # distance
    simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
        simResult[[Nsim]][[Ngroup2]], "d", "t", plot = F)
    testResult$p.value.d[i] = simTestResult$p.value
}
# reshape p-value results for each estimated
# parameter
testResult.Cephaloleia = testResult
dcast(testResult.Cephaloleia, combs ~ simulations,
    value.var = "p.value.j")
```

```
##                combs          100          150          200
## 1  Cp.mHxjN_Cb.mHxjN 4.476789e-11 2.313005e-18 9.669690e-24
## 2  Cp.mHxjN_Cb.mHxjY 2.015718e-12 4.282837e-16 4.861736e-20
## 3  Cp.mHxjN_Cb.mLxjN 3.679699e-11 1.032886e-15 5.083653e-22
## 4  Cp.mHxjN_Cb.mLxjY 1.716224e-08 1.354382e-13 2.155270e-17
## 5  Cp.mHxjY_Cb.mHxjN 2.111848e-10 1.053538e-17 1.628592e-22
## 6  Cp.mHxjY_Cb.mHxjY 7.788608e-12 1.440305e-15 4.424558e-19
## 7  Cp.mHxjY_Cb.mLxjN 1.101130e-10 3.036101e-15 4.413821e-21
## 8  Cp.mHxjY_Cb.mLxjY 4.644185e-08 3.890954e-13 1.568426e-16
## 9  Cp.mLxjN_Cb.mHxjN 3.859274e-11 2.275179e-19 2.267250e-25
## 10 Cp.mLxjN_Cb.mHxjY 1.659444e-12 6.120252e-17 2.329420e-21
## 11 Cp.mLxjN_Cb.mLxjN 3.025446e-11 1.747767e-16 2.543285e-23
## 12 Cp.mLxjN_Cb.mLxjY 1.432854e-08 2.394964e-14 1.354331e-18
## 13 Cp.mLxjY_Cb.mHxjN 1.417392e-11 6.457778e-20 2.890690e-26
## 14 Cp.mLxjY_Cb.mHxjY 7.172344e-13 2.237621e-17 4.622140e-22
## 15 Cp.mLxjY_Cb.mLxjN 1.558029e-11 7.177946e-17 5.304007e-24
## 16 Cp.mLxjY_Cb.mLxjY 7.815040e-09 9.933703e-15 3.136143e-19
```

```r
dcast(testResult.Cephaloleia, combs ~ simulations,
    value.var = "p.value.s")
```

```
##                combs          100          150          200
## 1  Cp.mHxjN_Cb.mHxjN 6.217382e-13 3.261113e-20 3.917914e-26
## 2  Cp.mHxjN_Cb.mHxjY 2.571541e-14 4.001581e-19 1.725411e-24
## 3  Cp.mHxjN_Cb.mLxjN 7.325191e-14 6.603974e-19 1.646445e-26
## 4  Cp.mHxjN_Cb.mLxjY 1.521360e-11 1.870196e-17 6.140489e-21
## 5  Cp.mHxjY_Cb.mHxjN 3.210548e-12 1.970846e-19 1.005429e-24
## 6  Cp.mHxjY_Cb.mHxjY 1.184998e-13 2.080658e-18 3.224478e-23
## 7  Cp.mHxjY_Cb.mLxjN 3.408455e-13 3.526209e-18 4.133825e-25
## 8  Cp.mHxjY_Cb.mLxjY 7.658772e-11 1.105853e-16 1.149385e-19
## 9  Cp.mLxjN_Cb.mHxjN 1.351784e-13 1.900966e-21 1.000220e-27
## 10 Cp.mLxjN_Cb.mHxjY 6.224393e-15 2.940224e-20 6.250594e-26
## 11 Cp.mLxjN_Cb.mLxjN 1.755984e-14 4.651880e-20 4.314810e-28
## 12 Cp.mLxjN_Cb.mLxjY 3.368951e-12 1.116502e-18 2.180913e-22
## 13 Cp.mLxjY_Cb.mHxjN 7.434223e-14 8.383300e-22 5.321850e-28
## 14 Cp.mLxjY_Cb.mHxjY 3.590616e-15 1.384218e-20 3.529239e-26
## 15 Cp.mLxjY_Cb.mLxjN 1.007594e-14 2.161946e-20 2.307824e-28
## 16 Cp.mLxjY_Cb.mLxjY 1.858176e-12 4.923404e-19 1.221408e-22
```

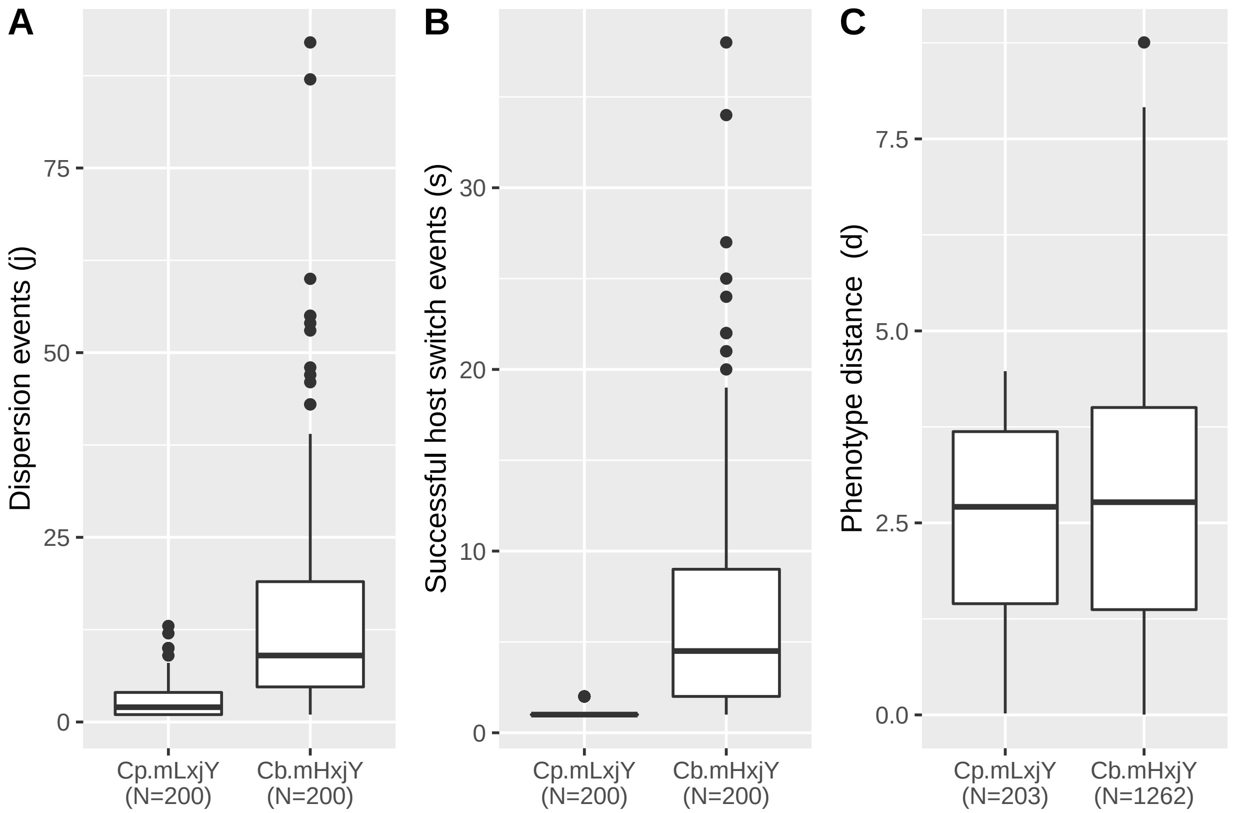
```r
dcast(testResult.Cephaloleia, combs ~ simulations,
    value.var = "p.value.d")
```

```
##                combs          100          150          200
## 1  Cp.mHxjN_Cb.mHxjN 0.4878877377 9.581379e-01 8.882705e-01
## 2  Cp.mHxjN_Cb.mHxjY 0.7533598917 1.993735e-01 2.439203e-01
## 3  Cp.mHxjN_Cb.mLxjN 0.0289345625 2.150971e-03 1.192113e-03
## 4  Cp.mHxjN_Cb.mLxjY 0.0011101184 3.231848e-06 3.699167e-06
## 5  Cp.mHxjY_Cb.mHxjN 0.1344493948 2.344102e-01 3.342520e-01
## 6  Cp.mHxjY_Cb.mHxjY 0.7102271451 8.379813e-01 6.208820e-01
## 7  Cp.mHxjY_Cb.mLxjN 0.0837818535 2.687223e-02 4.905075e-03
## 8  Cp.mHxjY_Cb.mLxjY 0.0031639355 5.453258e-05 1.211737e-05
## 9  Cp.mLxjN_Cb.mHxjN 0.8831183513 9.321297e-01 8.218317e-01
## 10 Cp.mLxjN_Cb.mHxjY 0.3772622534 2.340559e-01 2.646676e-01
## 11 Cp.mLxjN_Cb.mLxjN 0.0053006948 2.364061e-03 1.161424e-03
## 12 Cp.mLxjN_Cb.mLxjY 0.0001142616 2.818006e-06 2.989778e-06
## 13 Cp.mLxjY_Cb.mHxjN 0.5423813300 5.993765e-01 2.957937e-01
## 14 Cp.mLxjY_Cb.mHxjY 0.6686491935 8.609989e-02 2.179861e-02
## 15 Cp.mLxjY_Cb.mLxjN 0.0186691001 5.671991e-04 1.779197e-05
## 16 Cp.mLxjY_Cb.mLxjY 0.0005613414 6.623014e-07 2.226651e-08
```

Plot for Cephaloleia

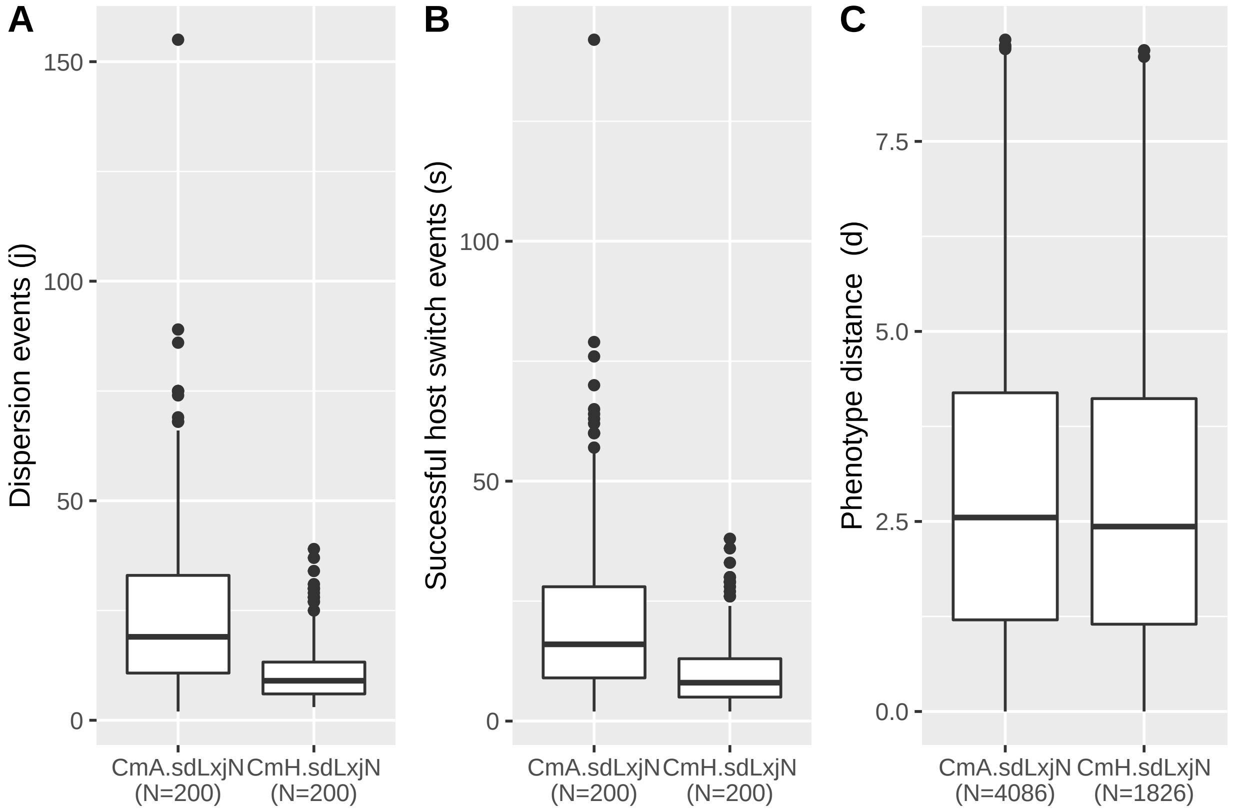
```r
# Choose one combination defining Ngroup1 and
# Ngroup2 this can be customized to get different
# plot
Ngroup1 = "Cp.mLxjY"
Ngroup2 = "Cb.mHxjY"
# Choose the data from a specific saved n_sim list
# of objects this can be customized to get
# different plot
Nsim = "n_sim_200"

# Build the plot for # of of dispersing events (j)
simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
    simResult[[Nsim]][[Ngroup2]], "j", "t", plot = F)

# simTestResult@.Data[[11]] -> groups = simulation1
# and simulation2 simTestResult@.Data[[12]] ->
# values
plotInput = data.frame(x = simTestResult@.Data[[11]],
    values = simTestResult@.Data[[12]])
plotInput$x = as.factor(plotInput$x)
xlabs <- paste((as.factor(c(Ngroup1, Ngroup2))), "\n(N=",
    table(plotInput$x), ")", sep = "")

j.ceph = ggplot(data = plotInput, aes(x = x, y = values,
    group = x)) + geom_boxplot() + labs(x = "", y = "Dispersion events (j)") +
    scale_x_discrete(labels = xlabs)

# Build the plot for # of successful host switch s
simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
    simResult[[Nsim]][[Ngroup2]], "s", "t", plot = F)

# simTestResult@.Data[[11]] -> groups = simulation1
# and simulation2 simTestResult@.Data[[12]] ->
# values
plotInput = data.frame(x = simTestResult@.Data[[11]],
    values = simTestResult@.Data[[12]])
plotInput$x = as.factor(plotInput$x)
xlabs <- paste((as.factor(c(Ngroup1, Ngroup2))), "\n(N=",
    table(plotInput$x), ")", sep = "")

s.ceph = ggplot(data = plotInput, aes(x = x, y = values,
    group = x)) + geom_boxplot() + labs(x = "", y = "Successful host switch events (s)") +
    scale_x_discrete(labels = xlabs)

# Build the plot for distance between the pRes_sim
# and pRes_new_sim when successful switch occurs d
simTestResult = testHostSwitch(simResult[[Nsim]][[Ngroup1]],
    simResult[[Nsim]][[Ngroup2]], "d", "t", plot = F)

# simTestResult@.Data[[11]] -> groups = simulation1
# and simulation2 simTestResult@.Data[[12]] ->
# values
plotInput = data.frame(x = simTestResult@.Data[[11]],
    values = simTestResult@.Data[[12]])
plotInput$x = as.factor(plotInput$x)
```

```
xlabs <- paste((as.factor(c(Ngroup1, Ngroup2))), "\n(N=",
    table(plotInput$x), ")", sep = "")

d.ceph = ggplot(data = plotInput, aes(x = x, y = values,
    group = x)) + geom_boxplot() + labs(x = "", y = "Phenotype distance  (d)") +
    scale_x_discrete(labels = xlabs)

figure1 <- ggarrange(j.ceph, s.ceph, d.ceph, labels = c("A",
    "B", "C"), ncol = 3, nrow = 1)
figure1
```



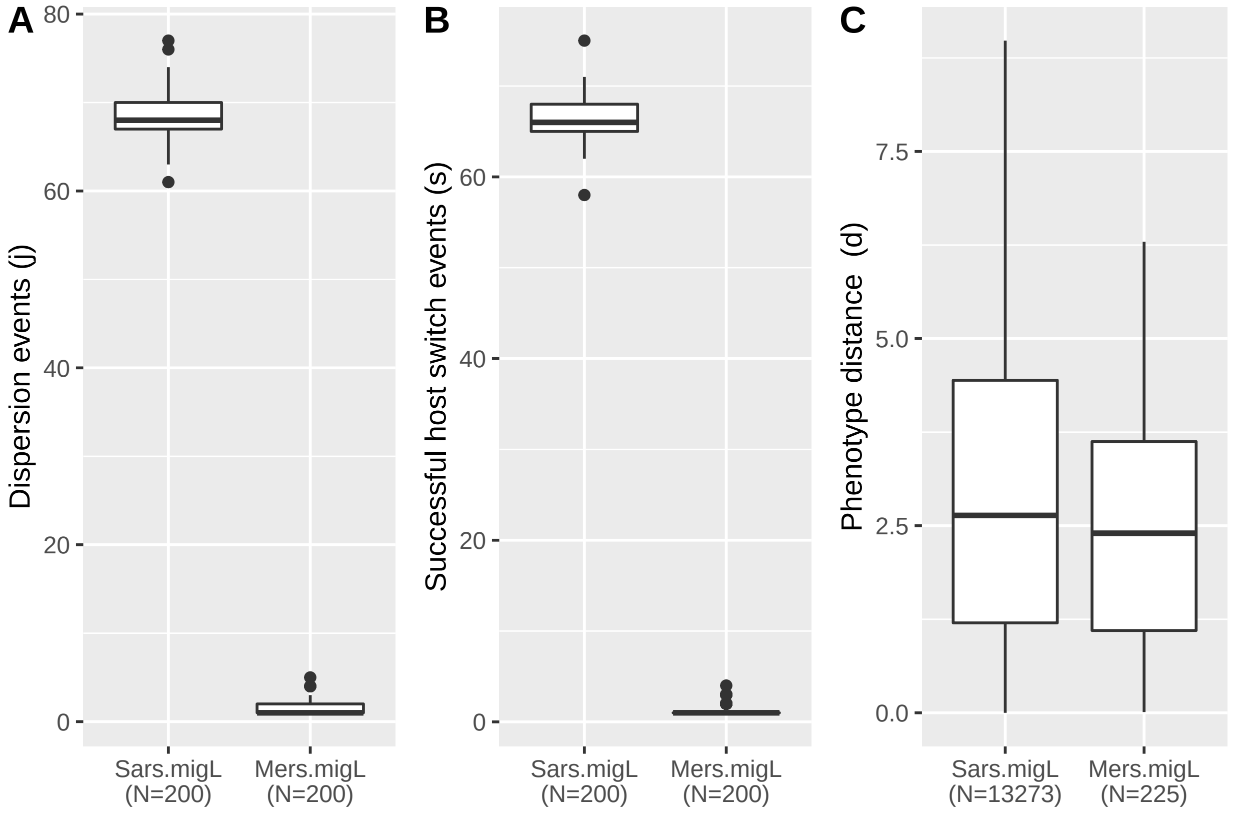
Scenario 2: Cacopsylla melanoneura-Rosaceae (agricultural pests)

Plot for Cacopsylla



Scenario 3: Sarbecovirus sp. and Merbacovirus sp. (SARS-MERS)-Mammals (zoonotic pathogens)

Plot for SarsMers



System information

```
R.Version()
```

```
## $platform
## [1] "x86_64-w64-mingw32"
##
## $arch
## [1] "x86_64"
##
## $os
## [1] "mingw32"
##
## $system
## [1] "x86_64, mingw32"
##
## $status
## [1] ""
##
## $major
## [1] "4"
##
```

```
## $minor
## [1] "0.5"
##
## $year
## [1] "2021"
##
## $month
## [1] "03"
##
## $day
## [1] "31"
##
## $‘svn rev‘
## [1] "80133"
##
## $language
## [1] "R"
##
## $version.string
## [1] "R version 4.0.5 (2021-03-31)"
##
## $nickname
## [1] "Shake and Throw"
```