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[bomeara/BMhyb] Time from donor (#13)

1 message

Paul Bastide <notifications@github.com> Fri, Oct 6, 2017 at 4:23 PM
Reply-To: bomeara/BMhyb
<reply+013c4595b7a7b08283814bcc962f60a5cbd797e7a915ff1392cf0000000115eeff7a92a169ce0fb2b2ff@reply.github.com>
To: bomeara/BMhyb <BMhyb@noreply.github.com>
Cc: Tony Jhwueng <djhwueng@umail.iu.edu>, Mention <mention@noreply.github.com>

Hi @bomeara and @djhwueng,

I have been trying to test your function `GetVModified` on the example network you show on your preprint, but I ran into a problem.

I used the following function to create this network (with `t1`, `t2` and `t3` as in the preprint):

```
create_paper_network <- function(gamma, t1, t2, t3){
    phy <- read.tree(text = paste0("((R:", t3, ",Y:", t3, "):", t1 + t2, ",X:", t1 + t2 + t3,
");"))
    network <- list(phy = phy,
                    flow = data.frame(donor = "X",
                                      recipient = "R",
                                      gamma = gamma,
                                      time.from.root.donor = t1,
                                      time.from.root.recipient = t1 + t2))
    network$flow$donor <- as.character(network$flow$donor)
    network$flow$recipient <- as.character(network$flow$recipient)
    return(network)
}
```

To plot an example:

```
gamma <- 0.5
t1 <- 0.3; t2 <- 0.4; t3 <- 0.3; # unit height
network <- create_paper_network(gamma, t1, t2, t3)

PlotNetwork(network$phy, network$flow)
axis(1, at = c(0, t1, t1+t2, t1+t2+t3), labels = c("0", "t1", "t1+t2", "t1+t2+t3"))
```

Is this network correct ? I tried to copy the format given by outputs of your function `SimulateNetwork`, but I might have made a mistake.

Using this network, I had a problem computing the induced variance matrix using `GetVModified`:

```
sigma2 = 1
x <- c(sigma.sq = sigma2, mu = 0, SE = 0)
actual.params <- c("sigma.sq", "mu", "bt", "vh", "SE")

vcv_BMhyb <- GetVModified(x, network$phy, network$flow, actual.params)
```

This gave me the following result:

```
     R   Y    X
R 0.65 0.7 0.35
Y 0.70 1.0 0.00
X 0.35 0.0 1.00
```

There is a problem here with Cov[Y,R] and Cov[X,R]. Applying the formulas, I get:

```
Cov[X, R] = sigma^2 * gamma * t1 = 0.5*0.3 = 0.15 \neq 0.35
Cov[Y, R] = sigma^2 * (1-gamma) * (t1 + t2) = 0.35 \neq 0.7
```

I could not explain this discrepancy. Did I misused your functions ? Or are my computations wrong ?

One point that is unclear to me, is that I could find no reference to the parameters `time.from.root.donor` (t1) in the code of `GetVModified`, that seems essential for the computation of this matrix (but maybe it's hidden in the call of an other function, in which case I might have missed it).

Thank you for your help, and for your package !

Session infos:

```
> sessionInfo()
R version 3.4.2 (2017-09-28)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.3 LTS

Matrix products: default
BLAS: /usr/lib/openblas-base/libblas.so.3
LAPACK: /usr/lib/libopenblasp-r0.2.18.so

locale:
[1] LC_CTYPE=fr_FR.UTF-8       LC_NUMERIC=C               LC_TIME=fr_FR.UTF-8
LC_COLLATE=fr_FR.UTF-8
[5] LC_MONETARY=fr_FR.UTF-8    LC_MESSAGES=fr_FR.UTF-8    LC_PAPER=fr_FR.UTF-8       LC_NAME=C
[9] LC_ADDRESS=C               LC_TELEPHONE=C             LC_MEASUREMENT=fr_FR.UTF-8
LC_IDENTIFICATION=C

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] BMhyb_1.5.1 ape_4.1

loaded via a namespace (and not attached):
 [1] Rcpp_0.12.12            subplex_1.4-1           msm_1.6.4               mvtnorm_1.0-6
 [5] lattice_0.20-35         tidyr_0.7.1             corpcor_1.6.9           prettyunits_1.0.2
 [9] assertthat_0.2.0        digest_0.6.12           foreach_1.4.3           R6_2.2.2
[13] plyr_1.8.4              phytools_0.6-20         coda_0.19-1             httr_1.3.1
[17] ggplot2_2.2.1           progress_1.1.2          rlang_0.1.2.9000        uuid_0.1-2
[21] lazyeval_0.2.0          curl_2.8.1              data.table_1.10.4       taxize_0.9.0
[25] phangorn_2.2.0          Matrix_1.2-11           RNeXML_2.0.7            combinat_0.0-8
[29] splines_3.4.2           stringr_1.2.0           igraph_1.1.2            munsell_0.4.3
[33] compiler_3.4.2          numDeriv_2016.8-1       geiger_2.0.6            pkgconfig_2.0.1
[37] mnormt_1.5-5            tibble_1.3.4            gridExtra_2.2.1         TreeSim_2.3
[41] expm_0.999-2            quadprog_1.5-5          codetools_0.2-15        XML_3.98-1.9
[45] reshape_0.8.7           viridisLite_0.2.0       dplyr_0.7.2             MASS_7.3-47
[49] crul_0.3.8              grid_3.4.2              nlme_3.1-131            jsonlite_1.5
[53] gtable_0.2.0            magrittr_1.5            scales_0.5.0            stringi_1.1.5
[57] reshape2_1.4.2          viridis_0.4.0           bindrcpp_0.2            scatterplot3d_0.3-40
[61] phylobase_0.8.4         xml2_1.1.1              fastmatch_1.1-0         deSolve_1.20
[65] iterators_1.0.8         tools_3.4.2             rncl_0.8.2              ade4_1.7-8
[69] bold_0.5.0              glue_1.1.1              purrr_0.2.3             maps_3.2.0
[73] plotrix_3.6-6           parallel_3.4.2          survival_2.41-3         colorspace_1.3-2
[77] bindr_0.1               animation_2.5           clusterGeneration_1.3.4
```

—