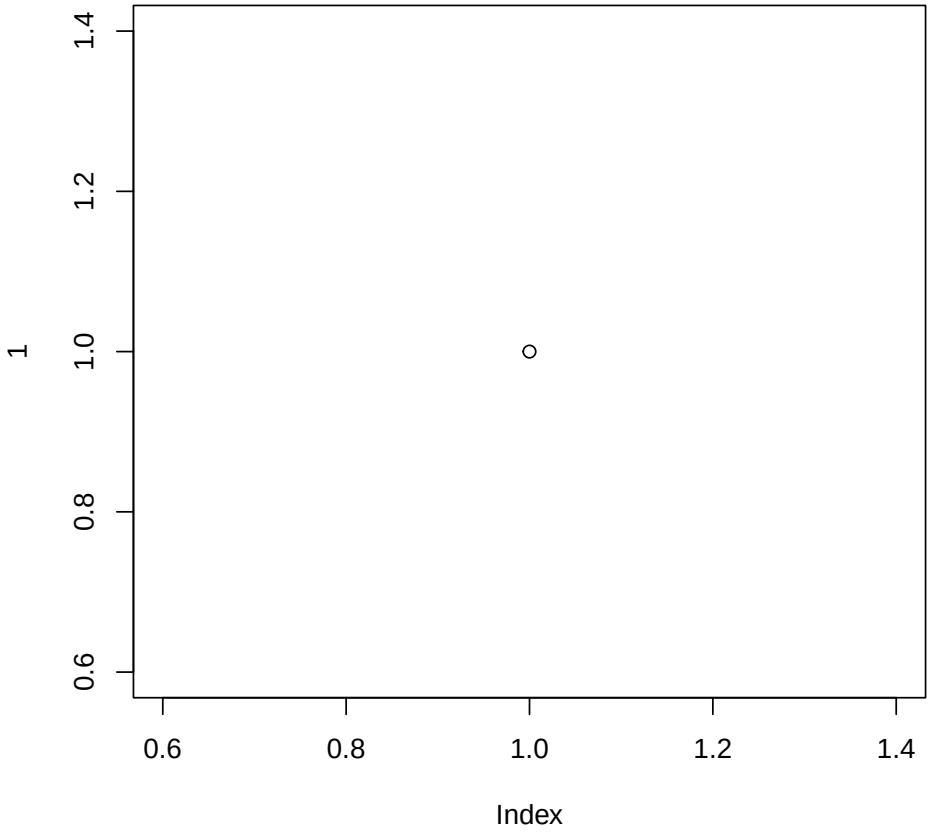
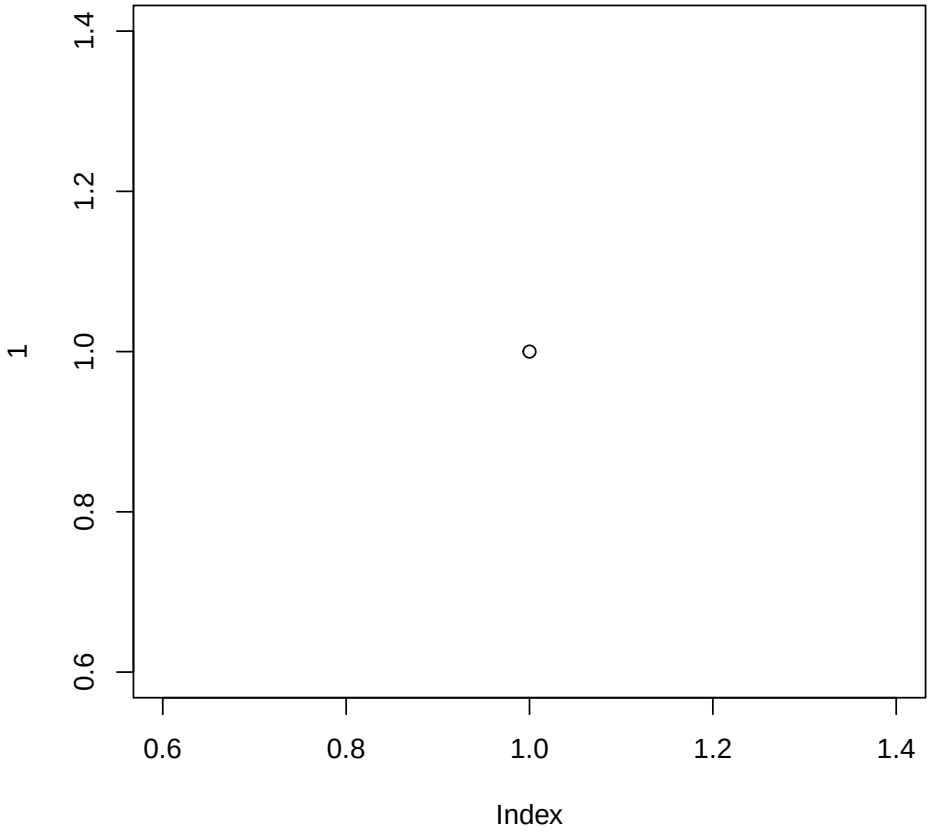
```
> theCppFile = tempfile(fileext='.cpp')
> file.copy(system.file('extsrc/02_disease.cpp',package='aghq'),theCppFile)

[1] TRUE

> # set the seed
> set.seed(563478)
> if(requireNamespace("EpiILMCT", quietly=TRUE)) {
+   # Create the functions
+ data("tswv", package = "EpiILMCT")
+ dat <- tswv$tswvsir
+ dat$epidat <- dat$epidat[order(dat$epidat[ ,4]), ]
+
+ I <- dat$epidat[ ,4]
+ R <- dat$epidat[ ,2]
+ infected <- !is.infinite(I)
+
+ datlist <- list(
+   D = as.matrix(dist(dat$location[dat$epidat[ ,1], ])),
+   I = I,
+   R = R,
+   infected = as.numeric(infected[infected])
+ )
+
+ } else {
+   print("missing EpiILMCT package, running model without data")
+   datalist = list()
+ }

[1] "missing EpiILMCT package, running model without data"

> haveTmbstan = requireNamespace('tmbstan', quietly=TRUE)
> haveTMB = requireNamespace("TMB", quietly=TRUE)
> if(haveTmbstan & haveTMB) {
+   print("have the packages, will run vignette")
+ } else {
+   print("missing some packages, vignette won't run.")
+ }

[1] "missing some packages, vignette won't run."

> if(haveTMB) {
+
+ # Compile TMB template-- only need to do once
+   TMB::compile(theCppFile)
+   theDll <- dyn.load(TMB::dynlib(gsub("[.]cpp$", "", theCppFile)))[[1]]
+
+ # Function and its derivatives
+   ff <- TMB::MakeADFun(data = datlist,
+                 parameters = list(theta1 = 0,
+                                   theta2 = 0),
+                 DLL = theDll,
+                 ADreport = FALSE,
+                 silent = TRUE)
+ }
```

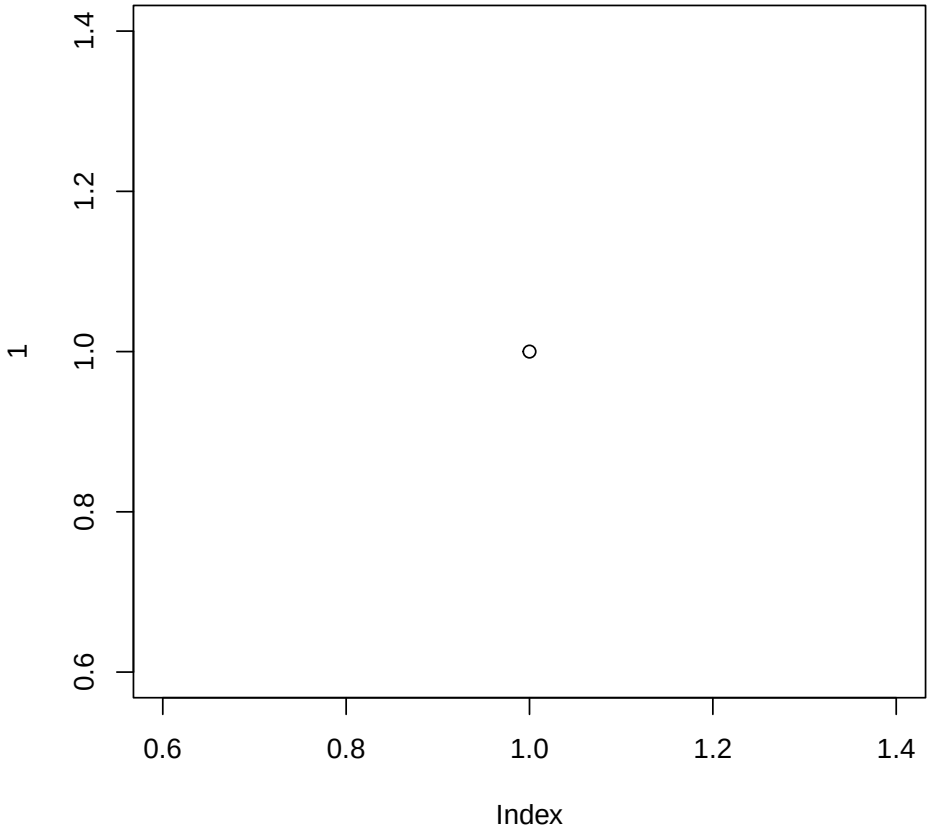
```
> if(haveTMB) {
+   quadmod <- aghq::aghq(ff,9,c(0,0),control = aghq::default_control(negate = TRUE, verbose=TRUE))
+ }
> if(haveTmbstan & haveTMB) {
+ stanmod <- tmbstan::tmbstan(
+   ff,
+   chains = 2,
+   cores = 2,
+   iter = 2e03,
+   warmup = 1e03,
+   init = quadmod$optresults$mode,
+   seed = 124698,
+   algorithm = "NUTS"
+ )
+ } else{
+         stanmod = NULL
+         print("need packages installed to build this vignette")
+ }

[1] "need packages installed to build this vignette"

> if(!is.null(stanmod) & requireNamespace("rstan", quietly=TRUE) ) {
+   rstan::traceplot(stanmod)
+ } else {
+   plot(1)
+ }
```




```
> if(!is.null(stanmod)) {
+ stansamps <- as.data.frame(stanmod)
+ stansamps$alpha <- exp(stansamps$`par[1]`)
+ stansamps$beta <- exp(stansamps$`par[2]`)
+
+ posttrans <- list(totheta = log,fromtheta = exp)
+ quaddens <- aghq::compute_pdf_and_cdf(quadmod,posttrans)
+ }

> if(!is.null(stanmod)) {
+         hist(stansamps$alpha,freq=FALSE,breaks=50,main = "",xlab = "",cex.lab=1.5,cex.axis = 1.5)
+         with(quaddens[[1]],lines(transparam,pdf_transparam))
+ } else {
+   plot(1)
+ }
```




```
> if(!is.null(stanmod)) {
+         hist(stansamps$beta,freq=FALSE,breaks=50,main = "",xlab = "",cex.lab=1.5,cex.axis = 1.5)
+         with(quaddens[[2]],lines(transparam,pdf_transparam))
+ } else {
+   plot(1)
+ }
```


1
0.6
0.8
1.0
1.2
1.4
0.6
0.8
1.0
1.2
1.4
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