Instructions for running the individual-based Dynamic Energy Budget Schistosoma population model (SIDEB) on Windows

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This document can be found at https://github.com/darwinanddavis/SchistoIBM/tree/master/windows

R session info

R version 3.5.0 (2018-04-23)

Platform: x86_64-apple-darwin15.6.0 (64-bit) Running under: OS X El Capitan 10.11.6

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib

locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:

[1] stats graphics grDevices utils datasets methods base

loaded via a namespace (and not attached):

[1] compiler_3.5.0 backports_1.1.2 magrittr_1.5 rprojroot_1.3-2 tools_3.5.0 htmltools_0.3.6 [7] pillar_1.2.3 tibble_1.4.2 yaml_2.2.0 Rcpp_0.12.18 stringi_1.2.3 rmarkdown_1.10

[13] knitr_1.20 stringr_1.3.1 digest_0.6.15 rlang_0.2.1 evaluate_0.10.1

Overview

Follow the instructions to run the simulation model from R or RStudio. All reports and bugs should be addresses to matthew.malishev@gmail.com.

Required files

Files required for running the simulation are outlined below and will be automatically loaded from the *Schistosoma* IBM Github page when running the model:

```
DEB_IBM.R
DEB_INF_GUTS_IBM.nlogo
FullStarve_shrink_production2.Rda
IndividualModel_IBM.c
IndividualModel_IBM.dll (Windows, generated from C)
```

Install R RStudio

Install RStudio from the RStudio website.

Install NetLogo

Install NetLogo from the NetLogo website.

Run RNetLogo

Load the 'DEB_IBM.R' file into your R session. Follow the instructions to load the model and execute the simulation.

References

- ¹ Installing R Studio
- ² Installing NetLogo