slendr: a framework for spatio-temporal population genomic simulations on geographic landscapes

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We present a new R package, *slendr* (slendr.net), designed for reproducible, declarative, and visually-focused encoding of complex spatio-temporal population models on real and abstract geographic landscapes. *slendr* uses a tailor-made SLiM script (messerlab.org/slim) as a simulation back end bundled with the package, and saves spatially-annotated tree sequences as outputs from its models. In addition to spatial models, *slendr* offers a new way to simulate traditional, random-mating demographic models—either with SLiM or using an alternative back end implemented with *msprime*. With its R-idiomatic interface to the tree sequence analysis library *tskit* (tskit.dev), *slendr* opens up the possibility of efficient, reproducible population genetic simulations and analyses entirely in R. In this poster we demonstrate the features of the R package on several complete examples.

website: slendr.net

tutorials: slendr.net/articles

preprint: biorxiv.org/content/10.1101/2022.03.20.485041v1
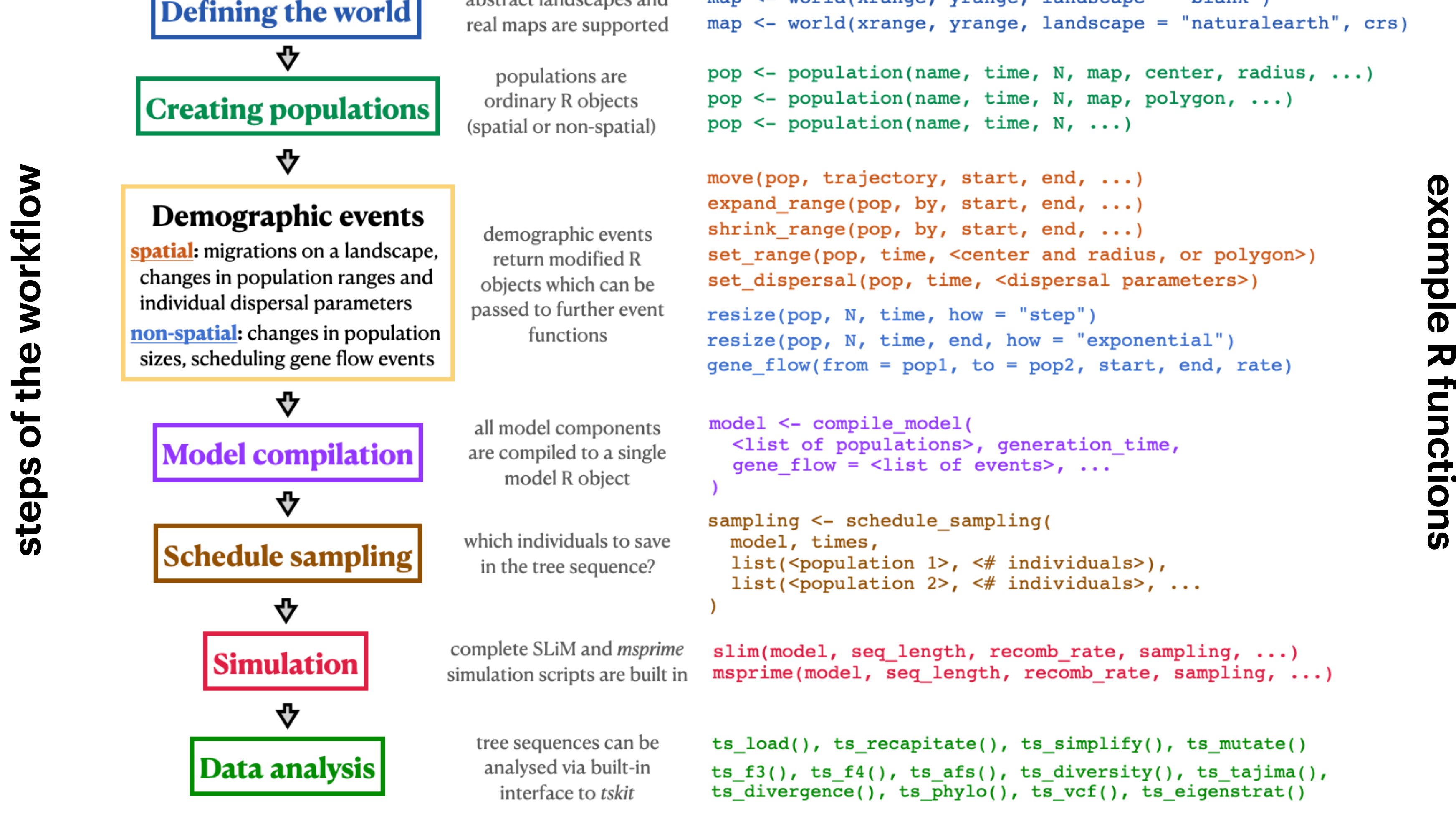
interactive examples from this poster: github.com/bodkan/probgen2022

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Overview of a typical *slendr* workflow

Model definition, simulation, and data analysis steps are all parts of a single reproducible R script, without having to write code in multiple languages or convert data between file formats.

Complete list of *slendr* functions can be found at slendr.net/reference

Traditional, non-spatial demographic models

slendr provides a new way to specify demographic models (population splits, population size changes, gene-flow events) using a straightforward, declarative interface entirely in R. Models can be simulated by built-in simulation engines written in SLiM and *msprime*.

run ex1.R in your browser on Binder: github.com/bodkan/probgen2022
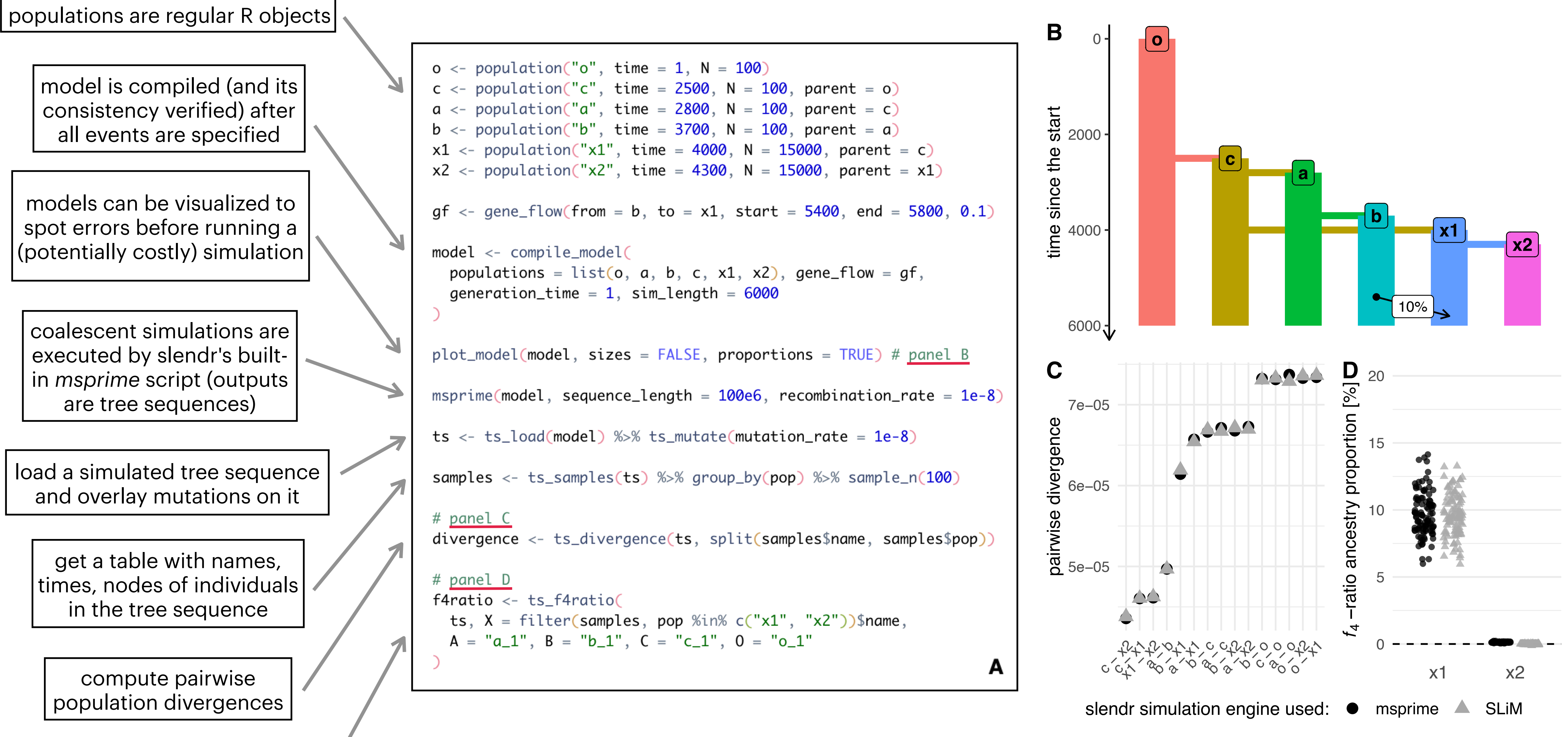
Spatial model on an abstract landscape

If the user defines a simulation world map (in this example an abstract, featureless map), the model can be simulated with a built-in SLiM back end script.
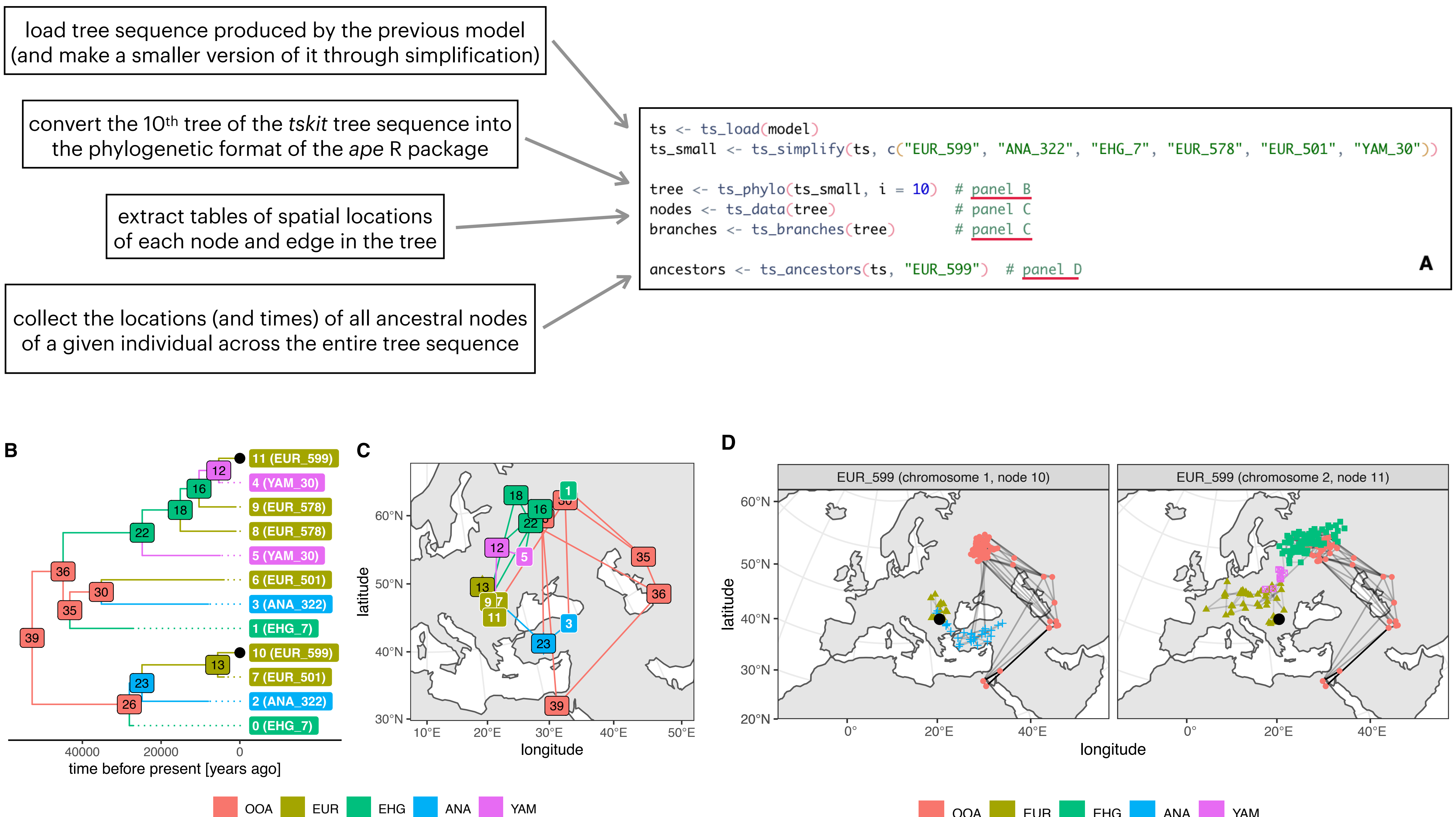

run ex2.R in your browser on Binder: github.com/bodkan/probgen2022
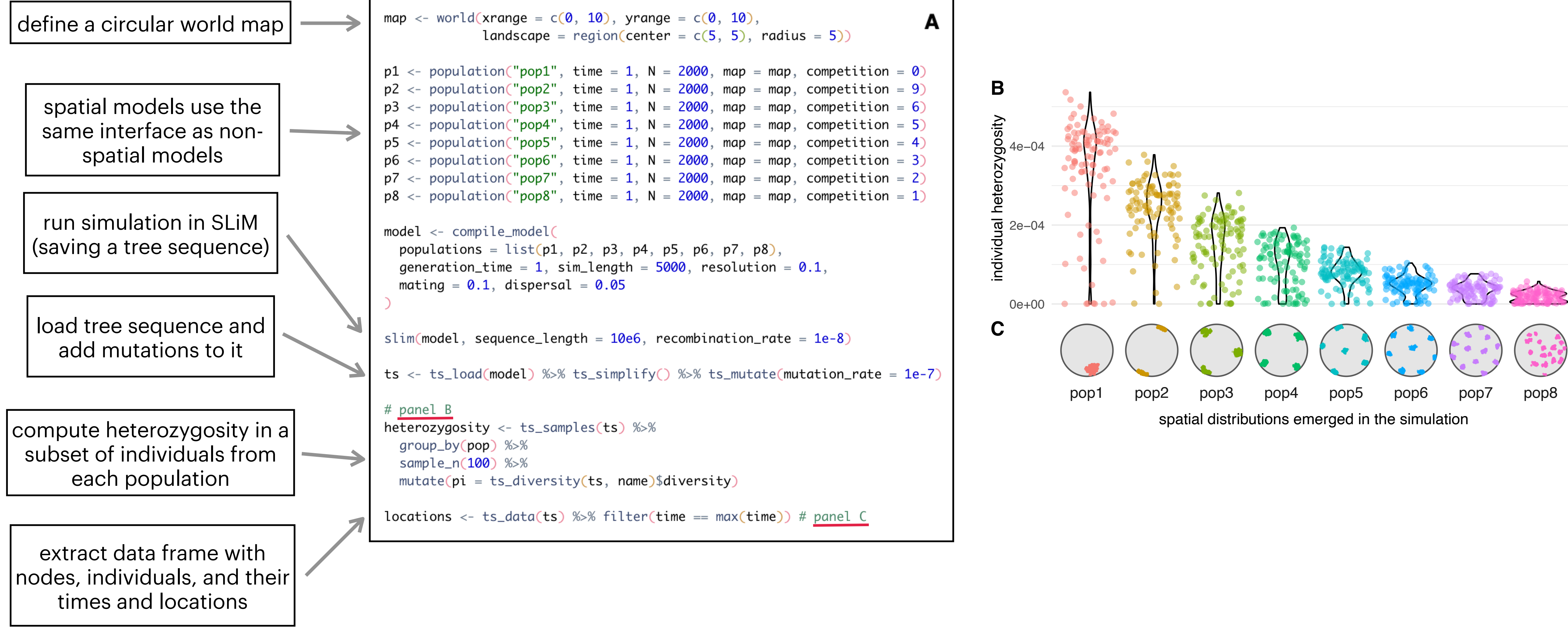
Spatial model on realistic geographic landscape

slendr allows scheduling of large-scale population migrations and range expansions using a set of dedicated functions, without the need for handling spatial geometric operations. These events can occur on abstract landscapes but can be also defined on realistic regions on Earth (such as in this example).

run ex3-4.R in your browser on Binder: github.com/bodkan/probgen2022
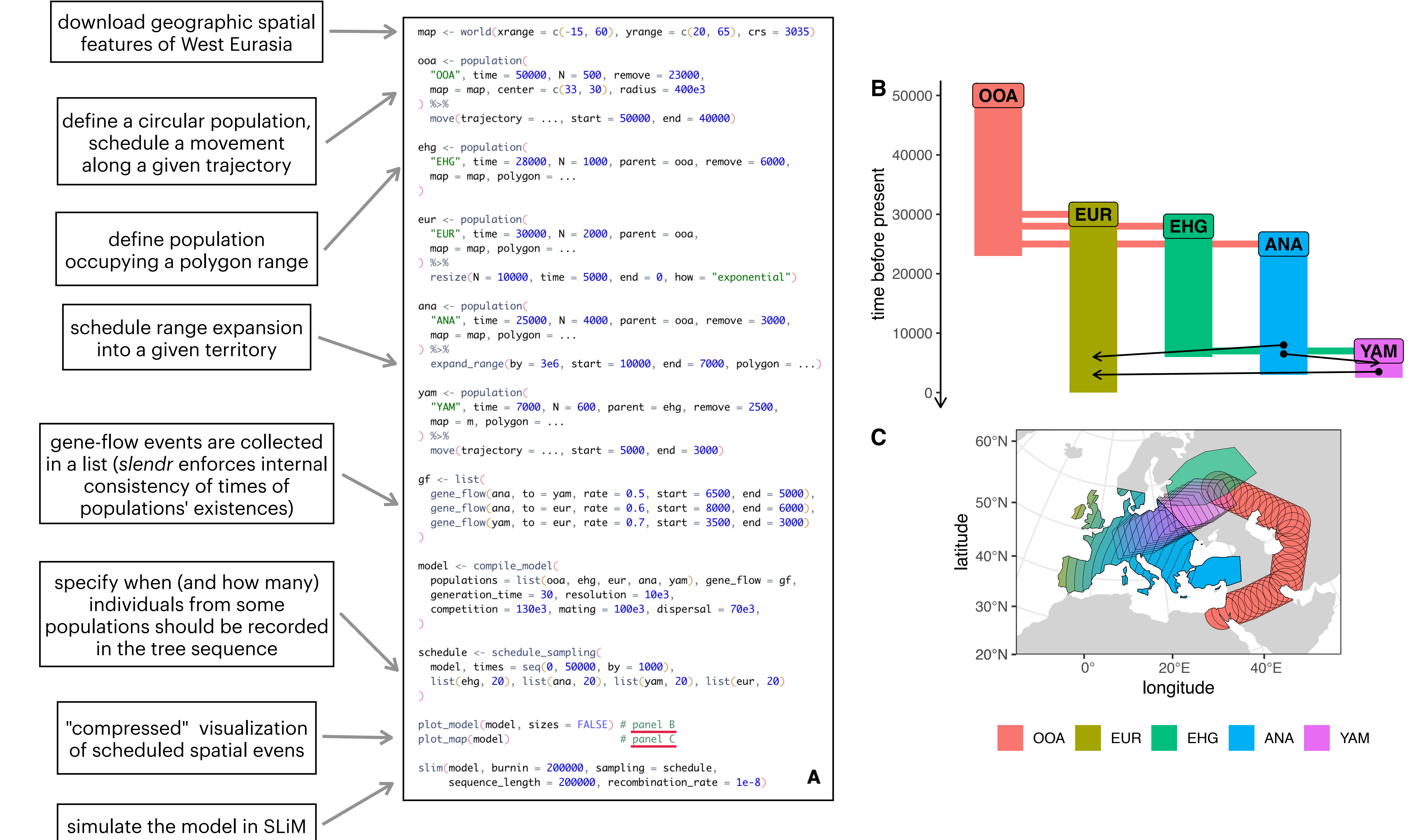
Analysis of spatio-temporal ancestry relationships

slendr automatically translates spatial information in tree sequences to data frames of the class *sf*, allowing analysis using the vast array of R packages for geospatial data analysis. For instance, support for this data type is built into the *ggplot2* R package (see panels B, C, and D below).

run ex3-4.R in your browser on Binder: github.com/bodkan/probgen2022