# ***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* provides a new way to simulate traditional, random-mating demographic models 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, large-scale population genetic simulations and analyses entirely using the tools of the R ecosystem. In this poster we demonstrate the usage 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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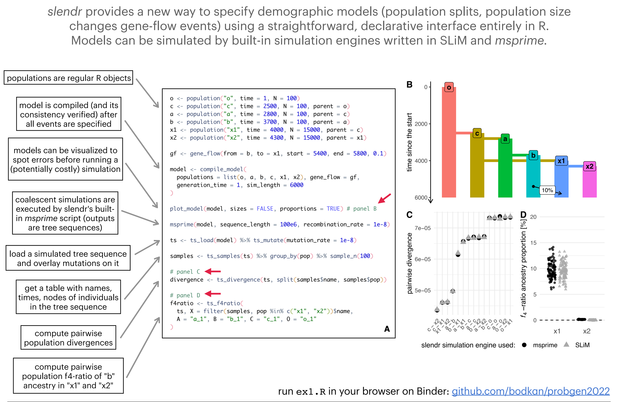
## Overview of a typical *slendr* workflow

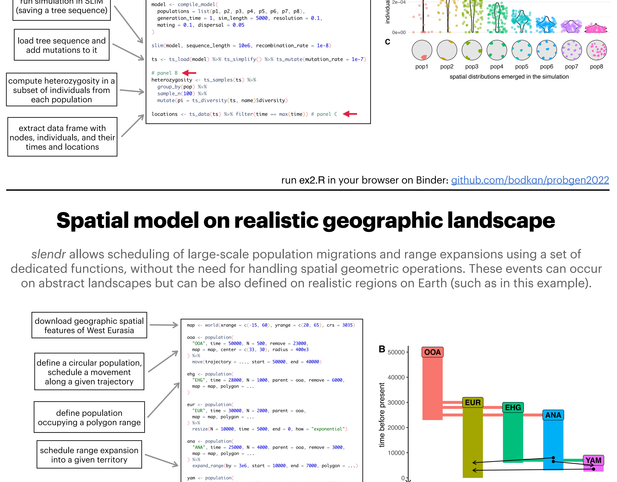
Model definition, simulation, and data analysis steps are all parts of a single reproducible R script, without having to write code in multiple languages or convert data between file formats.




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

## Traditional, non-spatial demographic models

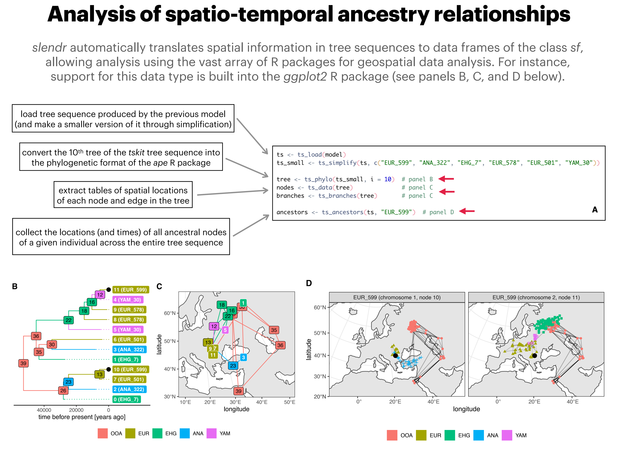
*slendr* provides a new way to specify demographic models (population splits, population size changes gene-flow events) using a straightforward, declarative interface entirely in R. Models can be simulated by built-in simulation engines written in SLiM and *msprime*.




run `ex1.R` in your browser on Binder: github.com/bodkan/probgen2022

## Spatial model on an abstract spatial landscape

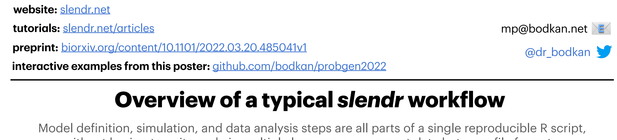
If the user defines a simulation world map (in this example, an abstract, featureless map), the model can be simulated with a built-in SLiM back end script.




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

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