RAREsim Vignette

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This vigette describes how to use the RAREsim R package to simulate rare variant genetic data.

Here we will walk through an example using RAREsim to simulate one cM block on chromosome 19, to match the data from the African ancestry group from gnomAD v2.1 (Karczewski, et al., 2020).

## Install the package

library(RAREsim)

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