

# The SimEVO project

Kári Hlynsson

<https://github.com/lvthnn/SimEVO>

## Abstract

We discuss the theoretical basis of the SimEVO simulation project and how it can be used to obtain data for use in biological research. Mathematical notation is covered and some useful methods of analysis are proposed. We discuss some ideas on how to obtain and process data in order to deduce conclusions regarding forces of selection and evolutionary processes. For more information on installation or usage, see the `README.md` file located in the GitHub repository.

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Theoretical basis</b>	<b>1</b>

## 1 Introduction

Write introduction please.

## 2 Theoretical basis

In traditional evolutionary biology, the scope of observation is limited to a particular population within a location.