

Statistical Genetics Analyses in R

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Preface

Why read this book

Structure of the book

Software information and conventions

All analyses are run on R version 3.3.2 (2016-10-31) – “Sincere Pumpkin Patch” on a x86_64-w64-mingw32/x64 (64-bit) platform.

Some packages are available via [CRAN](#), while others are hosted at [Bioconductor](#). I will provide package installation instructions at the beginning of each example, indicating where each package can be found.

I will also be using the **library()** function, rather than **require()** for loading packages to make sure that we will get an error message in case packages have not been installed correctly.

The example workflows included are meant to illustrate the theoretical concepts and get you started on your own analysis. They are minimal examples of the necessary steps but are not meant to substitute the package manuals. When you want to apply the workflows to your own data, I highly recommend going back to the package documentation to find out about additional functions and using the `help()` function to explore parameter options. I will be using the same naming and code schemes as in the package manuals to make finding the relevant parts easy.

Acknowledgments

About the Author

Chapter 1

Introduction to Statistical Genetics

Chapter 2

Quantitative Genetics

Chapter 3

Population Genetics

Chapter 4

Evolutionary Genetics

Chapter 5

Genetics of complex diseases

Chapter 6

Genetic Epidemiology

Chapter 7

Placeholder