

Fundamentals of computational biology

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Preface

Here we present a course centered book of the Fundamentals of Computational Biology. We will cover several topics, from using the unix tools, the importance of package manager systems (such as homebrew and conda), sequencing technologies, sequence alignments, molecular phylogenetics, genome assembly and annotation, and variant calling analysis.

1 Introduction

This is a book created from markdown and executable code.

See Knuth (1984) for additional discussion of literate programming.

2 Welcome the the command line

In this chapter we will explore the fundamentals of the command line. That is the concepts of Unix based systems the command line (CLI) and how we can use it to acess information programatically.

3 Summary

References

Knuth, Donald E. 1984. “Literate Programming.” *Comput. J.* 27 (2): 97–111. <https://doi.org/10.1093/comjnl/27.2.97>.