

# Introduction to Bioinformatics

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# About

This book includes some of the topics covered during the intensive course *Introduction to Bioinformatics* held in at Nagoya University in Dec 13-14, 2017. It does not try to be particularly comprehensive but serve as a small guide for the students.



# Prerequisites

This is a *sample* book written in **Markdown**. You can use anything that Pandoc's Markdown supports, e.g., a math equation  $a^2 + b^2 = c^2$ .

The **bookdown** package can be installed from CRAN or Github:

```
install.packages("bookdown")  
# or the development version  
# devtools::install_github("rstudio/bookdown")
```

Remember each Rmd file contains one and only one chapter, and a chapter is defined by the first-level heading #.

To compile this example to PDF, you need to install XeLaTeX.





# Chapter 1

## Introduction

1.1 Sequence analysis

1.2 Omics analysis

1.3 Structural analysis



## Chapter 2

# Sequence analysis

### 2.1 Introduction

### 2.2 Two sequence alignment

#### 2.2.1 Comparing two sequences of different lengths

#### 2.2.2 Smith-waterman (global alignment)

#### 2.2.3 Needleman- (local alignment)

#### 2.2.4 Blast

### 2.3 Multiple sequence alignment

### 2.4 Domains and motifs

### 2.5 Phylogenetic methods



## Chapter 3

# Omics analysis

3.1 Introduction

3.2 Microarrays

3.3 Next-generation sequencing

3.4 Mass spectromics methods

3.5 Single cell omics



## Chapter 4

# Bioinformatics resources

### 4.1 Gene Ontology

### 4.2 Pathway databases

#### 4.2.1 KEGG

#### 4.2.2 Reactome

### 4.3 Domain databases

#### 4.3.1 PFAM

### 4.4 Motif databases

### 4.5 Interaction networks

#### 4.5.1 Biogrid

#### 4.5.2 STRING





## Chapter 5

# Reproducible research

### 5.1 Git

#### 5.1.1 Github

### 5.2 Literate programming

#### 5.2.1 RMarkdown notebooks

#### 5.2.2 Jupyter notebooks



# Bibliography