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GTO 2: The genomics-proteomics toolkit



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Preface

License

This document was written in RMarkdown¹ using the bookdown² package.

¹<https://rmarkdown.rstudio.com>

²<https://bookdown.org>



0

Introduction

to do

0.1 SubSection

to do

```
.dashboard > div:not(.dashboard-content)
  display: none;
}
```



FIGURE 1: Settings for creating filters charts



Part I

Tools



0

FASTQ Tools

0.2 gto2_fq_to_fasta

to do

0.3 gto2_fq_to_mfasta

to do

0.4 gto2_fq_exclude_n

to do

0.5 gto2_fq_extract_quality_scores

to do

0.6 gto2_fq_info

to do

0.7 gto2_fq_maximum_read_size

to do

0.8 gto2_fq_minimum_quality_score

to do

0.9 gto2_fq_minimum_read_size

to do

0.10 gto2_fq_rand_extra_chars

to do

0.11 gto2_fq_from_seq

to do

0.12 gto2_fq_mutate

to do

0.13 gto2_fq_split

to do

0.14 gto2_fq_pack

to do

0.15 gto2_fq_unpack

to do

0.16 gto2_fq_quality_score_info

to do

0.17 gto2_fq_quality_score_min

to do

0.18 gto2_fq_quality_score_max

to do

0.19 gto2_fq_cut

to do

0.20 gto2_fq_minimum_local_quality_score_forward

to do

0.21 gto2_fq_minimum_local_quality_score_reverse

to do

0.22 gto2_fq_xs

to do

0.23 gto2_fq_clust_reads

to do

0.24 gto2_fq_complement

to do

0.25 gto2_fq_reverse

to do

0.26 gto2_fq_variation_map

to do

0.27 gto2_fq_variation_filter

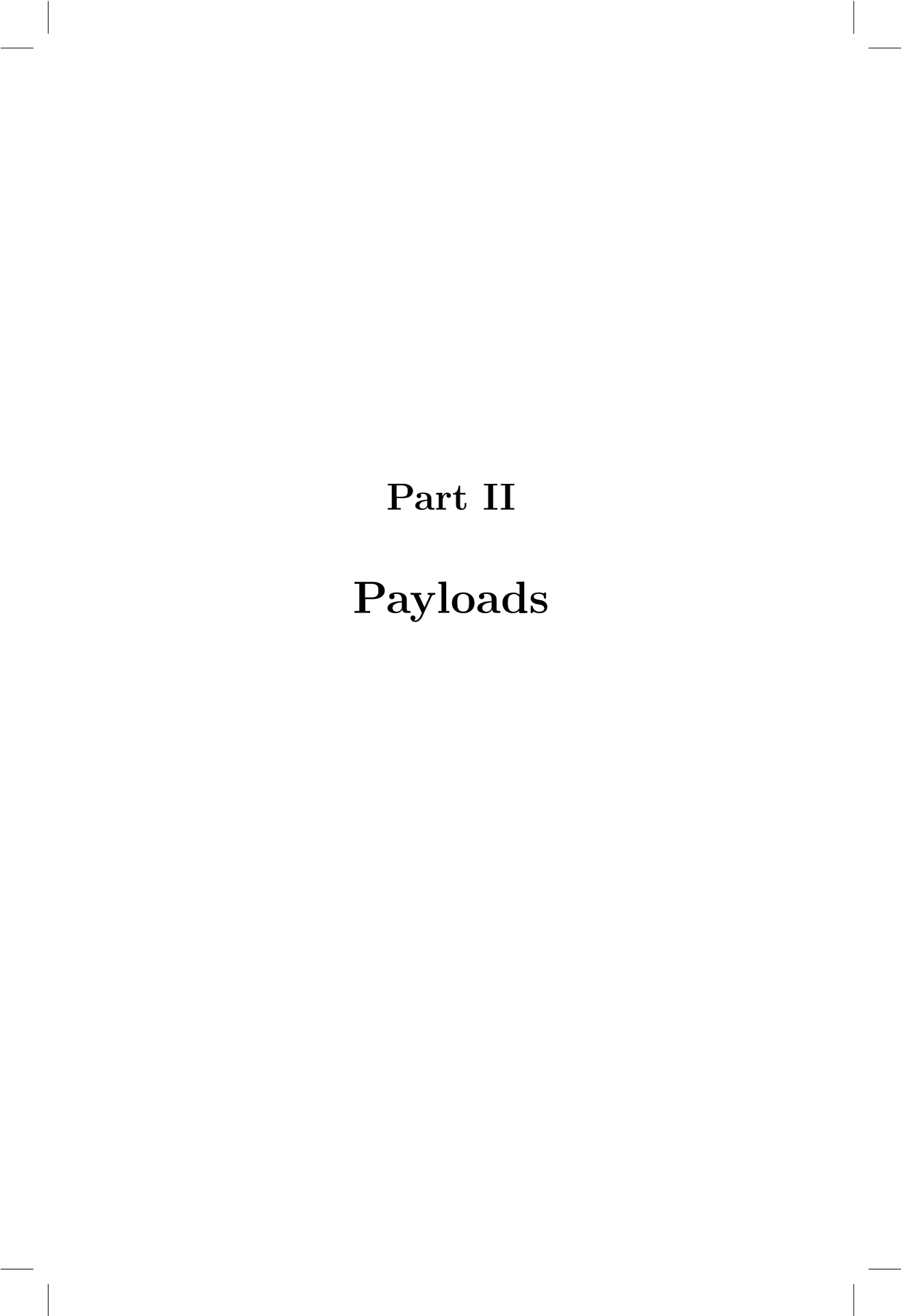
to do

0.28 gto2_fq_variation_visual

to do

0.29 gto2_fq_metagenomics

to do



Part II

Payloads



0

Server Side Template Injection





Part III

Scripts



0

TO DO