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# ***GTO 2: The genomics-proteomics toolkit***



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# *Preface*

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## License

This document was written in RMarkdown<sup>1</sup> using the bookdown<sup>2</sup> package.

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<sup>1</sup><https://rmarkdown.rstudio.com>

<sup>2</sup><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

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## *FASTQ Tools*

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### 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

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## 0.9 gto2\_fq\_minimum\_read\_size

to do

---

## 0.10 gto2\_fq\_rand\_extra\_chars

to do



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**0.11 gto2\_fq\_from\_seq**

to do

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**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

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**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

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**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

---

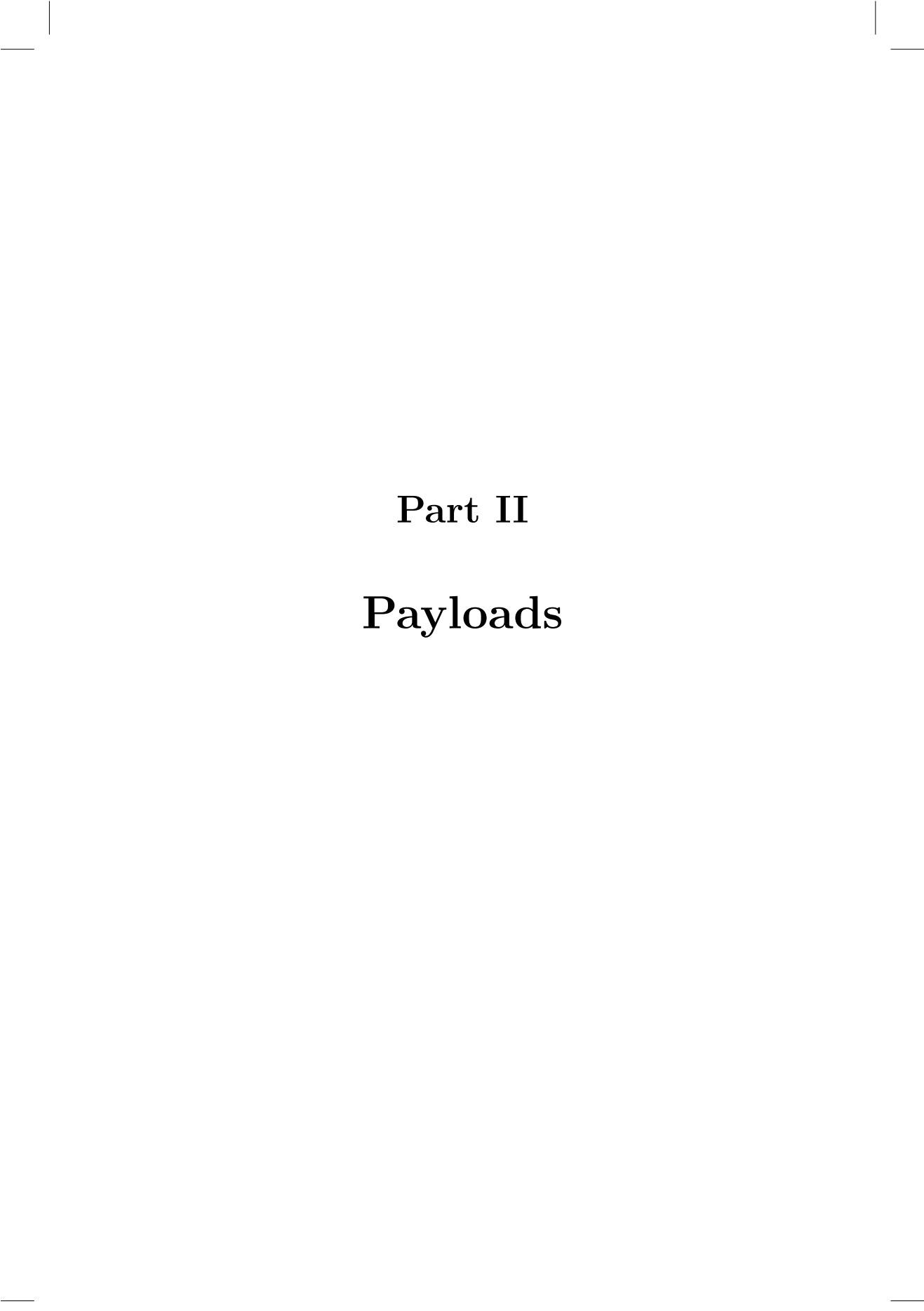
## 0.28 gto2\_fq\_variation\_visual

to do

---

## 0.29 gto2\_fq\_metagenomics

to do



## **Part II**

# **Payloads**



# 0

## *Server Side Template Injection*







## Part III

# Scripts



**0**

*TO DO*