Mapping

Requirements

Before diving into this slide deck, we recommend you to have a look at:

- Galaxy introduction

? Questions

- What two things are crucial for a correct mapping?

- What is BAM?

🎯 Objectives

- You will learn what mapping is

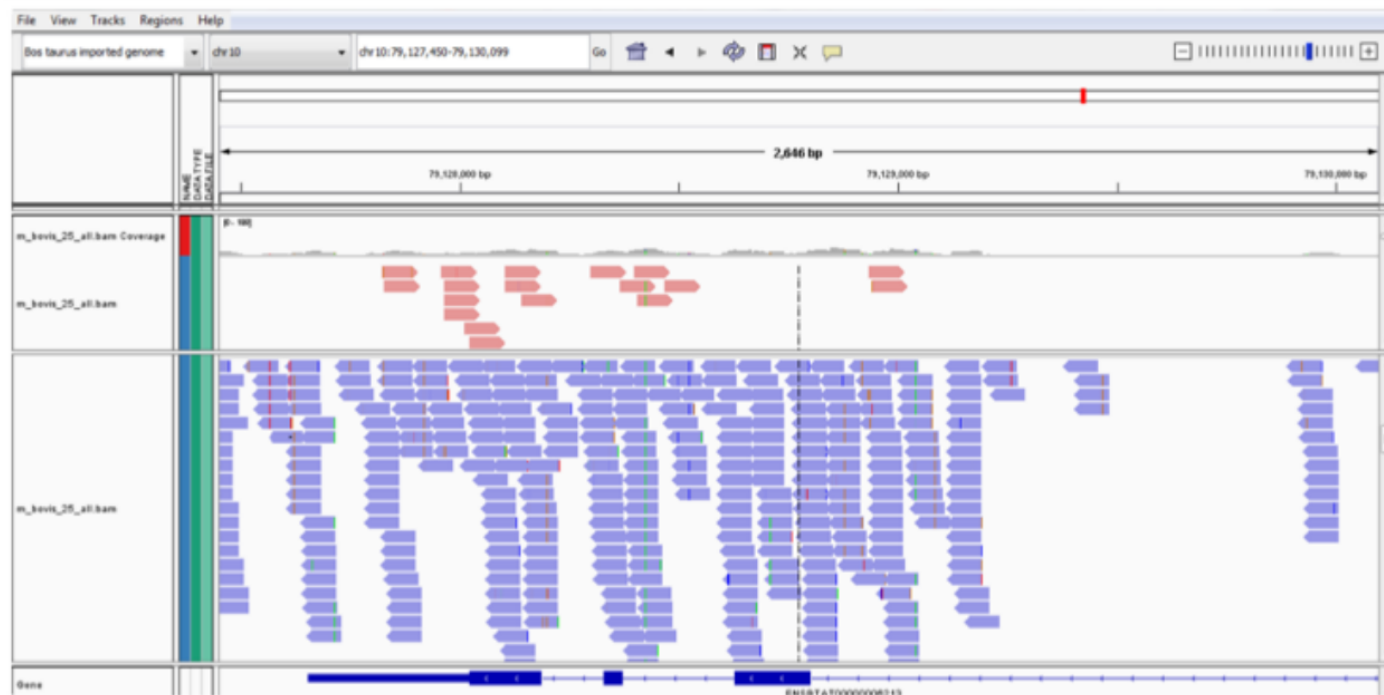- A genome browser is shown that helps you to understand your data

What is mapping?

Mapping

- Search the position of a read in the genome

Sequence alignment

A A C C G C C T T

A G G G G C C T T

1 2 3 4 5 6 7 8 9

Sequence alignment

```
A A C C G C C T T
|       | | | | |
A G G G C C T T

1 2 3 4 5 6 7 8 9
```

Looks easy...

Lego time: Who wants to volunteer?

- Know your data!
- Maybe not the "best" result is the one you are searching for
- Try different mappers

Tools, tools, tools

- Bowtie
- HISAT
- MAQ
- BWA
- Eland
- SOAP
- STAR
- BISMARCK

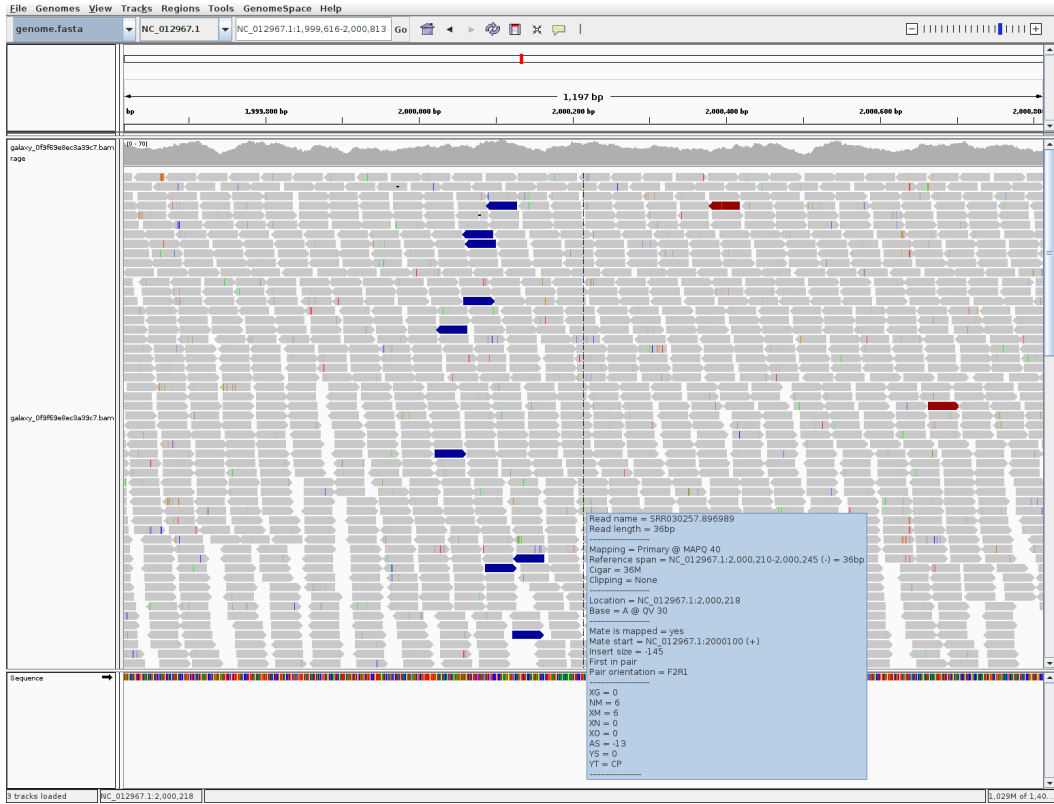And many more!

SAM/BAM file format

SAM/BAM file format

SAM: Sequence Alignment/Map format

BAM: Binary SAM

IGV Browser -- Hands-on

! Key points

- Know your data!

- Mapping is not trivial

- There are many mapping algorithms, it depends on your data which one to choose

Thank you!

This material is the result of a collaborative work. Thanks the Galaxy Training Network and all the contributors (Joachim Wolff) !