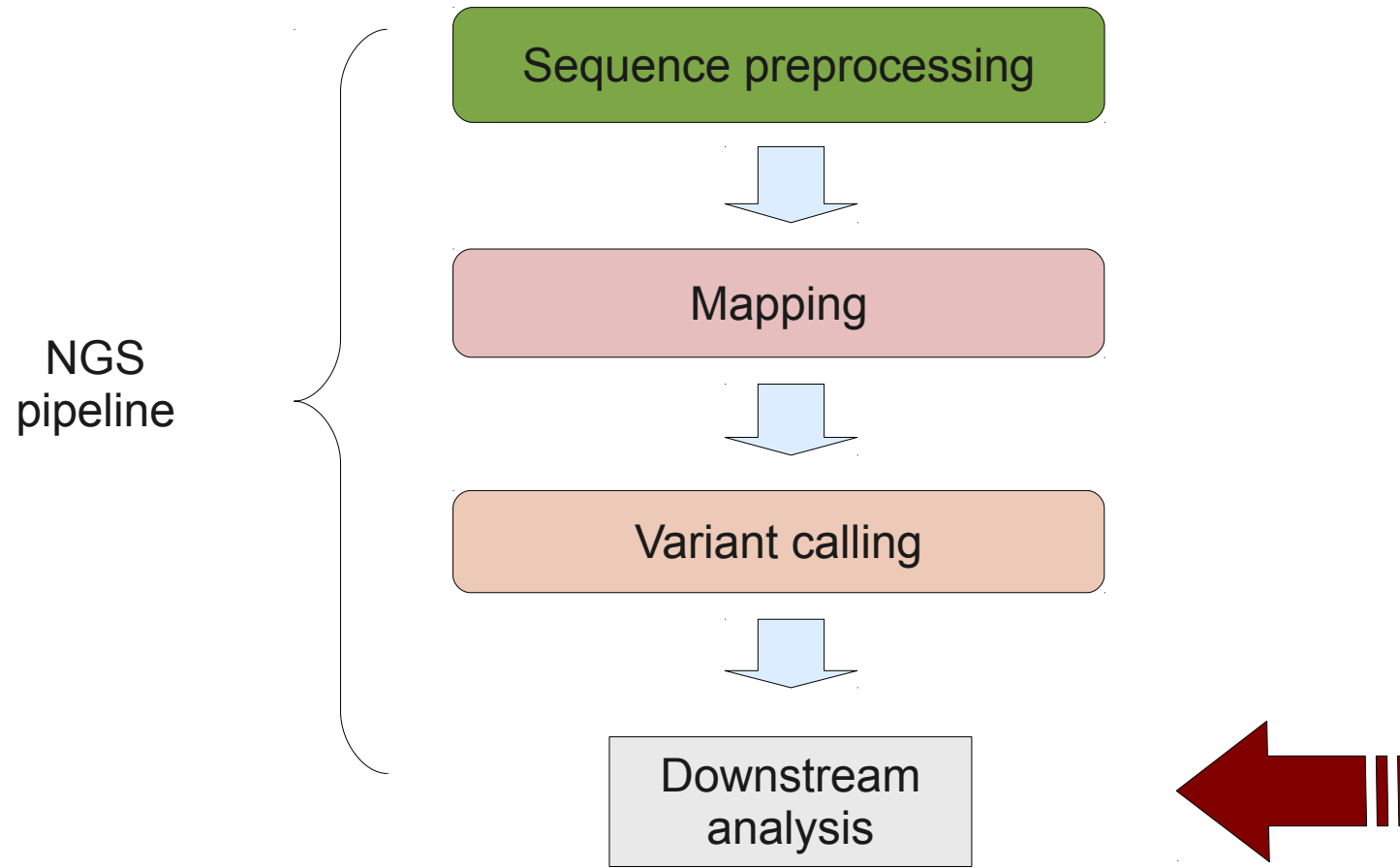


# Results interpretation

Jorge Jiménez  
jjimeneza@cipf.es  
BIER - CIBERER  
Genomics Department  
Centro de Investigación Principe Felipe (CIPF)  
(Valencia, Spain)

# NGS Sequence preprocessing

Where we are?



<http://bioinfo.cipf.es/bierwiki>

[[group:grinberg:sidebar]]

**ciberer BIER**  
PLATAFORMA DE INFORMACIÓN PARA LA INVESTIGACIÓN BÁSICA

Show page Old revisions      Recent changes      Sitemap      Login

Search

## Login

You are currently not logged in! Enter your authentication credentials below to log in. You need to have cookies enabled to log in.

Login

**Username**

**Password**

Remember me

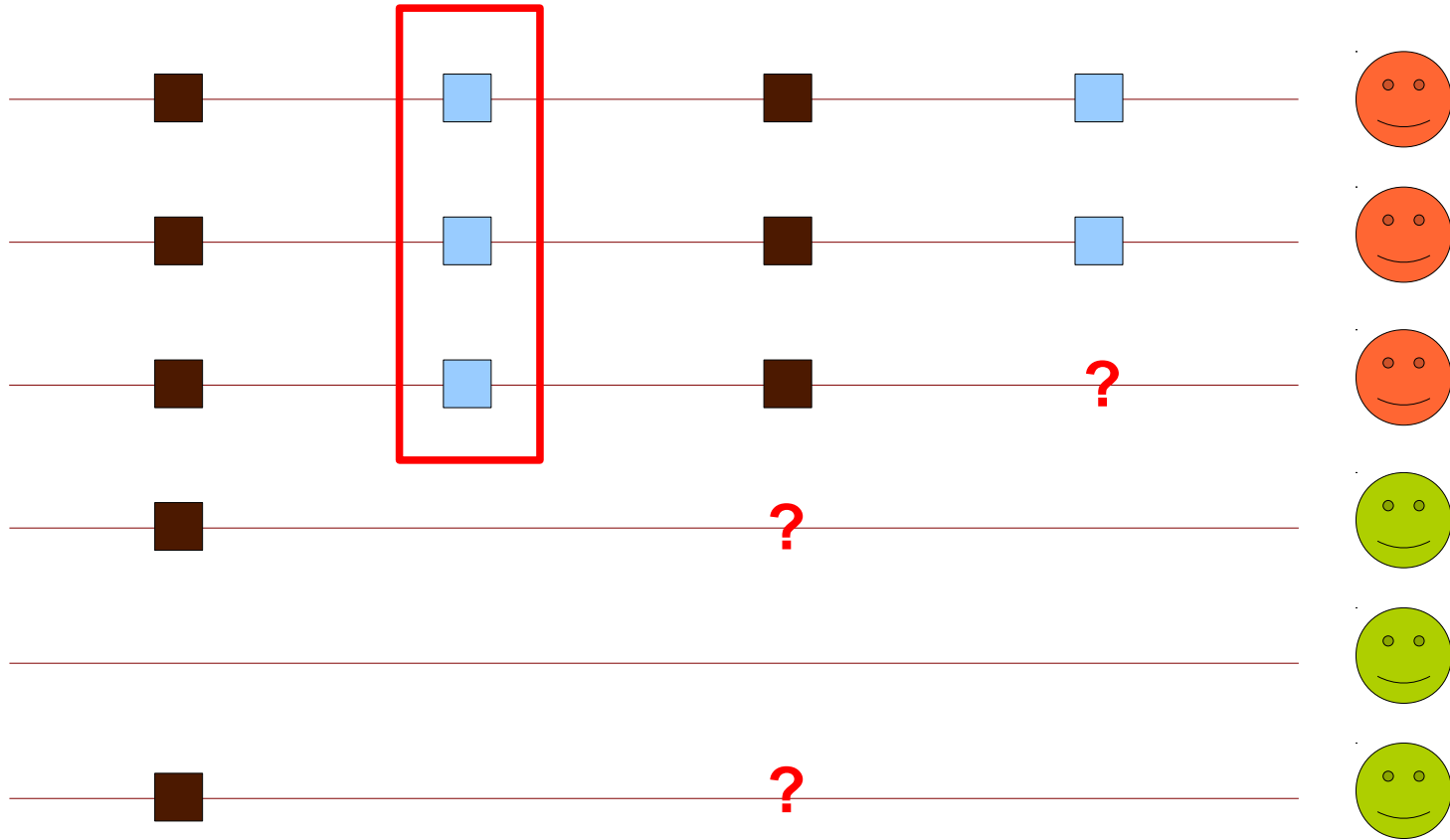
Login

You don't have an account yet? Just get one: [Register](#)

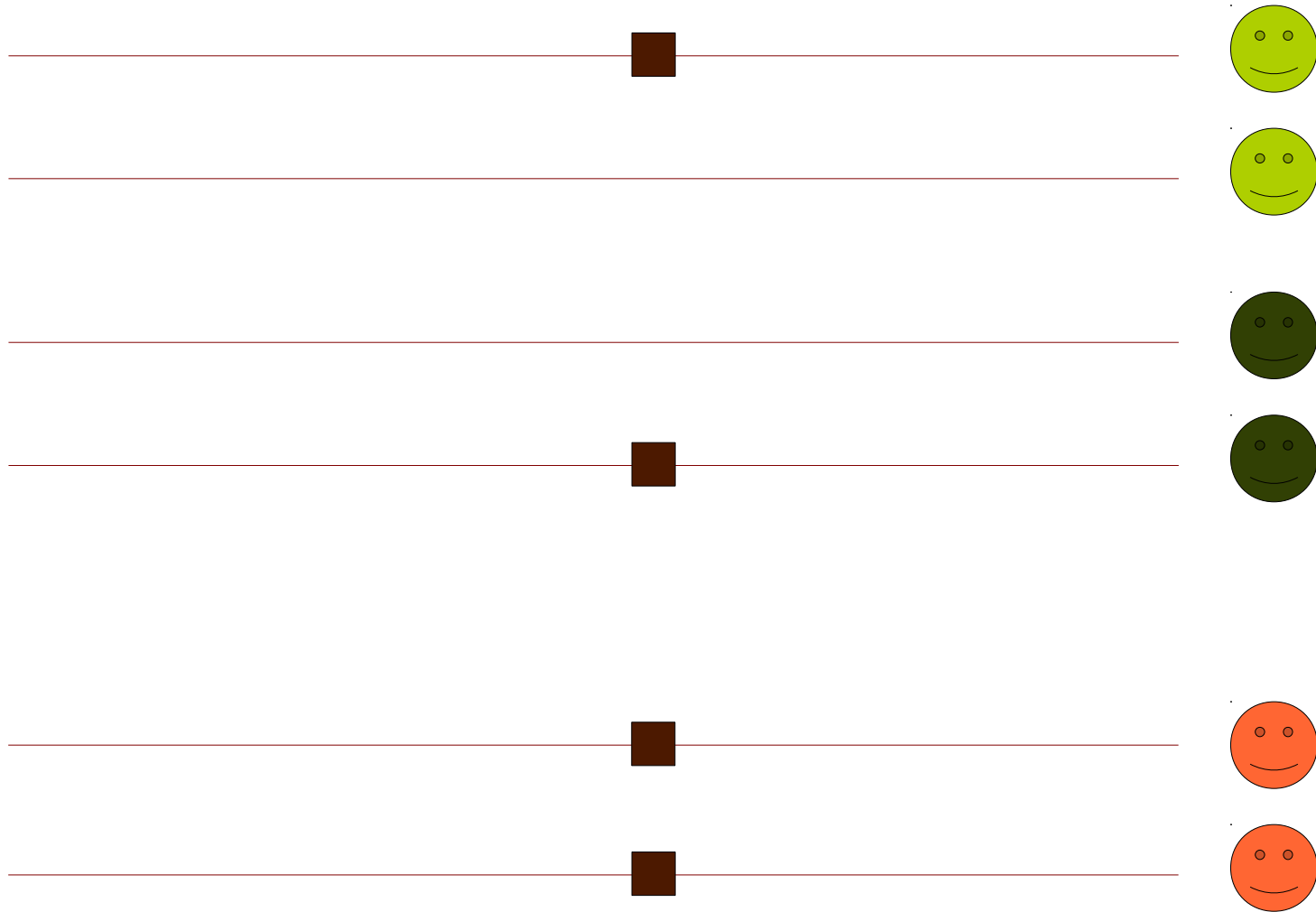
Forgotten your password? Get a new one: [Send new password](#)

Show page Old revisions      [Back to top](#) [unknown link type]

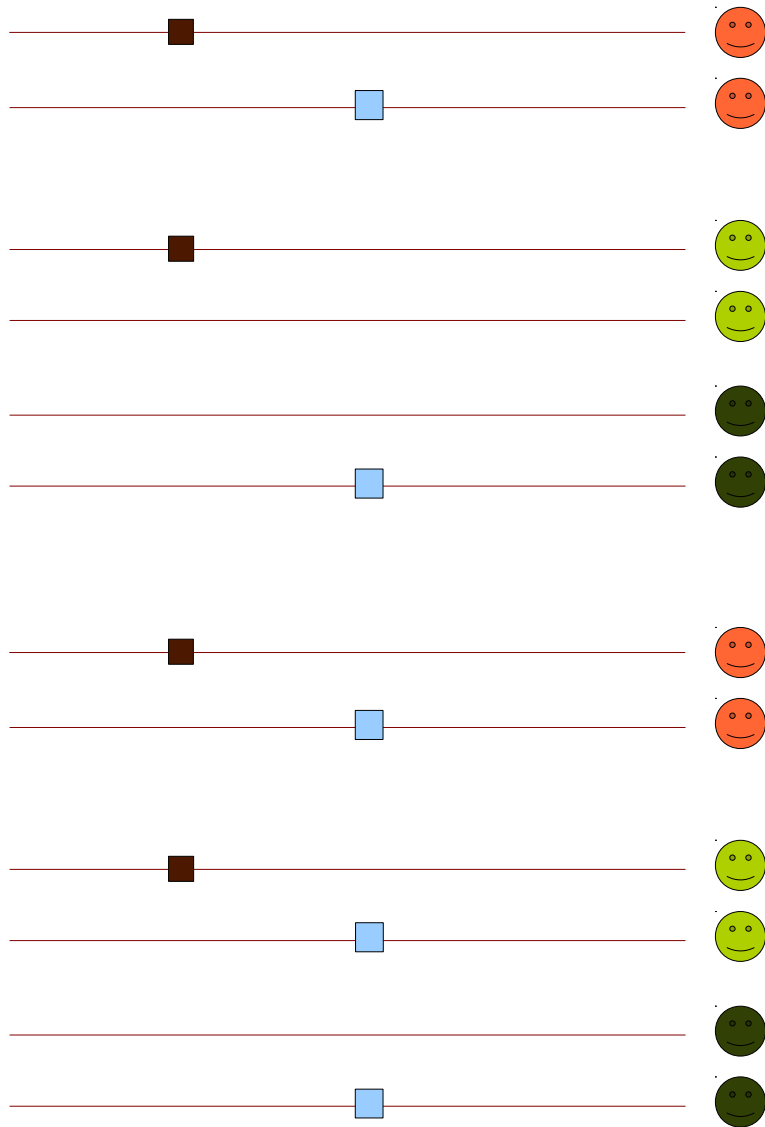
# Dominant



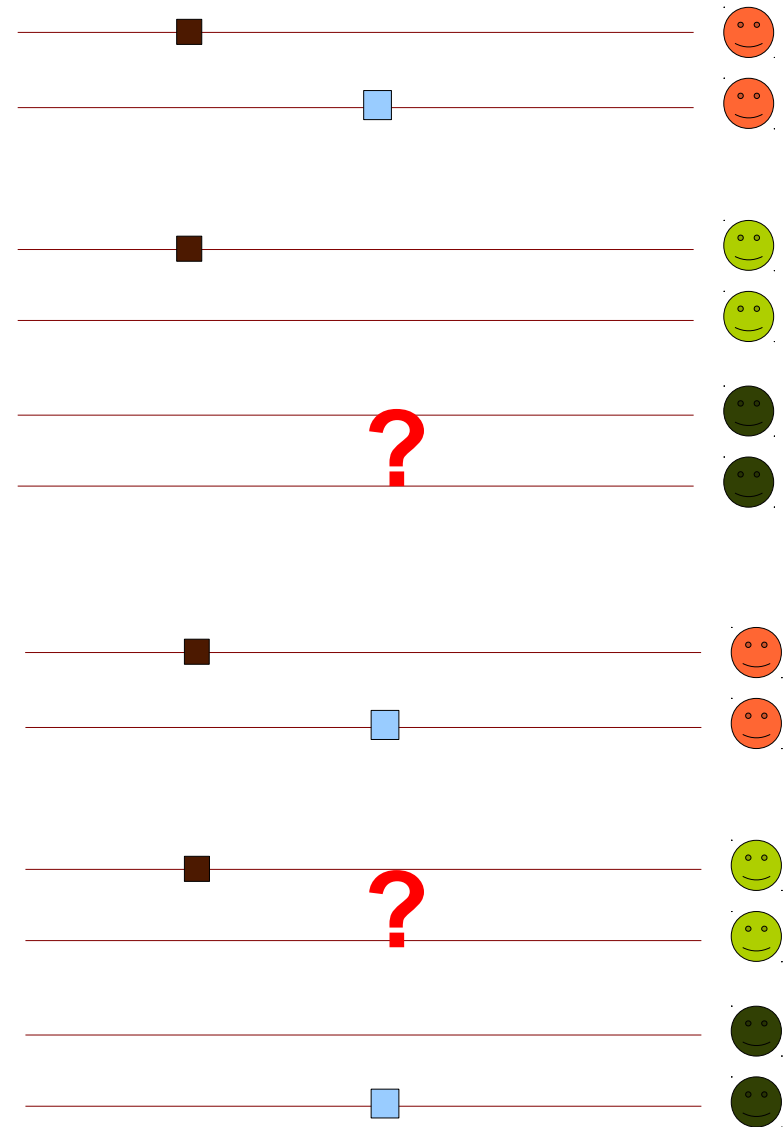
# Recessive - homozygous



# Recessive – compound heterozygosity



X



# FILTERS

---

## **Available:**

- Consequence type
- % cases and controls with variant
- SNVs and indels
- 1000 genomes allele frequency
- Recessive: genes with deleterious variants

## **To do:**

- present in dbSNP.
- All cases with the same genotype.
- Filter by GO terms.
- (...)

# Questions?

---

