

# Bioinformatica 2016/17

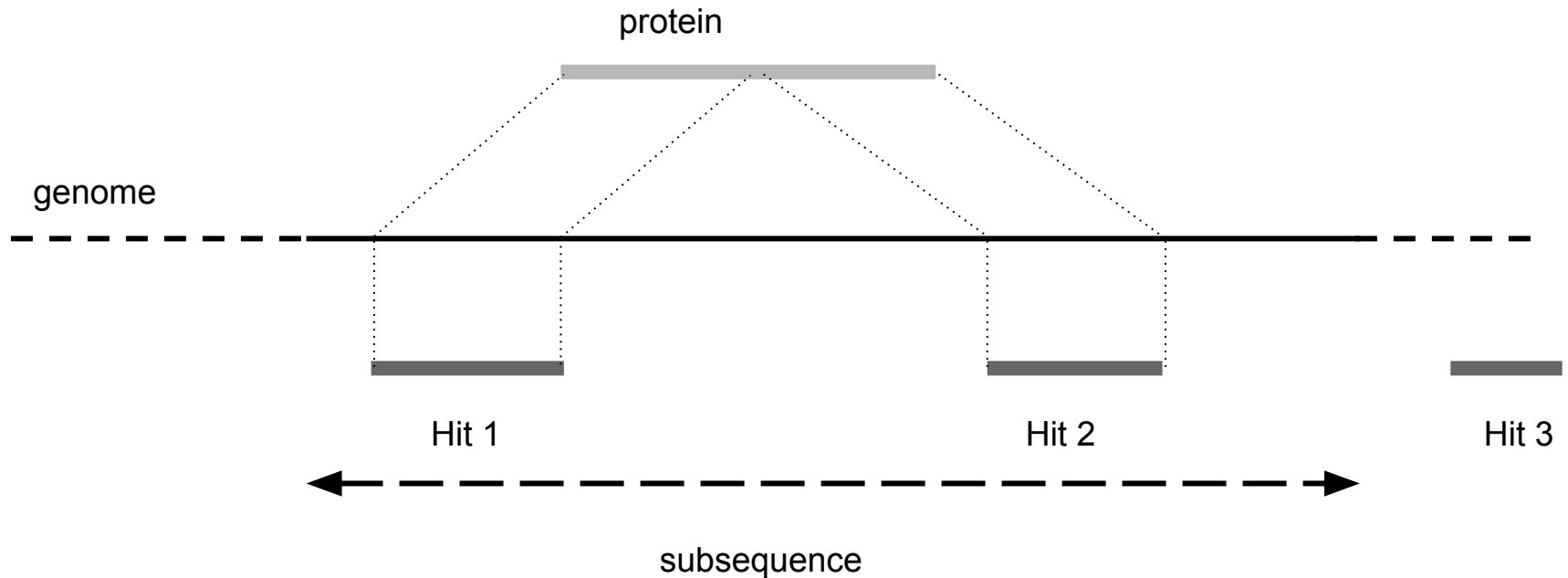
[didac.santesmasses@crg.cat](mailto:didac.santesmasses@crg.cat)

# Genome

/cursos/20428/BI/genomes/2016/Genus\_species/genome.fa

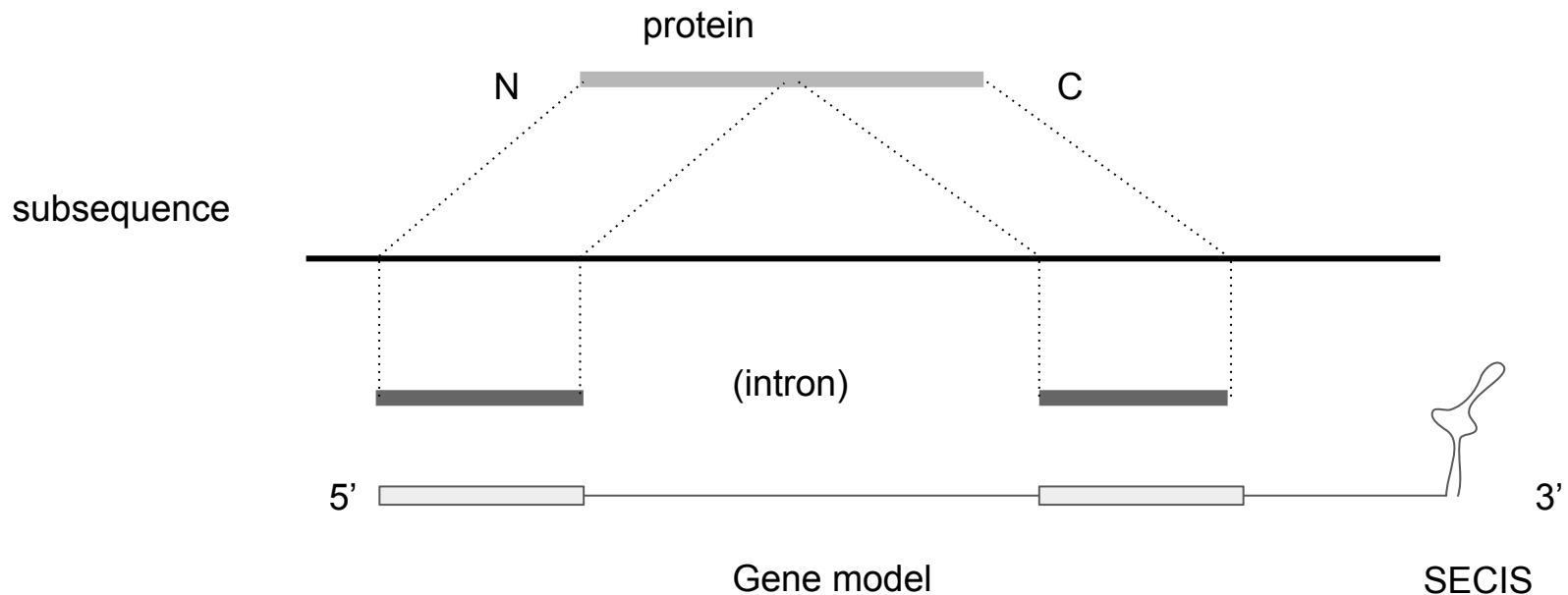
# Protocol overview

- **Tblastn**: locate gene region  
exons as independent blast hits



# Protocol overview

- **exonerate** or **genewise**: multi-exonic gene model
- **Seblastian**: SECIS prediction (<http://seblastian.crg.cat>)



# 1st step: get selenoprotein sequences

## SelenoDB

<http://www.selenodb.org/> (2.0; automatic annotation)

<http://www1.selenodb.org/> (1.0; manually curated, less species)

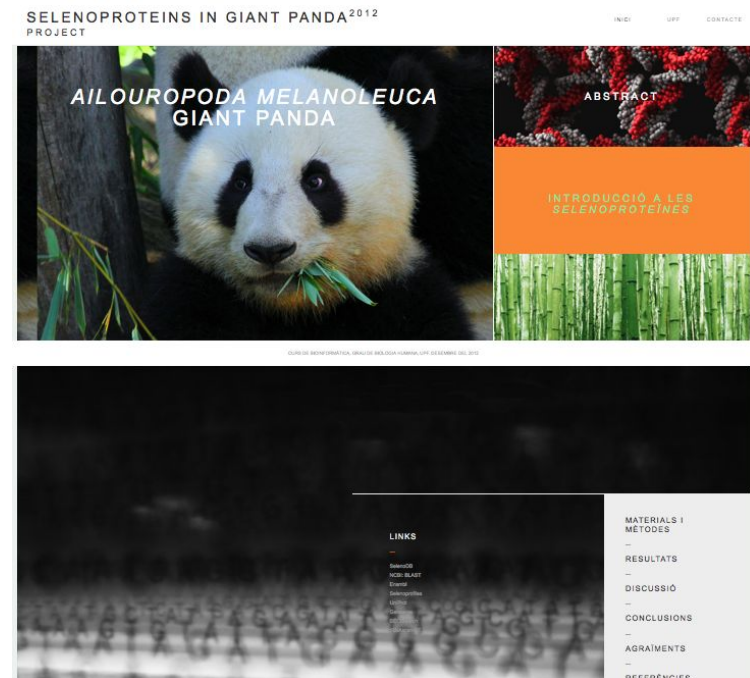
## Past year projects

<http://bioinformatica.upf.edu/>

## Protein databases

<http://www.ncbi.nlm.nih.gov/protein>

<http://www.uniprot.org/>



# Executables

```
module load modulepath/goolf-1.7.20
```

```
module load BLAST+/2.2.30-goolf-1.7.20
```

```
module load Exonerate/2.2.0-goolf-1.7.20
```

```
module load T-Coffee/11.00.8cbe486-goolf-1.7.20
```

```
export PATH=/cursos/20428/BI/bin:$PATH
```

```
export PATH=/cursos/20428/BI/soft/genewise/x86_64/bin:$PATH
```

```
export WISECONFIGDIR=/cursos/20428/BI/soft/genewise/x86_64/wise2.2.0/wisecfg/
```

# Cluster

- VPN connection <https://www.upf.edu/bibtic/en/guiesiajudes/recinfo/vpn/>
- ssh UXXXXX@sitdoc.s.upf.edu (campus global password)
- File `blastJob.sh`

```
#!/bin/bash
#$ -o tblastn.stdout
#$ -e tblastn.stderr
#$ -q all.q
#$ -N blastJob
#$ -cwd
module load modulepath/goolf-1.7.20
module load BLAST+/2.2.30-goolf-1.7.20
tblastn -query fitxerquery.fa -db nombbddBLAST -out fitxerdesortida
```

# Cluster

- Queue system

```
$ qsub blastJob.sh
```

```
$ qstat
```

```
job-ID  prior   name       user          state submit/start at   queue                          slots ja-task-ID
-----  -
      231  0.55500  blastJob    UXXXXX        r    02/10/2010 11:42:09  llicen.q@luke                    1
```

- To kill a running job

```
$ qdel 231
```



# Adding genes to SelenDB

Before adding genes to selenodb, you need to fill the information

[http://selenodb.crg.cat/selenodb\\_barcelona/add\\_author.html](http://selenodb.crg.cat/selenodb_barcelona/add_author.html)

Then you can use your email as author in

[http://selenodb.crg.cat/selenodb\\_barcelona/add\\_gene.html.mako](http://selenodb.crg.cat/selenodb_barcelona/add_gene.html.mako)