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Using Galaxy for the FMI NGS Pipeline

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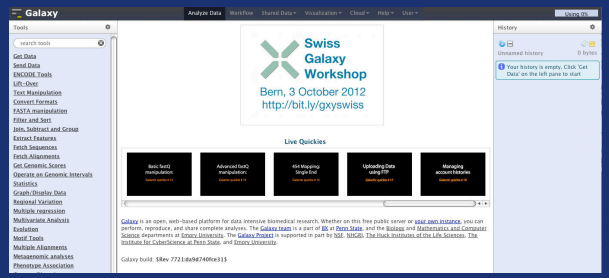
Galaxy at FMI is...

- in production for more than 5 years (3 years for NGS)
- used to reduce the workload of the core facilities
- used to bridge the gap

the “average” lab scientist

?

the “modern” lab scientist



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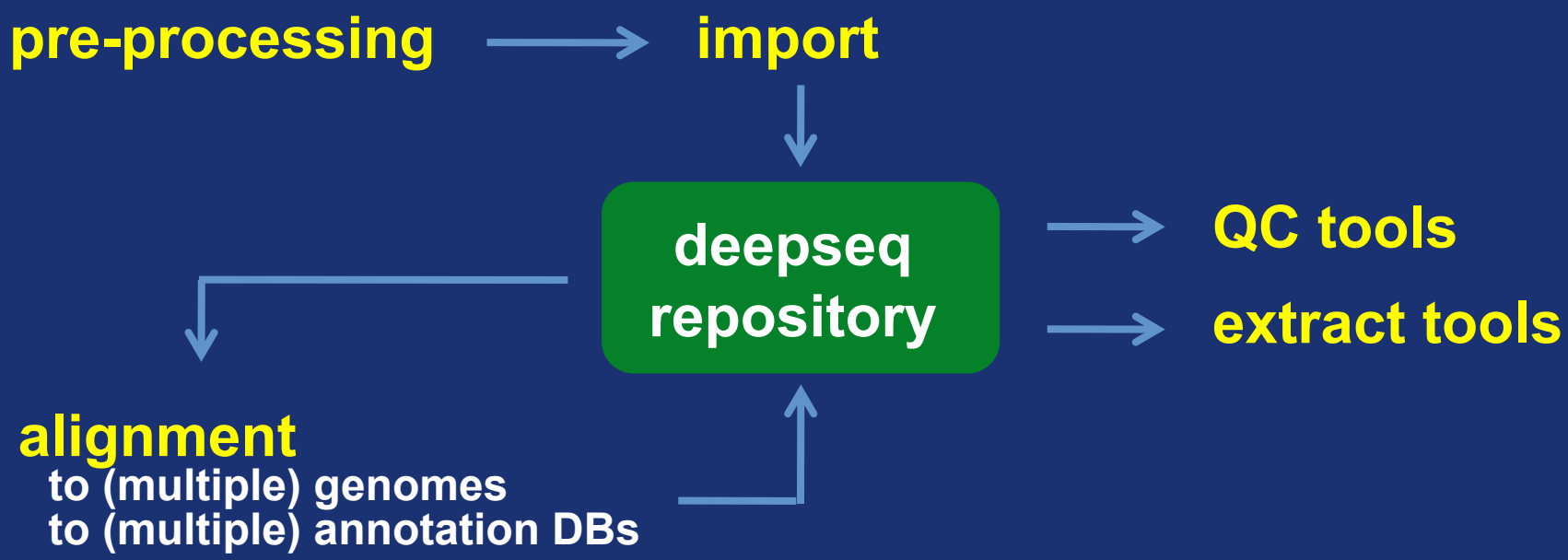
The (current) FMI Deep Sequencing Pipeline

(developed by Michael Stadler and Dimos Gaidatzis)



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The FMI Deep Sequencing is

....just a bunch of Perl scripts *(currently)*

→ which can be easily added to Galaxy

....just a simple file system *(currently)*

....which cannot be added to Galaxy.
(Galaxy uses its own data directory)

→ we don't have to, we just have to give Galaxy access to the file system
(without using "Data Libraries")

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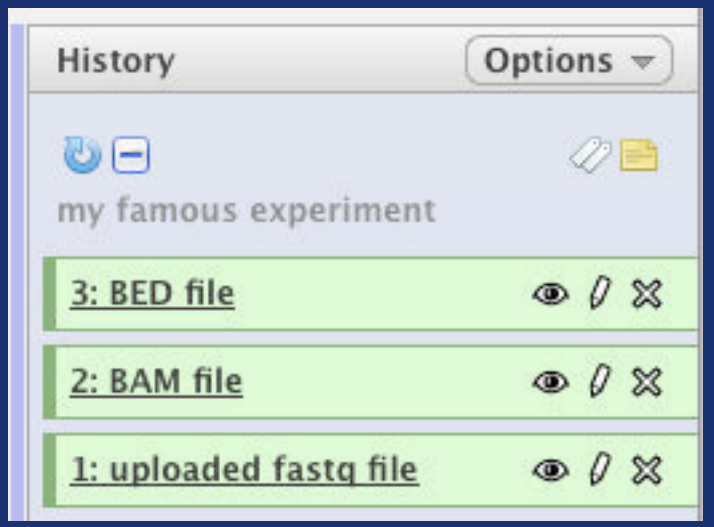
a simple NGS workflow

- your famous aligner

- your famous extract tool



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a simple NGS workflow

- do you need the first result (ie the alignment) as a new history item?
- does your tool require a Galaxy history item as input?

- the ‘famous aligner’ has a wrapper storing the BAM file in the central NGS repository and creating just a log file for Galaxy
- your ‘famous extract tool’ knows the location of the NGS repository

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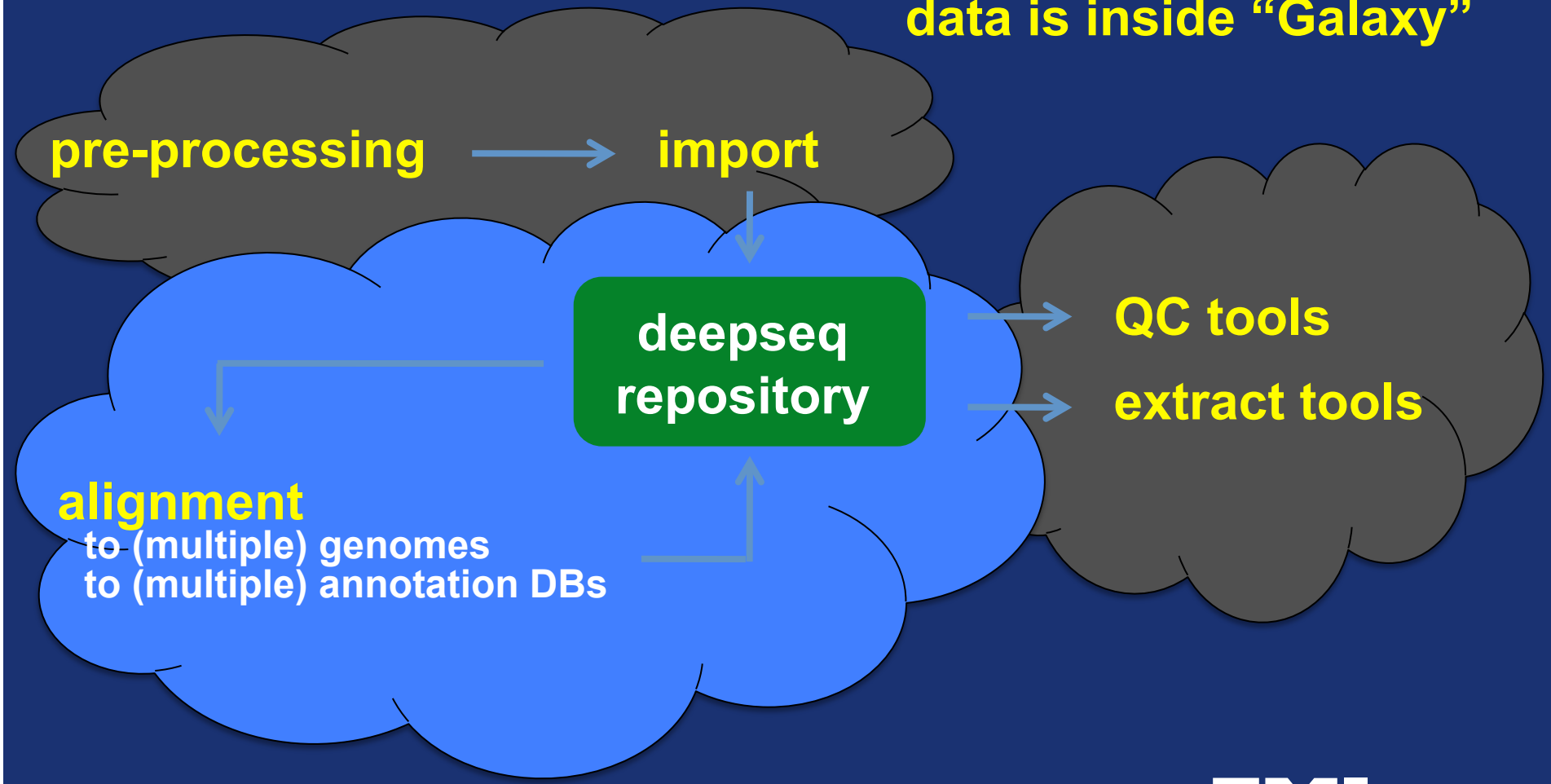
The FMI Deep Sequencing Pipeline



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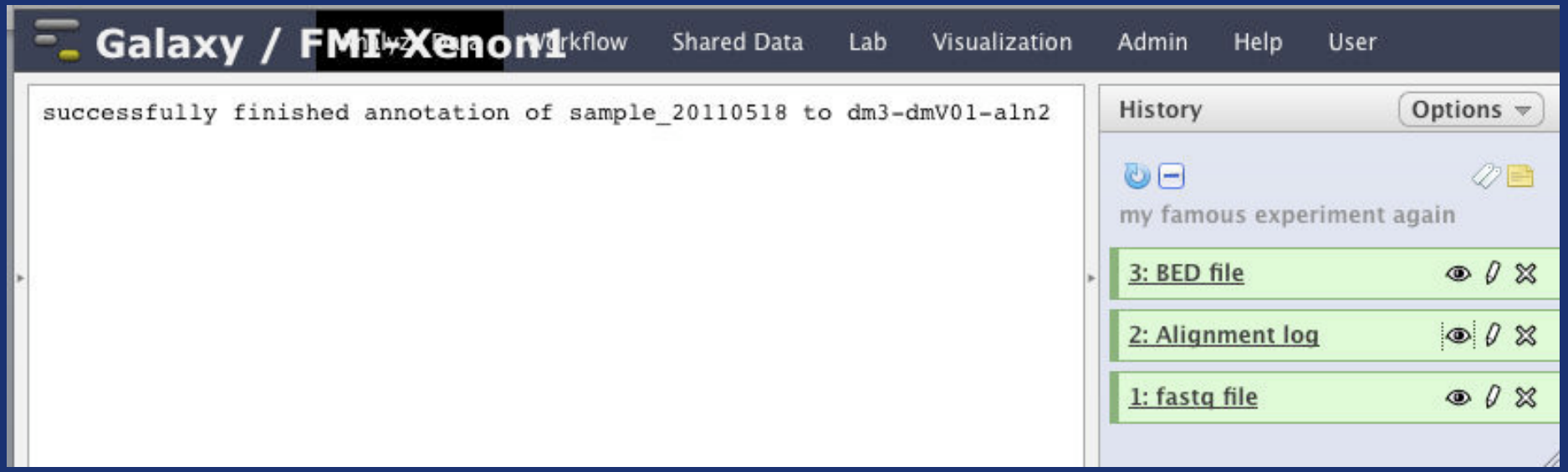
storing data outside of Galaxy

makes it easier to share with non-Galaxy users



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makes it easier to share with non-Galaxy users

```
successfully finished annotation of
sampleId_20110518 to dm3-dmV01-aln2
```

and now the command line geek can do

```
[geek@xenon1 ~]$ extractData.pl -f -s p -m
100 -i mySampleId_20110518 dm3-dmV01-aln2
genome |frag2bed.pl -t -q -U - | head -5
track name='mySampleId_20110518'
chr2L   10493   10528   sq39319 1       +
chr2L   10736   10764   sq74484 1       +
chr2L   11442   11477   sq1340  1       +
chr2L   13799   13834   sq84955 1       +
[geek@xenon1 ~]$
```

makes it easier to share with non-Galaxy users

command line

```
extractData.pl -f -s p -m 100 -i
mySampleId_20110518 dm3-dmV01-aln2 genome |
frag2bed.pl -t -q -U -
```

Galaxy tool definition file

```
 #elif ($summary.mode=="bed")#extractData.pl
-f $strand $maxhits $ignCnts
$sampleSelect.sampleId $genome-$annot-aln2
genome | frag2bed.pl -t -q $summary.ucsc -
> $output
```

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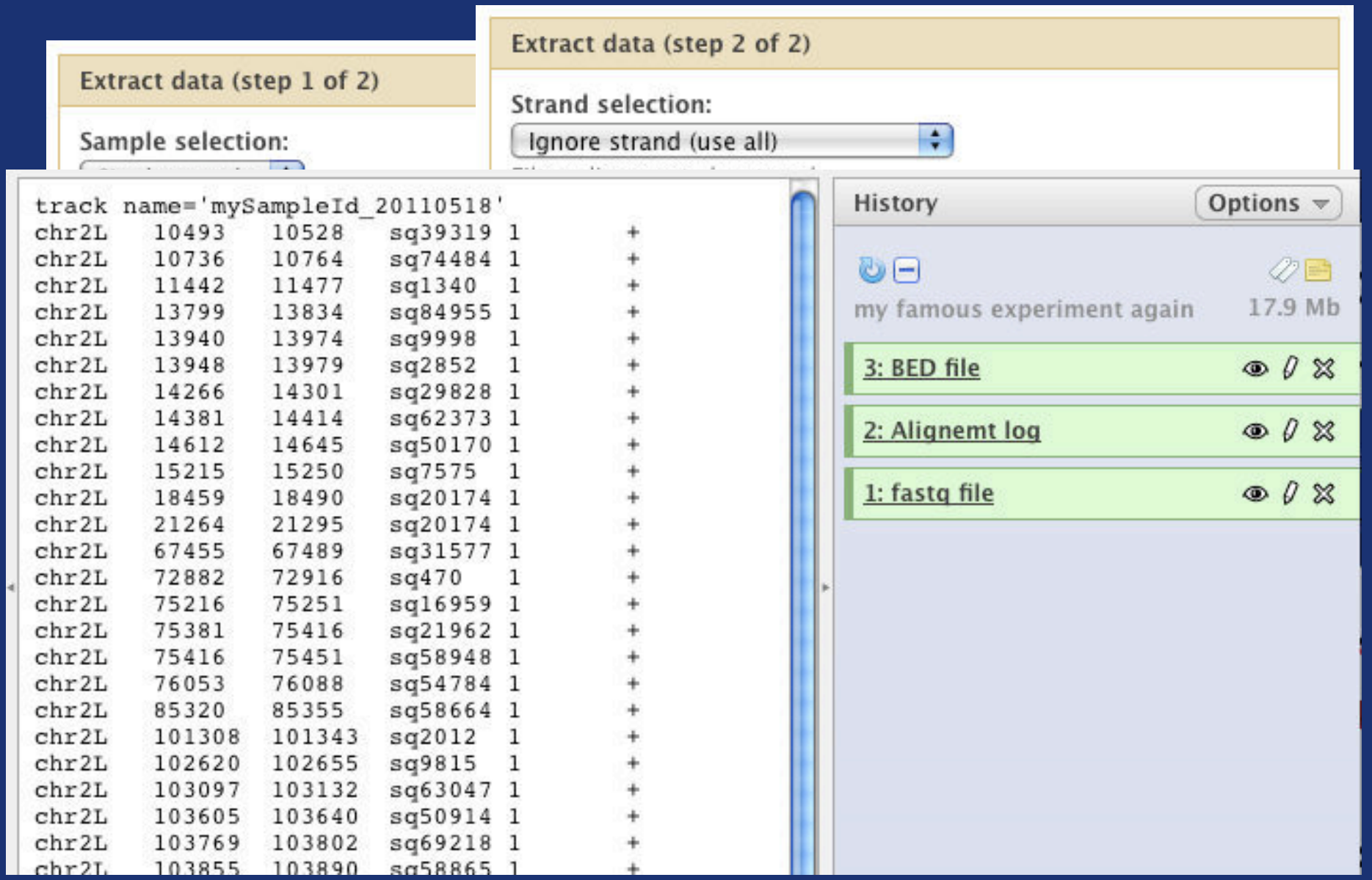
and doing the same in Galaxy



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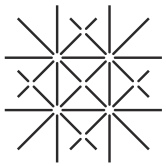
....and all the people from the "Galaxy"

Swiss Institute of Bioinformatics



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