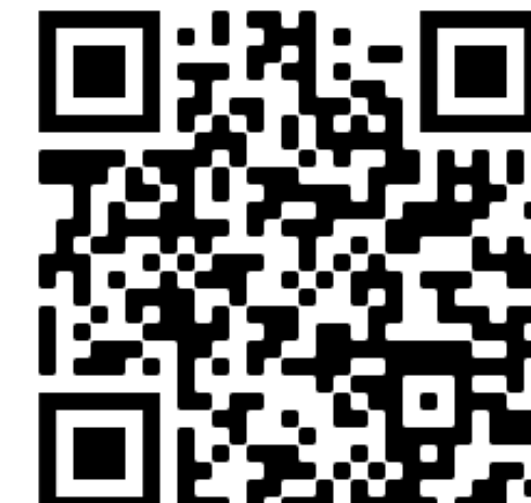
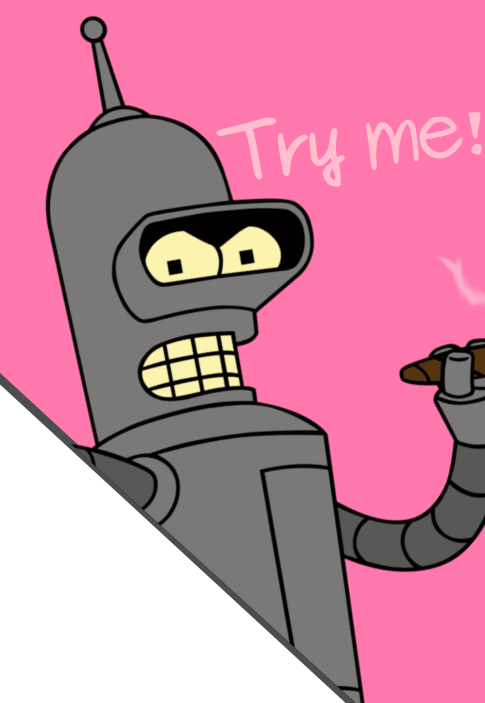
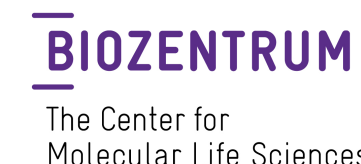


RNA-SEQ ANALYSIS MADE EASY

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 2. Swiss Institute of Bioinformatics, Switzerland
 3. Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland



...previously in The Lab:

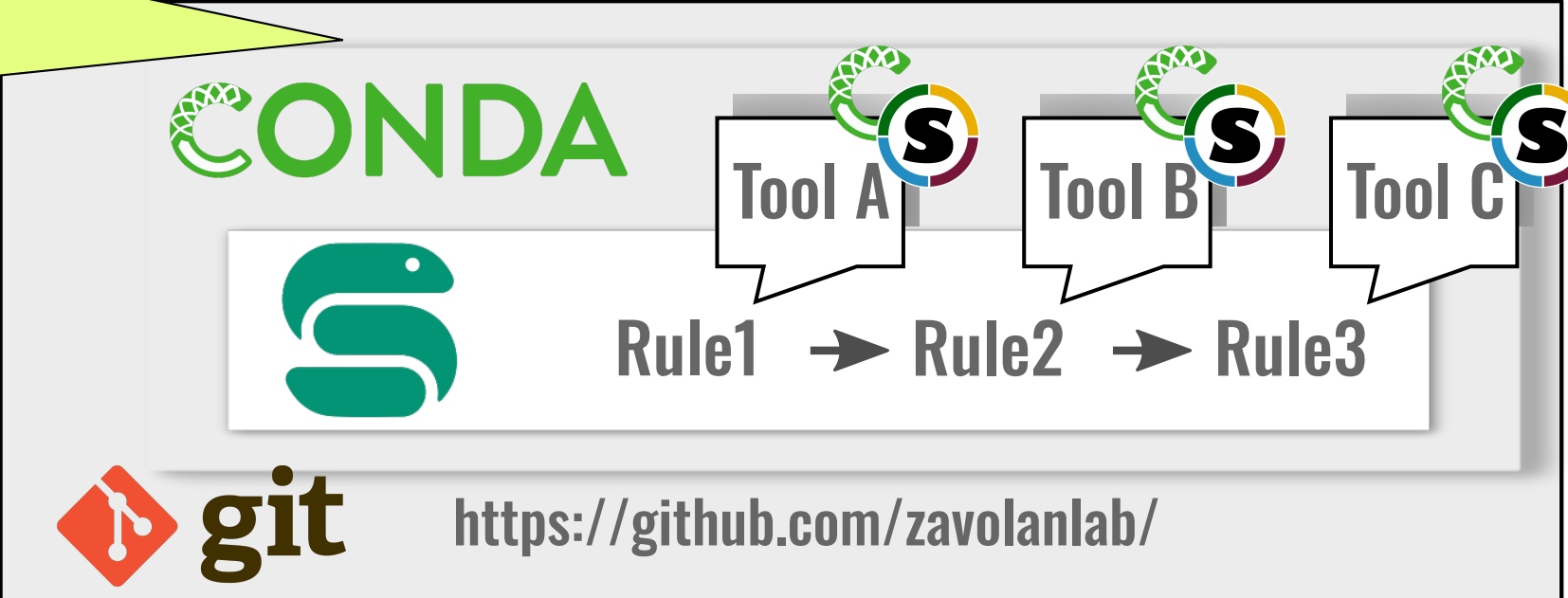
I really need these results for my deadline (ya, I only realized that today), but our bioinformatician is busy fighting bears on her self-discovery trip.

I should analyze all these 263 libraries from SRA, if I do those one by one my PhD is gonna take 17 years!

Aww, I have those RNA-Seq samples and no clue how to check whether they are any good!

ZARP

How is ZARP built?

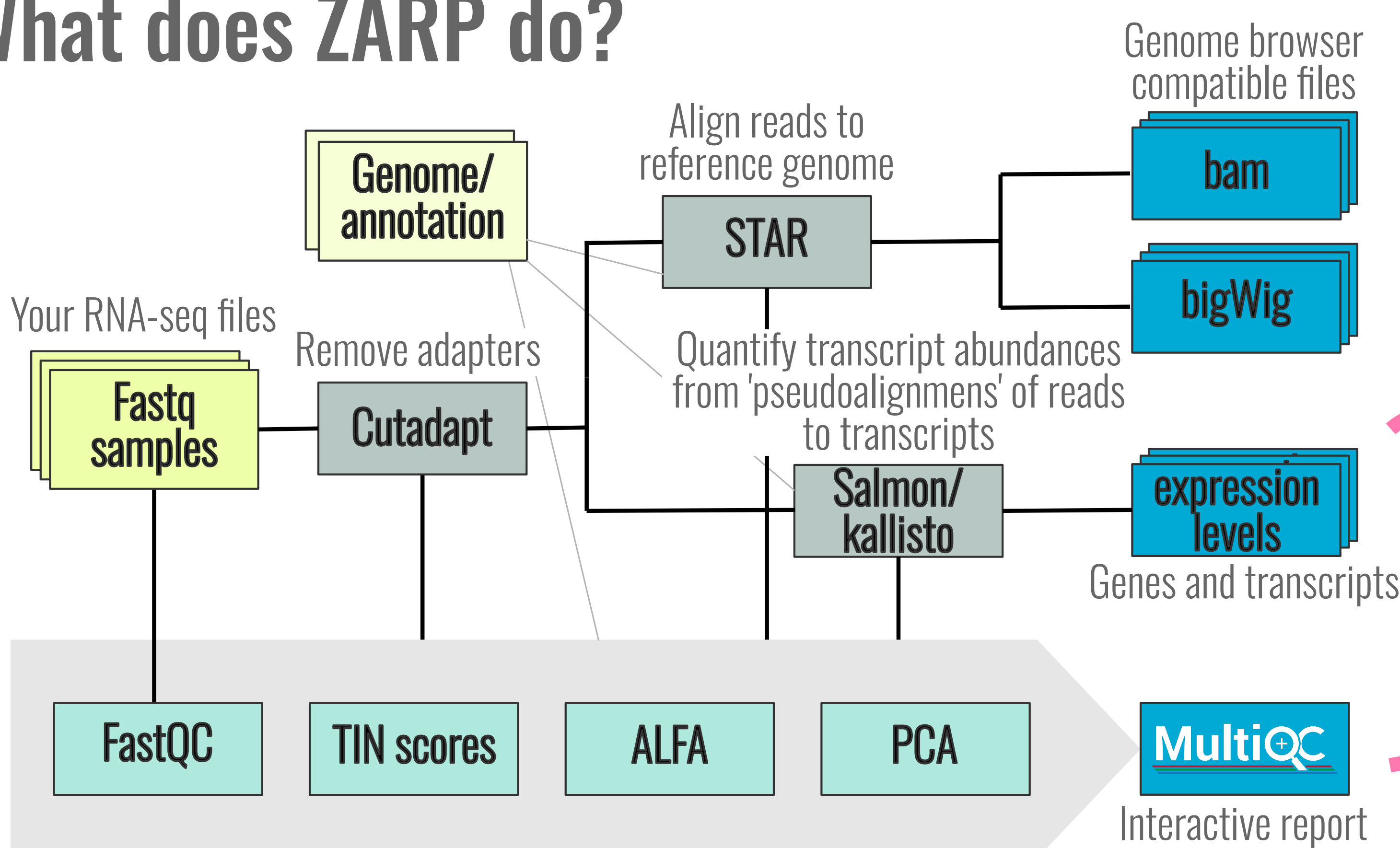


What does ZARP give?

yes, you can really view the results in a browser window!

runtimes for all rules

What does ZARP do?



your reads
 publicly available annotation
 other publicly available tracks
 your reads but in a 100x smaller file which is great for genome browsers

showing 3 of many plots

PCAs for genome & transcriptome

genomic categories

What does ZARP need?

Samples table

sample	seqmode	fq1	fq2	organism	gtf	genome	index	kmer	mean	multi
M10_1	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
M10_2	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
M10_3	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
M30_1	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
M30_2	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
M30_3	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
CR_1	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
CR_2	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250
CR_3	se	input_files/Samp	GAGATCGGAAC	XXXXXXXXXX	mus_musculus	input_files/annot	input_files/genom	75	31	250

Meeeh, ZARP! Such a pain to fill out those stupid sample tables... Why do we have bioinformaticians? I'll just keep sending it their way...

And wait months until they'll get to it? Just use ZARP-cli! Thank me later...

Why ZARP?

- Easy to set up
- Easy to run
- Explore results in browser
- Fast, free, fun*

- Configurable
- Reproducible
- Extendable
- Fast, free, fun*

* depending on personal disposition

Now with CLI:

Runs ZARP on

local files
 SRA accessions

sample tables

> zarp sample_1.fq.gz

> zarp SRR1234 SRR1235

> zarp table:samples.tsv

Manages your ZARP default configuration

Fetches and manages genome resources

Infers sample metadata:
 - Organism
 - 3' adapters
 - Read orientation

ZARP-cli

ZARP

Launches ZARP

The happy END!