CPT Annotation Infrastructure

Eric Rasche

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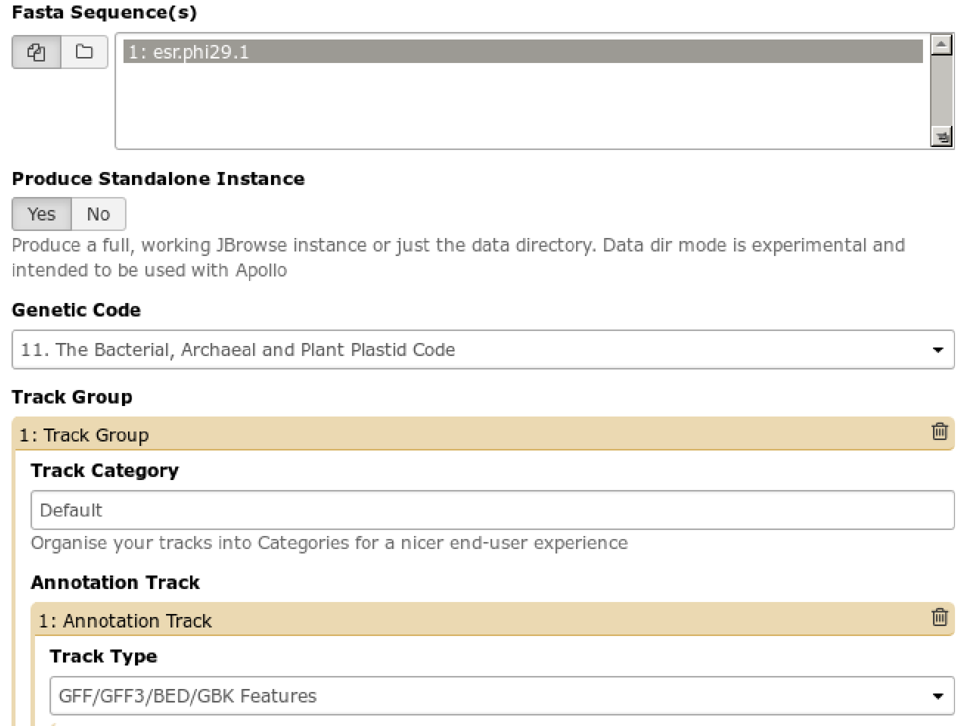
Data Analysis for Genome Annotation

- Sequencing Data
- Assembly to Contigs
- Structural Prediction
- Functional Prediction
- Publishing

Galaxy for Reproducible Genomics

- Standard interface to huge variety of tools
- "Histories" (audit logs) for later reference
- Workflows for sharing complex, multi-step analyses
- Collaboration between developers and end users



Fasta Sequence(s)

1: esr.phi29.1

Produce Standalone Instance

[✓ Yes] No

Produce a full, working JBrowse instance or just the data directory. Data dir mode is experimental and intended to be used with Apollo

Genetic Code

11. The Bacterial, Archaeal and Plant Plastid Code

Track Group

1: Track Group

Track Category

Default

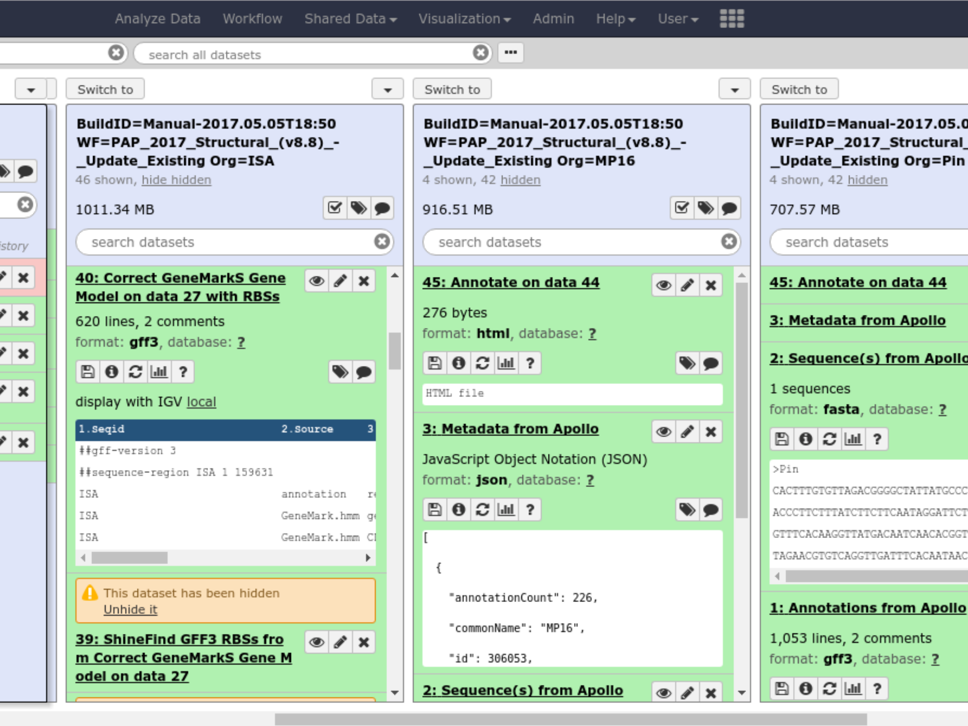
Organise your tracks into Categories for a nicer end-user experience

Annotation Track

1: Annotation Track

Track Type

GFF/GFF3/BED/GBK Features



BuildID=Manual-2017.05.05T18:50 WF=PAP_2017_Structural_(v8.8)_-_Update_Existing Org=ISA
46 shown, hide hidden
1011.34 MB

search datasets

40: Correct GeneMarkS Gene Model on data 27 with RBSs
620 lines, 2 comments
format: gff3, database: ?

display with IGV local

```
1.Seqid                   2.Source         3
##gff-version 3
##sequence-region ISA 1 159631
ISA                       annotation      r
ISA                       GeneMark.hmm    g
ISA                       GeneMark.hmm    C
```

This dataset has been hidden
Unhide it

39: ShineFind GFF3 RBSs from Correct GeneMarkS Gene Model on data 27

BuildID=Manual-2017.05.05T18:50 WF=PAP_2017_Structural_(v8.8)_-_Update_Existing Org=MP16
4 shown, 42 hidden
916.51 MB

search datasets

45: Annotate on data 44
276 bytes
format: html, database: ?

```
HTML file
```

3: Metadata from Apollo
JavaScript Object Notation (JSON)
format: json, database: ?

```
[
  {
    "annotationCount": 226,
    "commonName": "MP16",
    "id": 306053,
```

2: Sequence(s) from Apollo

BuildID=Manual-2017.05.0
WF=PAP_2017_Structural_
_Update_Existing Org=Pin
4 shown, 42 hidden
707.57 MB

search datasets

45: Annotate on data 44

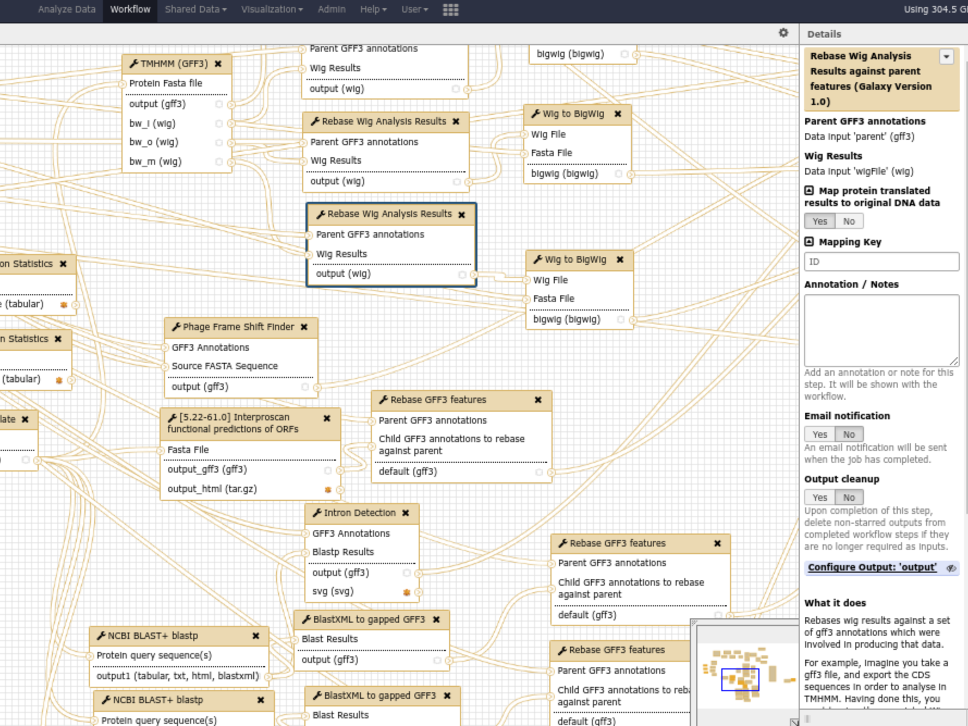
3: Metadata from Apollo

2: Sequence(s) from Apollo

1 sequences
format: fasta, database: ?

```
>Pin
CACTTTGTGTTAGACGGGGCTATTATGCCC
ACCCTTCTTTATCTTCTTCAATAGGATTCT
GTTTCACAAGGTTATGACAATCAACACGGT
TAGAACGTGTCAGGTTGATTTCACAATAAC
```

1: Annotations from Apollo
1,053 lines, 2 comments
format: gff3, database: ?



Rebase Wig Analysis Results against parent features (Galaxy Version 1.0)

Parent GFF3 annotations

Data input 'parent' (gff3)

Wig Results

Data input 'wigFile' (wig)

Map protein translated results to original DNA data

[✓ Yes] No

Mapping Key

ID

Annotation / Notes

Add an annotation or note for this step. It will be shown with the workflow.

Email notification

Yes [✓ No]

An email notification will be sent when the job has completed.

Output cleanup

Yes [✓ No]

Upon completion of this step, delete non-starred outputs from completed workflow steps if they are no longer required as inputs.

Configure Output: 'output'

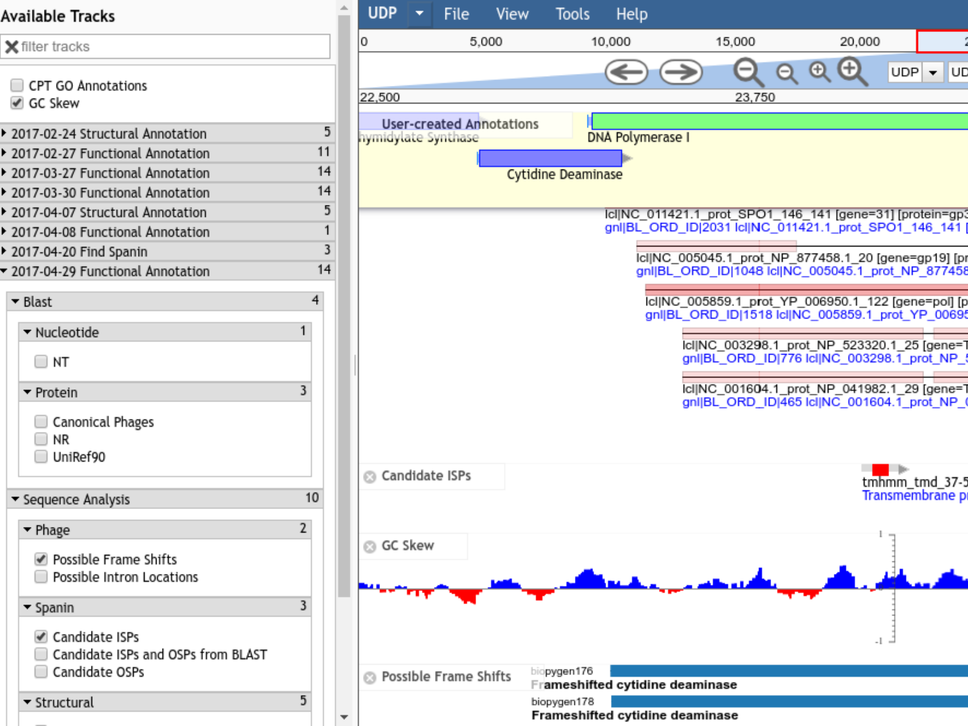
What it does

Rebases wig results against a set of gff3 annotations which were involved in producing that data.

For example, imagine you take a gff3 file, and export the CDS sequences in order to analyse in TMHMM. Having done this, you

Apollo for Interactive Annotation

- “Google Docs” for genome annotation
- Standard interface to analysis data
- Rapidly evolving service with a bright future



☐ CPT GO Annotations
☑ GC Skew

- 2017-02-24 Structural Annotation 5
- 2017-02-27 Functional Annotation 11
- 2017-03-27 Functional Annotation 14
- 2017-03-30 Functional Annotation 14
- 2017-04-07 Structural Annotation 5
- 2017-04-08 Functional Annotation 1
- 2017-04-20 Find Spanin 3
- 2017-04-29 Functional Annotation 14

Blast 4

Nucleotide 1

☐ NT

Protein 3

☐ Canonical Phages
☐ NR
☐ UniRef90

Sequence Analysis 10

Phage 2

☑ Possible Frame Shifts
☐ Possible Intron Locations

Spanin 3

☑ Candidate ISPs
☐ Candidate ISPs and OSPs from BLAST
☐ Candidate OSPs

Structural 5

User-created Annotations
hymidylate Synthase
DNA Polymerase I
Cytidine Deaminase

lcl|NC_011421.1_prot_SPO1_146_141 [gene=31] [protein=gp3
gnl|BL_ORD_ID|2031 lcl|NC_011421.1_prot_SPO1_146_141 [
lcl|NC_005045.1_prot_NP_877458.1_20 [gene=gp19] [pr
gnl|BL_ORD_ID|1048 lcl|NC_005045.1_prot_NP_877458
lcl|NC_005859.1_prot_YP_006950.1_122 [gene=pol] [p
gnl|BL_ORD_ID|1518 lcl|NC_005859.1_prot_YP_00695
lcl|NC_003298.1_prot_NP_523320.1_25 [gene=T
gnl|BL_ORD_ID|776 lcl|NC_003298.1_prot_NP_5
lcl|NC_001604.1_prot_NP_041982.1_29 [gene=T
gnl|BL_ORD_ID|465 lcl|NC_001604.1_prot_NP_0

Candidate ISPs
tmhmm_tmd_37-5
Transmembrane pr

GC Skew

Possible Frame Shifts
biopygen176
Frameshifted cytidine deaminase
biopygen178
Frameshifted cytidine deaminase

Phage Genomics with CPT Galaxy & Apollo

- Full-spectrum platform, *sequencing to publishing*
- *Collaboration*, genome annotation and analysis
- *Reproducible* science

Q&A

Thank you

GitHub	gh/@erasche
Work Email	esr@tamu.edu
GPG Fingerprint	F063 D331 6E63 E7B5 23FD B9EA C527 B0FC 0AF6 3592