http://http://edge-prod.lanl.gov/piret/form

Get Started | Analysis | Login

Set Project MetaData

Project Name

Description

Set Directory Path

Input Experimental Design File [Browse]

[Additional options]

[Set Analysis Parameters]

Additional options include:
1) # of CPUs to use
2) Config File Upload

---

http://http://edge-prod.lanl.gov/piret/form

Get Started | Analysis | Login

Set Analysis Parameters

Kingdom

◉ Prokarya   ○ Eukarya   ○ Both

Import Prokayotic Reference Fasta File

[Browse]

Import Prokayotic Reference GFF

[Browse]

[Additional options]

[< Back]   [Perform Analysis]

Additional options include:
1) Strandedness (Not stranded, forward, reverse)
2) Method ComboBox Drowdown (edgeR, DESeq2, ballgown, DEedge, balledgeR, DEgown)
3) Upload index file
4) Q value range slider

Get Started | Analysis | Login

Set up a new project   Abort Analysis

http://http://edge-prod.lanl.gov/piret/form

Project Name

Quick Project Summary

Run Details ⌄ ❮ ⊞

Transcriptomic Analysis [Optional Display of one or more reports ⌄]

┌─ QC Summary ─────────────────┐
│   │
│   │
│   │
└──────────────────────────────┘

┌─ Mapping Summary ────────────┐
│   │
│   │
│   │
└──────────────────────────────┘

┌─ Feature Count ──────────────┐
│   │
│   │
│   │
└──────────────────────────────┘

┌─ Differential Expression Analysis ─┐
│ [Display one or more analysis ⌄] │
│   │
│   ⊞ 🖼   │
│   │
└────────────────────────────────────┘
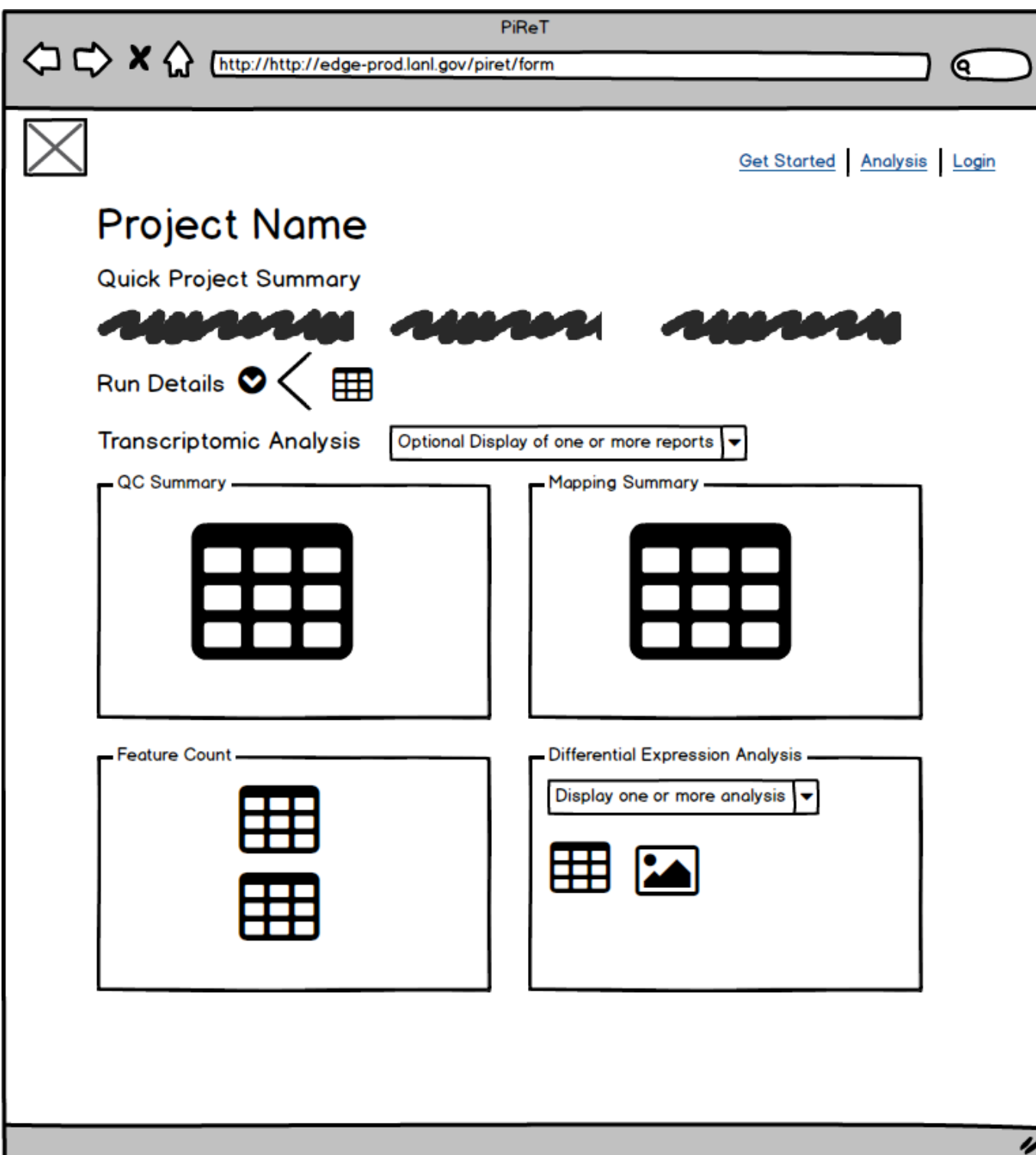
I like the idea of having a modal popup option for run details
Could also have a slide out menu if we expect a user to frequently navigate between the general output and the transcriptomic output