Bulk Upload UI Design Spec - v0.1

This is a collection of views that make up the UX of Bulk Upload. Included is the design spec, plus or minus some pixels.

Design

This document will contain 6 pages, as follows:

- 1. Overview page (this page).
- 2. Upload view.
- 3. Upload view with interaction details. [In progress]
- 4. Upload edit meta view.
- 5. Upload edit meta view with interaction details.
- 6. Active upload view. [In progress]

Implementation

[overview of front-end archectecture to follow]

Testing

[overview of front-end test harness to follow]

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Select files of interest and respective import types.

Calatiana	
Continue	\rightarrow

Quota
Q Search folders
Inbox
ecoli raw reads
bacillus subt genome dat
▼ my contigs
my contigs v1
folder
my contigs 562.8455

nbox /	bacillus subt genome data			
Q S	earch files			
(4)	Name	Size	Mod Time —	Import Type
	my_genome_1.gbk	8mb	30 secs ago	Genome ▼
	bacillus_subt_1.gbk	8mb	5 mins ago	Genome ▼
	bacillus_subt.genbank	8mb	3 hours ago	Genome ▼
✓	bacillus subt 3.fa	8mb	Jan 5, 2015	ContigSet ▼
✓	my_genome_4.fa	8mb	Jan 5, 2015	ContigSet ▼
~	my_genome_5.fa	8mb	Jan 5, 2015	ContigSet ▼
	foo.fa	8mb	Jan 5, 2015	ContigSet ▼
~	bar.fa	8mb	Jan 5, 2015	Genome ▼
	genomev1232.foops	8mb	Jan 5, 2015	no type found ▼
	bac_subt_pheno.csv	8mb	Jan 5, 2015	PhenotypeSet ▼
	phenotype.tsv	8mb	Jan 5, 2015	no type found

- A Vrl routing should be used to render views, with state going across various views. Note that there is no hash. While this isn't particularly important for upload views, the landing page views currently use "#", and so google won't index public landing pages, etc
- **Gobal search**. Feature/UX depends on how/if search will be supported API-wise. At the basic-level, we should support folder search client side.
- **Tree browser**. Single-click should select a folder. Double-click should expand a folder. Additionally, clicking a caret should expand a folder. Note: caret icons may be replaced with [+] icons.

Fixed headers should be implemented for best UX. Should include table head and everything above.



Edit required meta data of staged files, select a Narrative, and upload!

Q Select a na	arrative				Start Import		
contigSets (3)	Genomes	s (1)					
required fields							
Name*	Domain*	Tax ID*	Some Option?	•••	•••	•••	
bacillus_subt_3	Bacteria	▼ 12345.23					
my_genome_4	Bacteria	▼ 678.32					
my_genome_5	Bacteria	▼ not a number					

- Material Auto Completion. See htps://material.angularjs.org/latest/demo/autocomplete for UX. Should support arrow key functionality and be ordered by mod date.
- Auto-naming? Client side processing may aid by auto-generating names.
 I.e., replace spaces and special chars with underscores and strip suffixes for workspace storage. [silly workspaces!]





Edit required meta data of staged files, select a Narrative, and upload!

Q Bob Shew	nella Narrativ	e			Start Import	
ContigSets (3)	Genomes (1)				
* required fields						
Name*	Domain*	Tax ID*	Some Option?	•••	•••	•••
bacillus_subt_3	Bacteria	▼ 12345.23				
my_genome_4	Bacteria	→ 678.32				
my_genome_5	Bacteria	▼ 234532				
my_genome_5	Bacteria	▼ 234532				