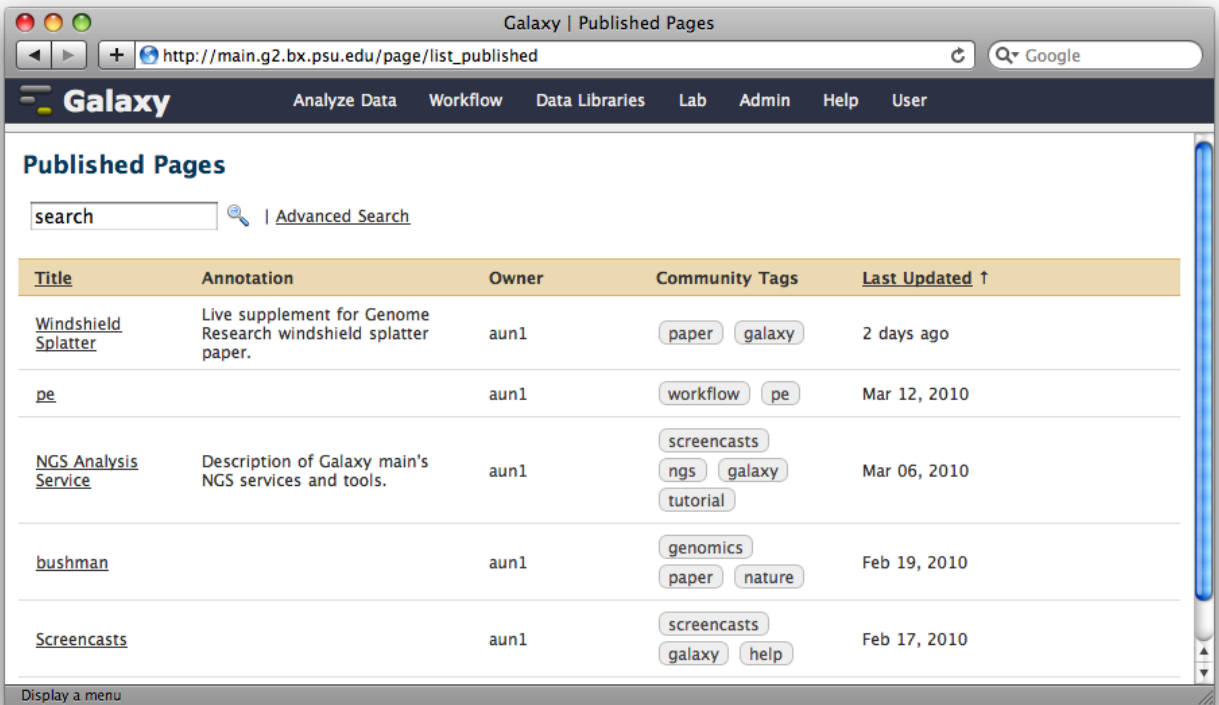


(a)



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Galaxy Analyze Data Workflow Data Libraries Lab Admin Help User

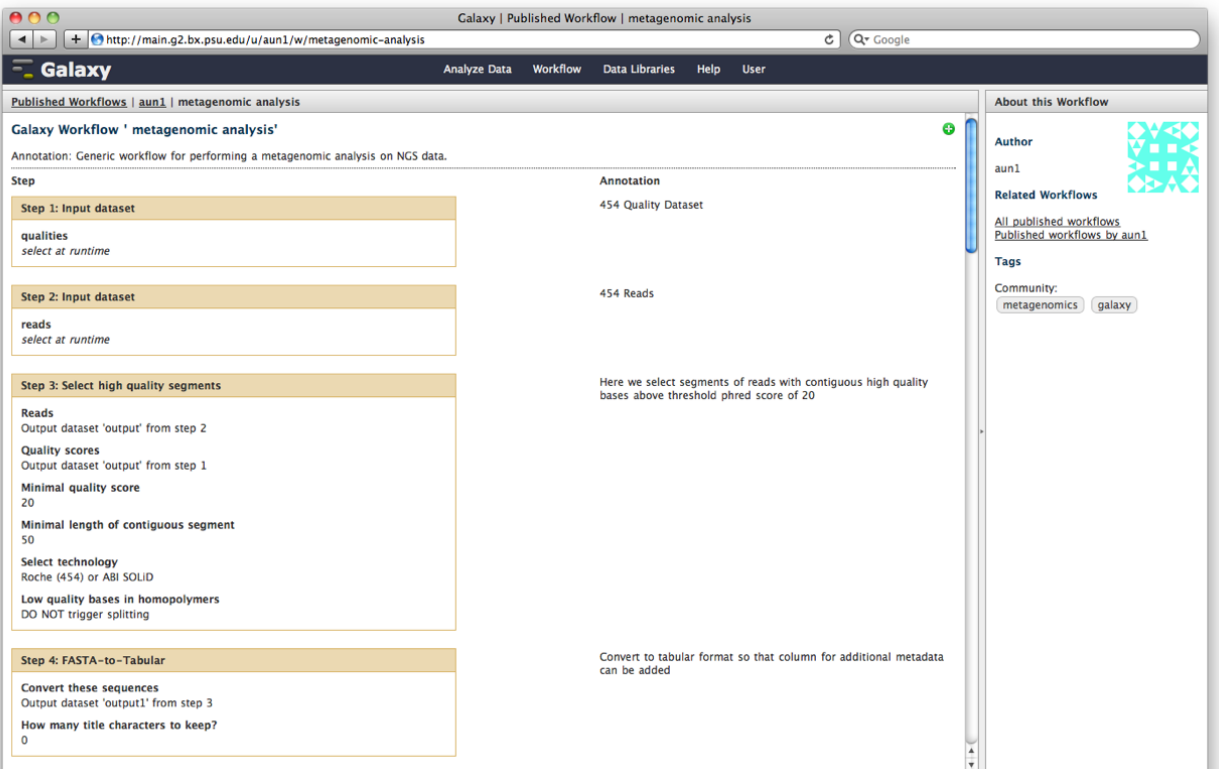
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(b)



Galaxy | Published Workflow | metagenomic analysis

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Published Workflows | aun1 | metagenomic analysis

### Galaxy Workflow ' metagenomic analysis'

Annotation: Generic workflow for performing a metagenomic analysis on NGS data.

Step	Annotation
<b>Step 1: Input dataset</b> qualities <i>select at runtime</i>	454 Quality Dataset
<b>Step 2: Input dataset</b> reads <i>select at runtime</i>	454 Reads
<b>Step 3: Select high quality segments</b> Reads Output dataset 'output' from step 2 Quality scores Output dataset 'output' from step 1 Minimal quality score 20 Minimal length of contiguous segment 50 Select technology Roche (454) or ABI SOLID Low quality bases in homopolymers DO NOT trigger splitting	Here we select segments of reads with contiguous high quality bases above threshold phred score of 20
<b>Step 4: FASTA-to-Tabular</b> Convert these sequences Output dataset 'output1' from step 3 How many title characters to keep? 0	Convert to tabular format so that column for additional metadata can be added

About this Workflow

Author  
aun1

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