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1 What was done where?

1.1 Galaxy Workflow

File imported as workflow in galaxy:
"..\\dev-gene-scripts-master\Galaxy-Workflow-Embryo_dev _genes.ga"

When opening workflow on galaxy the following messages appear:

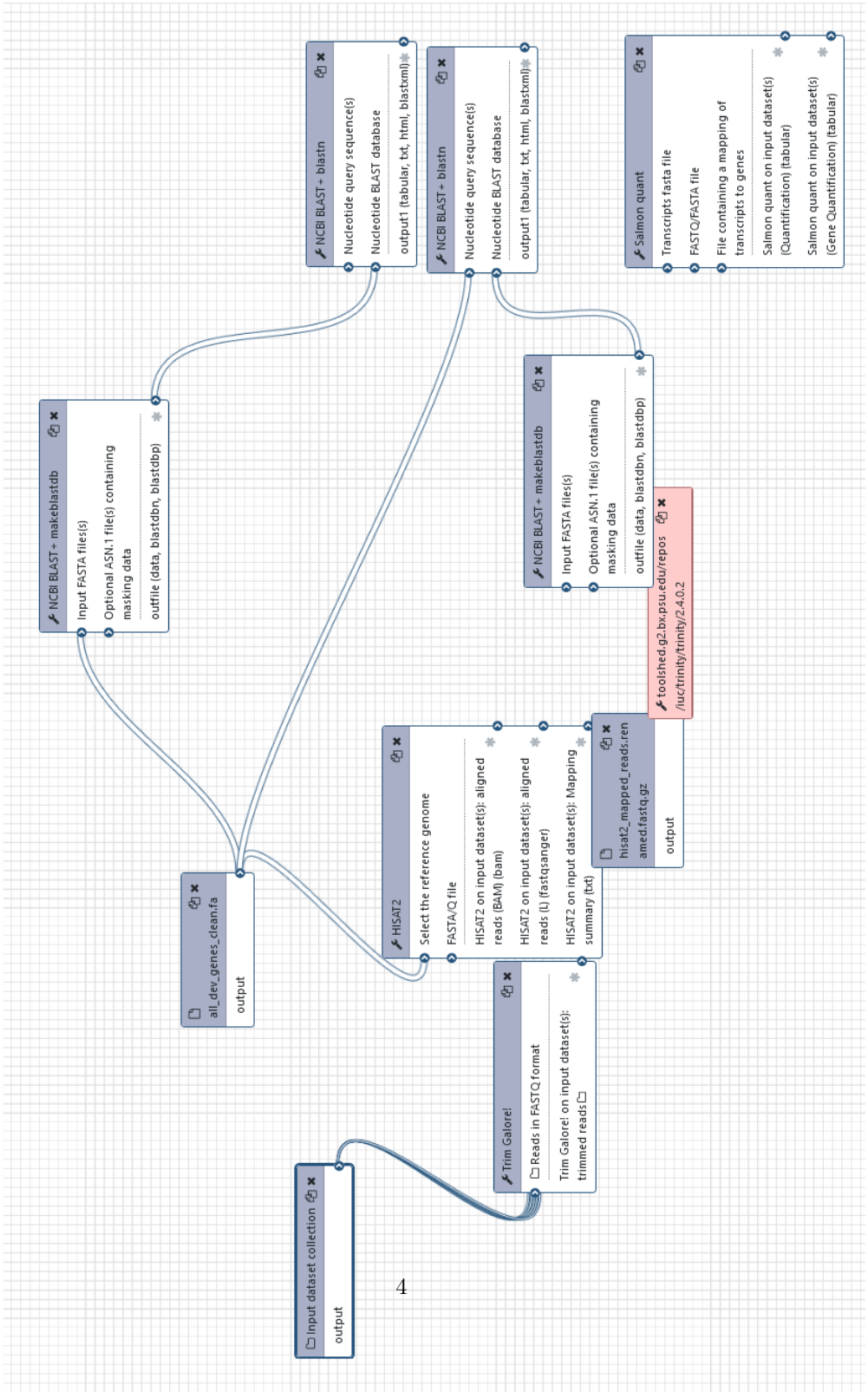
Issues loading this workflow
Please review the following issues, possibly resulting from tool upgrades or changes:

- Step 4: Trim Galore!
- Using version '0.6.3' instead of version '0.4.3.1' specified in this workflow.
- Step 5: NCBI BLAST+ makeblastdb
- Using version '0.3.3' instead of version '0.1.07' specified in this workflow.
- Step 6: toolshed.g2.bx.psu.edu/repos/iuc/trinity/trinity/2.4.0.2
- Tool is not installed
- Step 8: NCBI BLAST+ makeblastdb
- Using version '0.3.3' instead of version '0.1.07' specified in this workflow.
- Step 9: NCBI BLAST+ blastn
- Using version '0.3.3' instead of version '0.1.07' specified in this workflow.
- Step 10: Salmon quant
- No value found for 'Quasi Coverage'.
- No value found for 'Thinning factor'. Using default: '16'.
- No value found for 'Consistent Hits'. Using default: 'False'.

- No value found for 'skipQuant'. Using default: 'False'.
- No value found for 'Meta'. Using default: 'False'.
- No value found for 'incompatPrior'. Using default: '0.0'.
- No value found for 'Write Mappings to Bam File'. Using default: 'False'.
- No value found for 'Write orphan links'. Using default: 'False'.
- No value found for 'Minimum assigned fragments'.
- No value found for 'Type of index'. Using default: 'quasi'.
- No value found for 'Dump equivalence class counts including rich weights'. Using default: 'False'.
- No value found for 'Transcripts fasta file'. Using default: ''.
- No value found for 'Allow Dovetail'. Using default: 'False'.
- No value found for 'Consensus Slack'. Using default: '0'.
- No value found for 'Select a reference transcriptome from your history or use a built-in index?'. Using default: 'history'.
- No value found for 'Perfect Hash'. Using default: 'False'.
- No value found for 'No gamma draw'. Using default: 'False'.
- No value found for 'Discard orphan quasi'. Using default: 'False'.
- No value found for 'Range of factorization bins'. Using default: '0'.
- No value found for 'Specify the strandedness of the reads'. Using default: 'U'.
- No value found for 'Significant Digits'. Using default: '3'.
- No value found for 'FASTQ/FASTA file'. Using default: ''.
- No value found for 'Bootstrap reproject'. Using default: 'False'.
- No value found for 'Select salmon quantification mode:'. Using default: 'reads'.
- No value found for 'Validate mappings'. Using default: 'False'.
- No value found for 'Kmer length'. Using default: '31'.
- No value found for 'Use the traditional EM algorithm for optimization in the batch passes.'. Using default: 'False'.

- Using version '1.3.0+galaxy1' instead of version '0.9.1' specified in this workflow.
- No value found for 'Recover Orphans'. Using default: 'False'.
- No value found for 'Is this library mate-paired?'. Using default: 'single'.
- No value found for 'No length correction'. Using default: 'False'.
- Step 11: NCBI BLAST+ blastn
- Using version '0.3.3' instead of version '0.1.07' specified in this workflow.

1.2 Workflow Graphics



1.3 Run Workflow

When pressing run workflow, the following message appears:
Following tools missing: toolshed.g2.bx.psu.edu/repos/iuc/trinity/trinity/2.4.0.2