**A multi-track RNA-seq browser for visualization of Arabidopsis thaliana transcription patterns from different growth states and conditions.**

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1. Network analysis of local vs. iPlant BAM files. October 16, 2015

**Date**: October 16, 2015

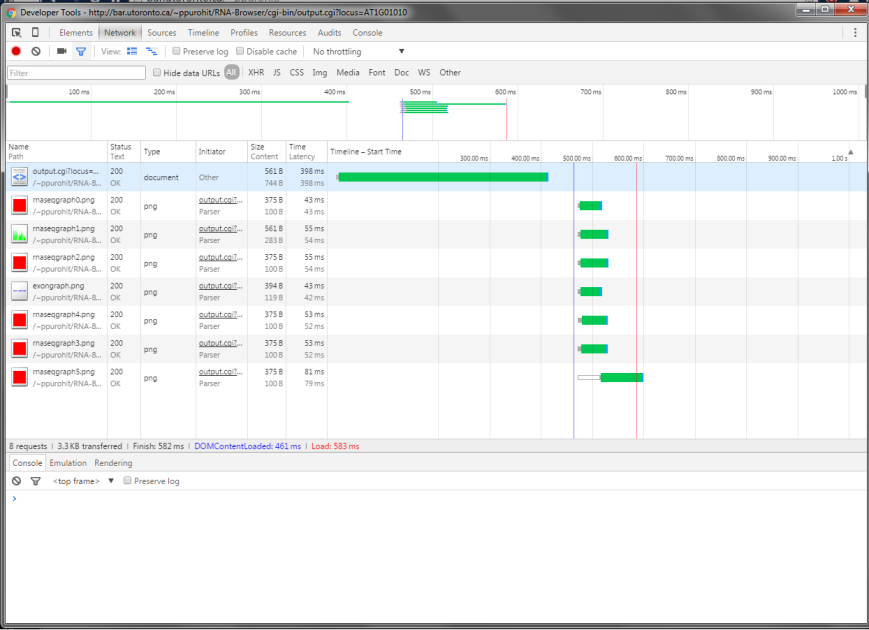
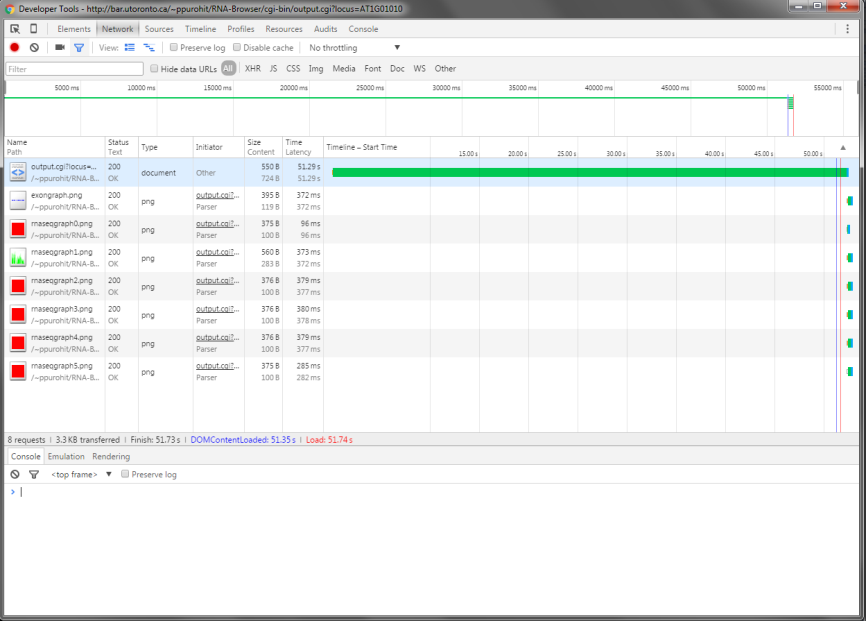
**Agenda**:

1. Check if local BAM files can speed up data retrieval using samtools’ mpileup () call.

**Protocol**:

1. Check if local BAM files can speed up data retrieval using samtools’ mpileup () call.
   1. Downloaded the BAM file for experiment SRR547531 using wget ().
   2. Executed mpileup () through SSH.
      1. Used local BAM file and compare to iPlant BAM file
   3. Ran the output.cgi script with the two BAM files (local vs. iPlant).
      1. Used Chrome Dev Tools to analyze the TTFB (time to first byte).

**Results**:

1. Check if local BAM files can speed up data retrieval using samtools’ mpileup () call.
   1. Done, file size = 662MB.
   2. Local BAM file mpileup call returns data instantly, iPlant BAM file takes 10-20 seconds.
   3. Local BAM file returns data in ~600ms! The iPlant BAM file takes ~50 seconds!
      1. Was calling the generate\_rnaseq\_graph() function only once to produce a single image.

**Date**:

**Agenda**:

**Protocol**:

**Results**:

**Notes**: