Real-Time Metagenomics Analysis

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Abstract

In the last few years a new technology called metagenomics has revolutionized biology. This technique allows biologists to sequence the DNA (genetic make up) of all the organisms in an environment. The Real-Time Metagenomics project provide biologists with a variety of tools to annotate metagenomes using web 2.0 technology, including web services (RTMg.web), Google's Android cell phone operating system (RTMg.mob), and all OpenSocial-based social network sites (RTMg.os). This technology allows biologists to perform useful, fast, and easy bioinformatics services on metagenomic data. In fact, annotations of DNA sequences are performed within minutes; something that used to take hours or days.

These annotations contain the genome functions and subsystems found in given DNA sequences. Using the SEED database of genome sequences, DNA sequences are compared against the SEED to determine annotation information.
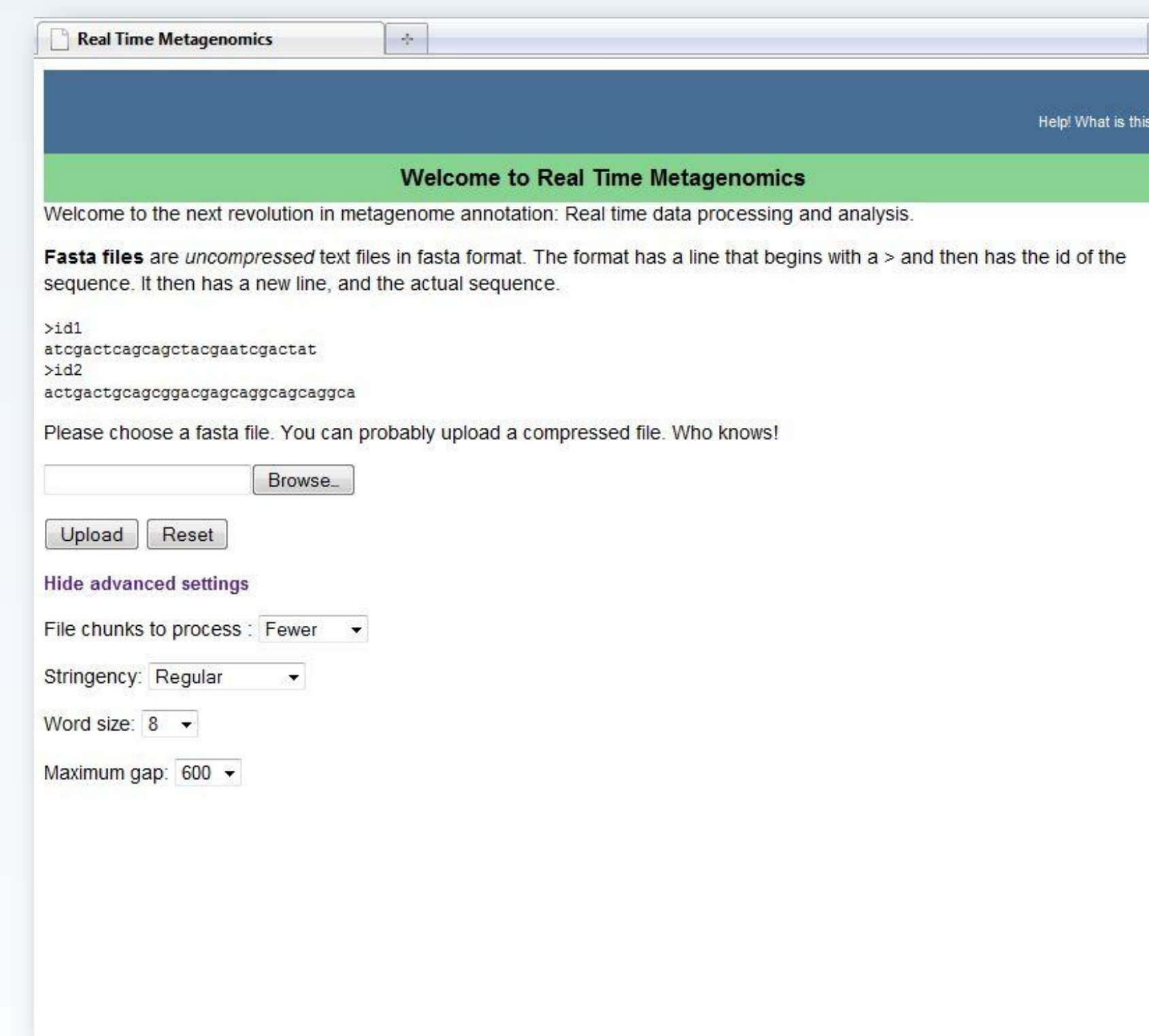
Objectives

➢ Utilize both current and new technologies to create a set of tools to use with metagenomic data.

➢ Further connect the bioinformatic community and expand their access of information.

➢ Create easy-to-use and user-friendly services to help organize and display metagenome-annotated data.

➢ Develop these services to seamlessly work together.

RTMg.web → RTMg.mob ↔ RTMg.os
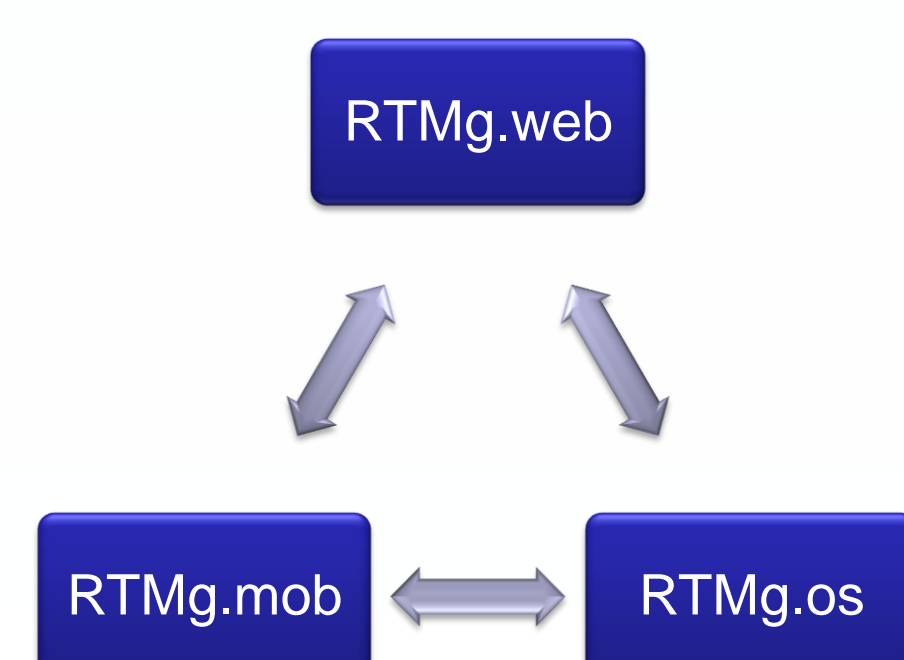
RTMg.web

The web portion of RTMg, this application allows you to upload fasta-formatted DNA sequence files. In return, the annotation results are sent back to you to examine, share and export. Then, you are able to view the protein functions, along with the different levels of subsystems found in the DNA sequences. These annotations can be stored on our server for use throughout the RTMg suite.

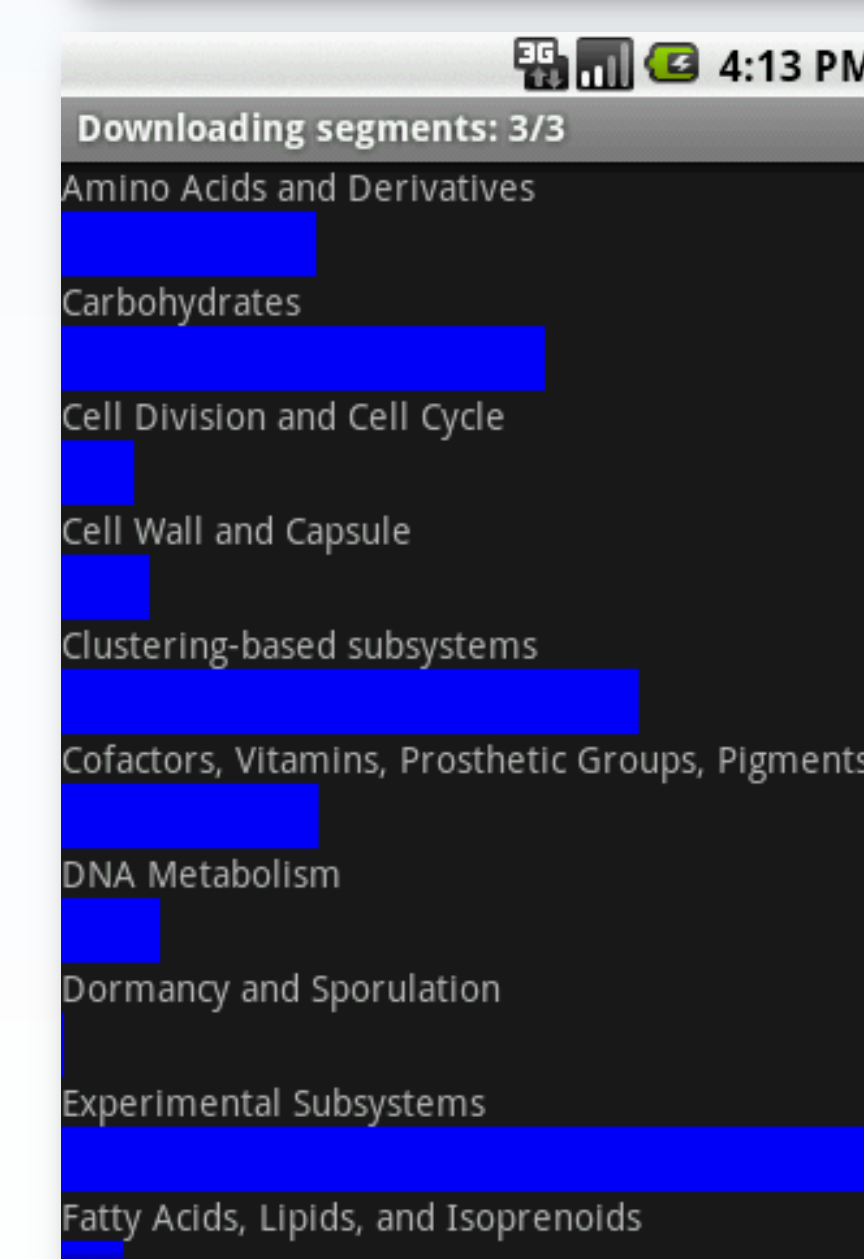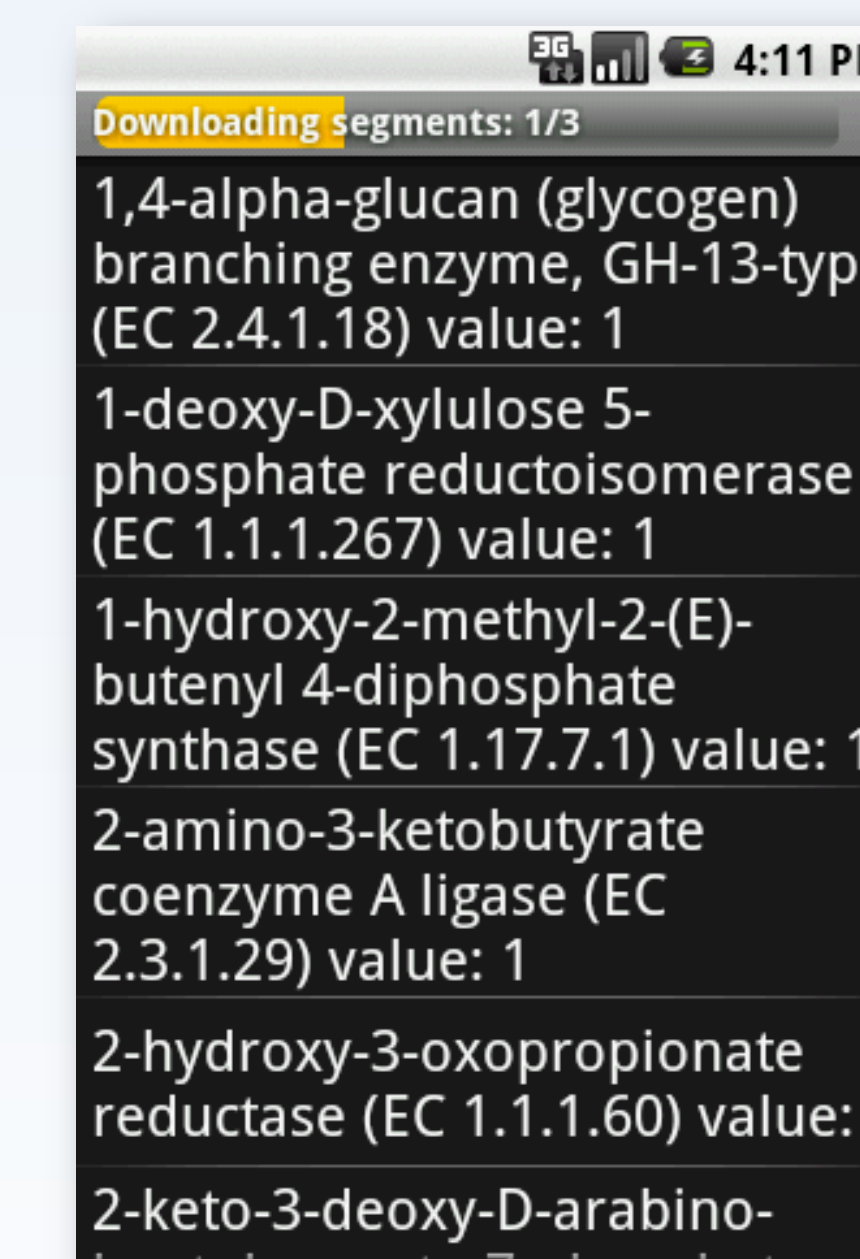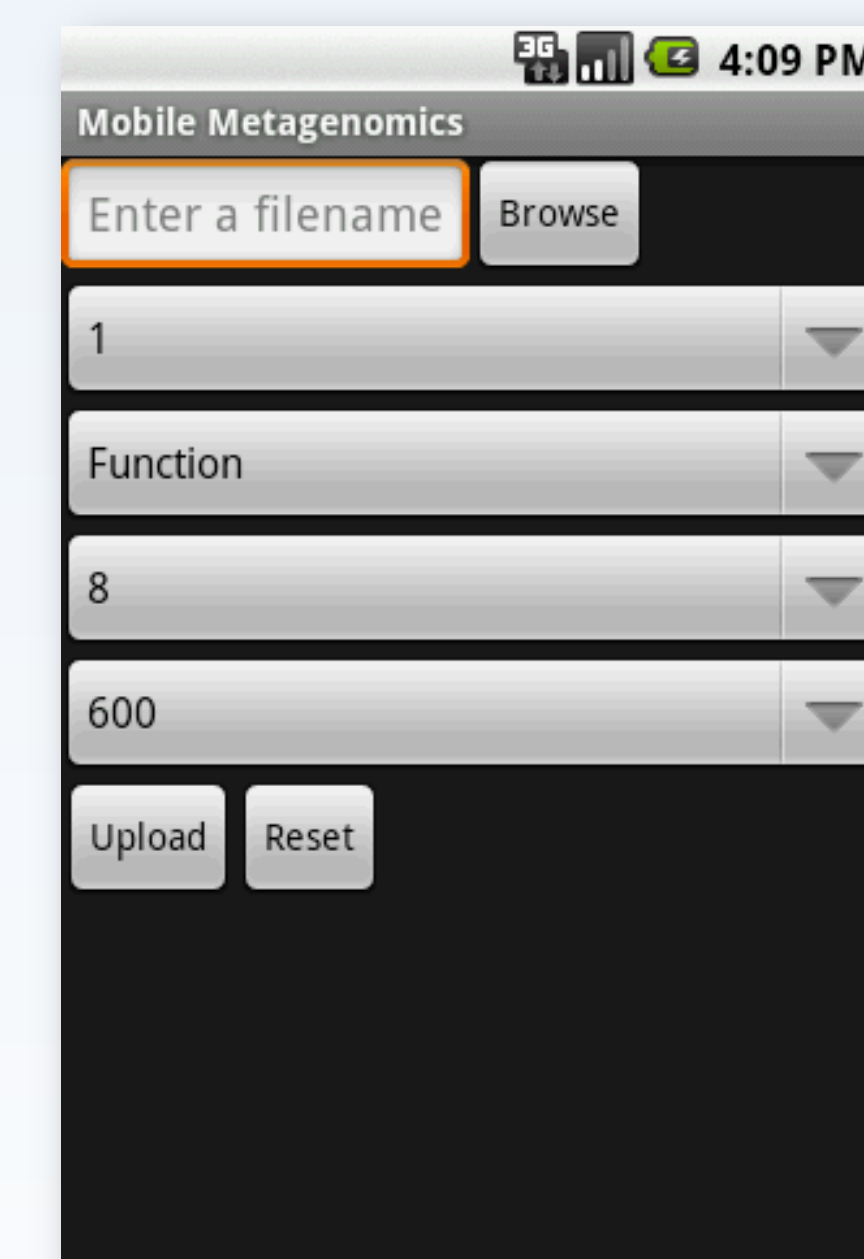| # of sequences	bp of sequence data	time to run (secs)
12,446	1,190,841	16.61
2,947	2,380,900	20.57
85,527	18,994,386	133.86
399,343	41,653,979	345.49

RTMg.mob

The mobile portion of RTMg, this Android-based application allows you to perform, view, and share your annotations right on your cell phone. RTMg.mob concurrently downloads the data letting you open other phone applications in tandem. This makes other Android applications (text message, web browsing, etc.) available for use as you wait for your annotations to finish downloading. After obtaining the annotations, you are then allowed to view the annotations in different aspects and share them via email or via our server.

Upon storing the annotations on our server, you then have a quicker mode of access to them, thus relieving you from performing the annotation process multiple times for the same sequence file.
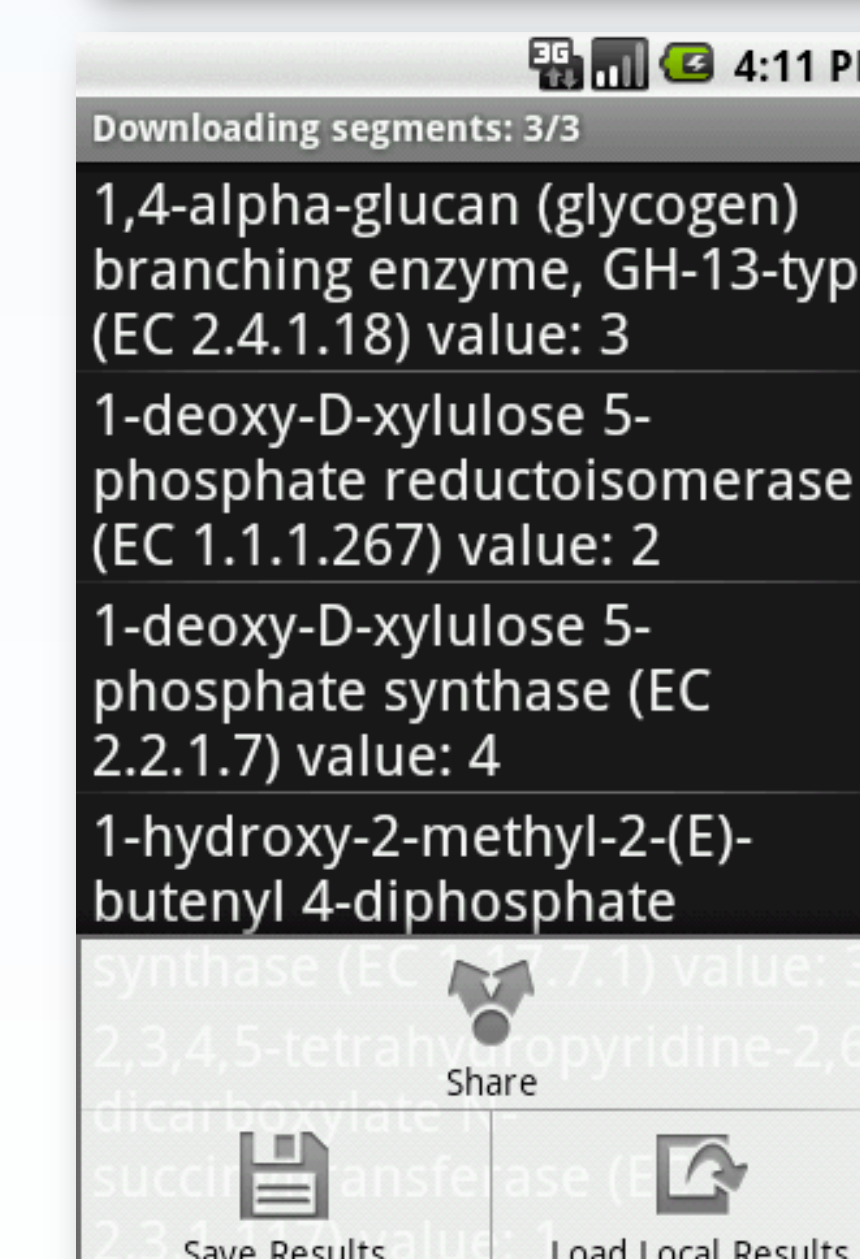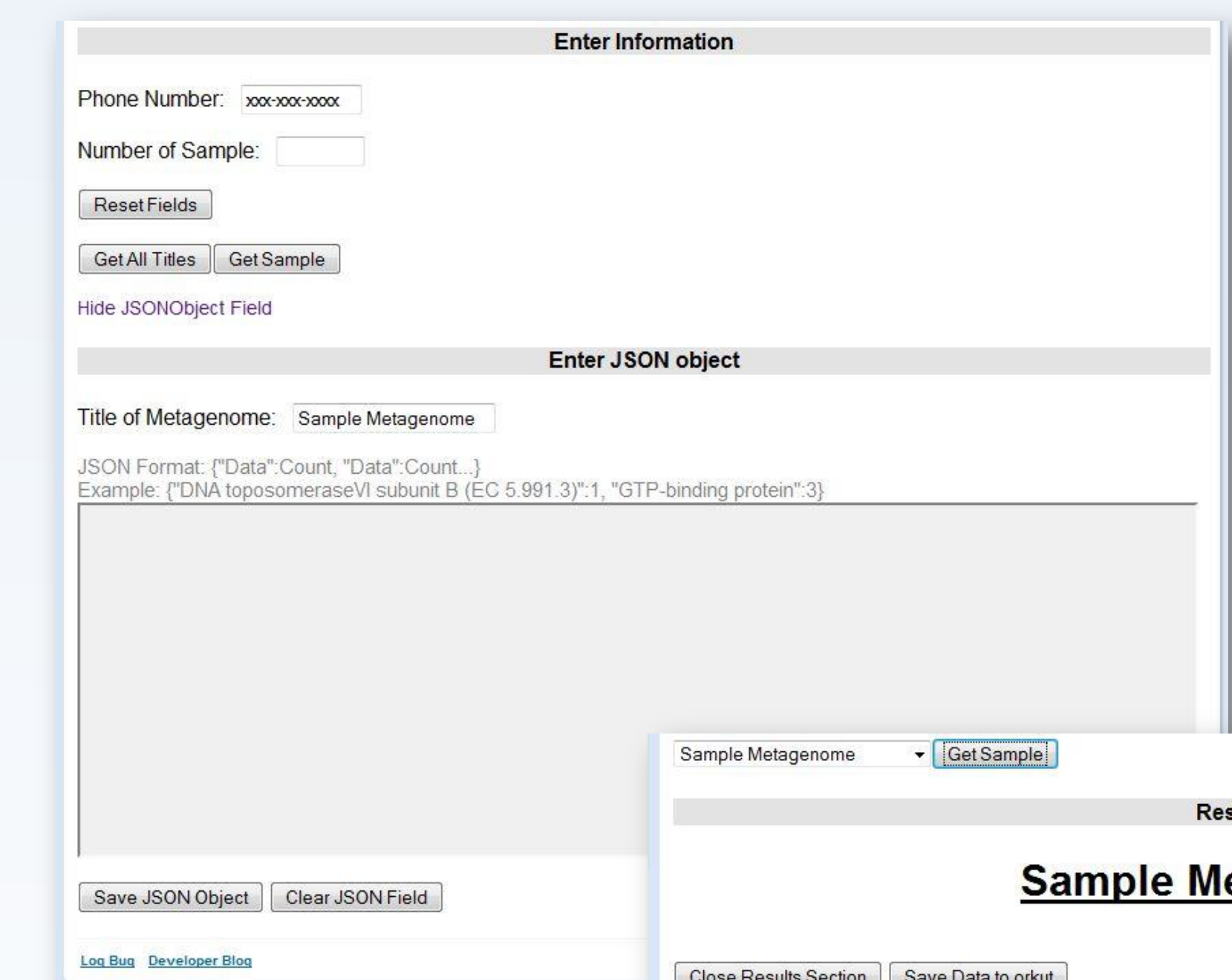
RTMg.os

The social-networking portion of RTMg, this OpenSocial-based application focuses on storing and sharing your annotated-metagenomic data from the same server used in RTMg.mob. Using Google's social network, orkut, RTMg.os brings a more social aspect to the RTMg project. It lets you display and share your data with any of your friends and colleagues.

As annotations are stored on our server they become publicly available for yourself and your friends to browse. This allows you to update your colleagues rapidly with every new metagenome you find.

SEED Website:

http://www.theseed.org/

RTMg Website:

http://edwards.sdsu.edu/rtmg