

Stylus Experiments Made Easy—A Free App for Personal Computers

Douglas D. Axe¹ and Winston Ewert²

Biologic Institute, Redmond, Washington, USA

Abstract

The Stylus model world offers intriguing parallels to the world of bacterial genetics. Combined with its computational tractability, this makes it an attractive system for evolutionary simulations. Here we describe a new app that adds ease of use to these advantages. The free Stylus app (for Mac, Windows, and Linux) brings all aspects of Stylus under the control of a simple graphical user interface and facilitates sharing of all key components of a Stylus project: genes, methods, and experiments. The ease of working with these components and of downloading data and graphics will suit both beginning and advanced users.

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¹daxe@biologicinstitute.org

²winstonewert@gmail.com

INTRODUCTION

Stylus is a model world that enables evolutionary experimentation *in silico* on objects analogous to bacterial genes and proteins [1]. At the core of the model is a rich set of structure-to-function relationships that mirror those of proteins in several respects. Instead of three-dimensional molecules capable of catalytic functions, the Stylus world is based upon two-dimensional line drawings capable of linguistic functions. Specifically, the codons in Stylus genes specify vectors from a set of twenty that, when joined end-to-end, form drawn objects called *vector proteins*. These vector proteins are functional to the extent that they resemble any of the Chinese written characters. To avoid subjective assessment of legibility, the Stylus uses an algorithm to quantify the similarity between a gene product and a given Chinese character, returning a score from 0 to 1 in a small fraction of a millisecond.

In its first implementation [1], users installed Stylus by compiling the open-source C++ code for their processor and linking the resulting executable file to a database containing character descriptions—one XML file per Chinese character. Then, to run an experiment they had to acquire an XML gene description file and hand edit another XML file containing the experimental details. With these in place, an appropriately configured terminal command launched the experiment. Output consisted of a collection of new gene XML files that were

processed with a supplied Python script, resulting in an HTML report for viewing the vector proteins produced during the run.

The prospective user of this system faced two immediate challenges, one being the absence of a convenient source of initial gene files and the other being the skills needed to perform the steps just described, which are atypical among life scientists. The first of these challenges was addressed by the publication of the first Stylus genome [2], consisting of 223 genes. The second challenge has now been addressed by developing a Stylus app that runs on personal computers, which we briefly describe here.

OVERVIEW

The new Stylus app is available as a free download [3] for Mac, Windows, and Linux users. It was built with Python, a dynamic programming language, and with Qt, a cross-platform graphical user interface framework [4]. The C++ scoring and processing engine at the heart of the new app comes from the original Stylus engine [1]. Built to take advantage of multi-core and multi-processor technology, this engine provides efficient performance that is readily scaled according to the size of the project.

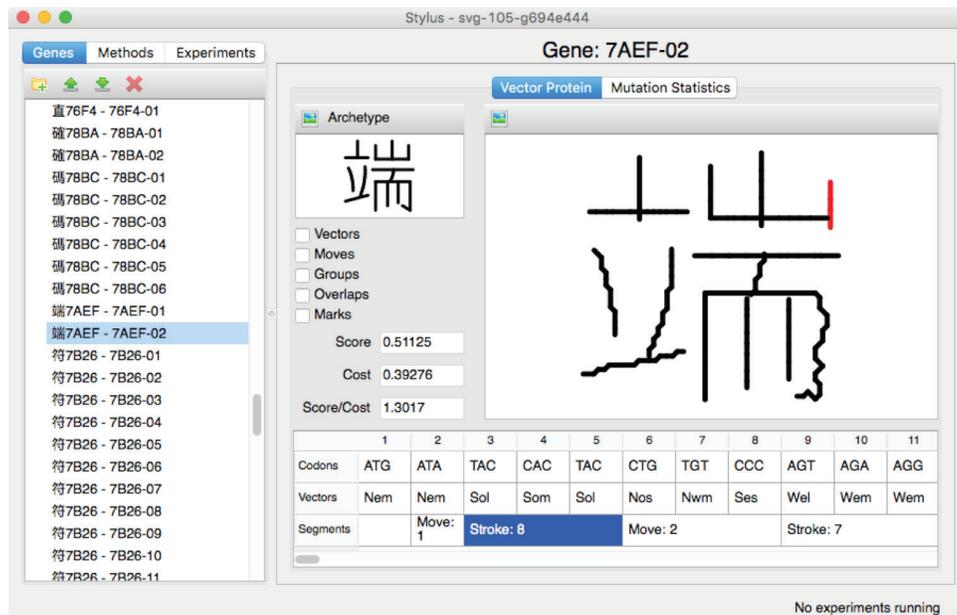


Figure 1: Screenshot of the Genes window with the Vector Protein pane selected.

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Under the headings Genes, Methods, and Experiments, the user interface presents windows that facilitate making, using, and sharing assets in these three essential categories.

WORKING WITH GENES

Clicking on the Genes tab brings up a window (Figure 1) with a panel at the left listing all 223 genes from the published genome [2] as well as any genes saved by the user. User-named folders facilitate organization of saved genes, as does drag-and-drop moving of genes between folders. Clicking on a gene in the list shows a pane with two tabs: Vector Protein and Mutation Statistics. When Vector Protein is selected, the pane gives complete information on the vector protein corresponding to the selected gene, including an interactive picture and a picture of the *archetype* (which Stylus treats as the ideal form). The whole Stylus window can be used to view this information by collapsing the Genes list on the left (dragging the right edge to the left). Check boxes to the left of the vector protein allow various structural features to be displayed, and clicking on any element in the sequence frame below highlights the corresponding portion of the vector protein. Both images (vector protein and archetype) can be downloaded in several formats by clicking the image-export icons.

The Mutation Statistics tab gives immediate access to a wealth of information on the effects of point mutations on the selected gene. Having automatically produced and scored all possible single-base substitutions, the Stylus app displays a histogram showing the distribution of effects of these mutations.

WORKING WITH METHODS

The Methods tab brings up a window for editing and viewing the specifications for one part of an experiment (each experiment consisting of one or more parts executed in order). For a typical line-of-descent experiment, each part is specified by choosing 1) the kinds of mutations that will be applied, 2) the selective criteria by which a mutant gene will be accepted as the next “point” in the line of descent, and 3) when the line should be considered complete. The Mutation Statistics option offers an exception to line-of-descent, where the user can gather statistics on the effects of mutations of any specified kind. For example, this option can be used to examine the effects of multiple simultaneous mutations. As with the Genes window, a list of methods on the left facilitates housekeeping, but here the addition of an icon for duplicating the selected method enables users to quickly base a new method on an existing one.

WORKING WITH EXPERIMENTS

Finally, the Experiments tab brings up a window for setting up and launching experiments and for viewing the results. Clicking on the + icon adds a new experiment to the list and brings up a pane with tabs labeled Data and Plan. The Data tab is active only after an experiment is run. The Plan tab enables the user to choose one or more methods to be run in order on one or more genes. This is done by dragging and dropping genes from the Genes list into the upper pane and methods from the Methods list into the lower pane. For example, Figure

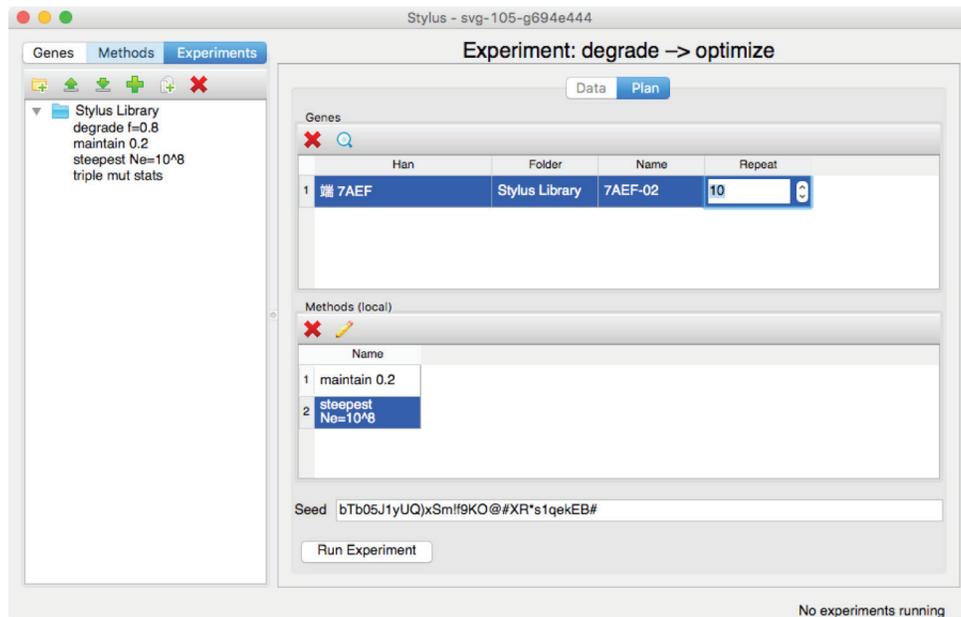


Figure 2: Screenshot of the Experiments window during plan construction. doi:10.5048/BIO-C.2016.1.f2

2 shows an experimental plan that applies a method called “degrade $f=0.8$ ” to gene 89D2-01 from the Stylus Library folder. A second method, called “steepest $N_e=10^8$,” is then applied to the gene produced by the first method. Any number of methods can be applied in succession, each one starting with the final gene from the prior method. Likewise, the ordered methods can be applied to any number of genes. As the Repeat setting in Figure 2 shows, a given set of methods may also be applied to the same gene multiple times, enabling the user to

see how much variability is caused from one run to the next by stochastic factors.¹

Clicking Run Experiment automatically switches from the Plan tab to the Data tab, where an interactive graph (powered by PyQtGraph [5]) displays results as they are being computed (Figure 3). The ability to move and scale plotted data

¹ As with all computational models, a seeded pseudo-random number generator is the determinant of these “chance” effects.

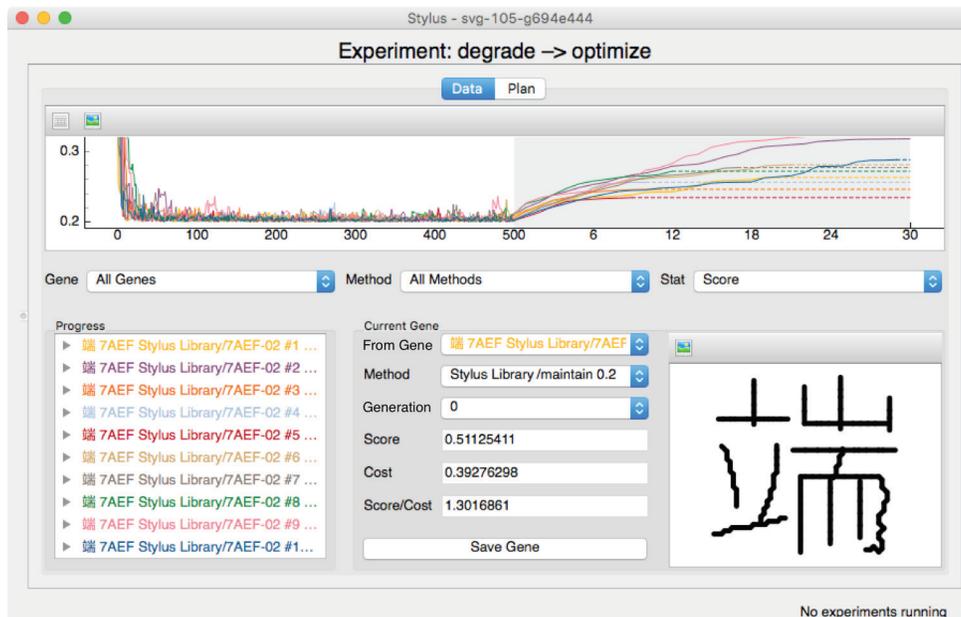


Figure 3: Screenshot of the Data pane of Experiments window after executing the experimental plan shown in Figure 2. The same experiment run on the same initial gene produces distinguishable results in each of the ten trials, as would be the case in a laboratory experiment. doi:10.5048/BIO-C.2016.1.f3

by dragging and scrolling makes it easy to view any region of interest at the desired magnification. Control over which runs are visible (one or all) is provided by the Gene dropdown menu. Any gene produced in the experiment can be selected either by clicking on the graph or by choosing the desired initial gene (using the From Gene pull-down) and Generation in the Current Gene pane. The selected gene can then be saved to any folder in the Genes list by clicking Save Gene.

Additionally, all data and graphics can be exported by clicking on the appropriate icon.

USERS AND USES

We anticipate that the major improvement in ease of use brought about by this new app will attract new users among professional researchers, teachers and students. A growing user base will help us attract funding for future development while keeping Stylus free to the end user.

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