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Similar to other genome browsers, TrawlerWeb supports the use of alternative gene names. For example, the same gene in an organism may be alternatively named in a number of ways such as *Homo sapiens* and *Homo sapiens sapiens*. Likewise, the same gene may also be annotated by multiple identifiers in the same species. While users can select and search among all three name types, the main purpose of gene organisation pages is to search and display all available data for a specific gene of interest. Users are free to explore gene organisation pages using either standard web browsers or TrawlerWeb directly. The TrawlerWeb client integrates into a web browser directly or can be downloaded as a client application to be used on its own, without requiring a web browser.

TrawlerWeb is intended to work on a web browser using an HTTP server. As of August 2018, it requires a web browser compatible with HTML5 to view TrawlerWeb pages. However, TrawlerWeb can be used to view the basic TrawlerWeb webpage, including in browsers and web servers that do not support HTML5. The Google Trends API allows you to download historical time-series data in XML format. This XML format is an interoperable format, based on the W3C Web Services Description Language (WSDL) 1.1, and can be read using a variety of tools. The utility is implemented as a Perl CGI script, with perl-base 5.24 or higher required on the user's computer. The interface is written in CGI.pm and uses CGI.pm methods to generate HTML pages, as well as the LwpQR code generator from qr-tools to generate the terminal flowchart. We have used customized versions of Unix tools such as uudecode and wget to allow users to download TrawlerWeb to their machines and run commands through the web interface. Additionally, for the command line interface, we have implemented the phantomJS browser and used it to construct the flowchart, with users able to modify the output by editing the terminal code manually, in addition to its generated version.

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As annotations for transcription factors are not available for many organisms, appropriate organisms can be selected for uploading in the web form by selecting from the organisms present in the TrawlerWeb database. This query can be improved by submitting an EnSEMBL query to retrieve genes with one or more expression tracks. In TrawlerWeb v1.0, results contain annotations where expression data were mapped to the transcript (mRNA

or ncRNA) corresponding to the furthest upstream transcription start site (transcription start site (TSS) of the transcript) where the expression track displayed the lowest level of expression, whenever possible. When multiple transcripts are annotated and display the same level of expression, TrawlerWeb draws upon their coding capacity (transcript length) to prioritise the first transcript. Expression levels are calculated using EnSEMBL's BioMart, which utilises local computations whenever possible and returns a value close to the most recent

genome assembly available [29]. Local computation of expression levels of the transcripts reported in the current analysis are described in more detail in the Assay page and are based on calculations using the STAR aligner [30] (version 2.5.2). Results can also be generated using default settings with no parameter modifications to facilitate comparisons of the effect of each parameter on search performance. Users can also access the complete dataset for download. This dataset contains the original FASTA sequence and

all calls to the BioMart to collect genomic coordinates and protein annotation for each transcript included. Regions can then be selected as necessary for the analysis of interest or, alternatively, gene lists can be generated using the TrawlerWeb FastQGatherer tool, which randomly selects specific regions for analysis [31]. The transcriptome data for each organism is thus generated by selecting or customising selected regions according to each users specific analysis needs. The FastQGatherer tool, available to all users, is a user-friendly way

for users to generate their own
gene lists for analysis in either
bed or BED format. 5ec8ef588b

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