

MAP2COV: Convert NGS data guide

MAP2COV is a free converter of NGS alignments file
It has been developed by the Laboratoire Pathogénèse des
Bactéries Anaérobies of the Institut Pasteur.

<http://cov2html.sourceforge.net/>

« One Click » graphical interface Tcl/Tk



Windows

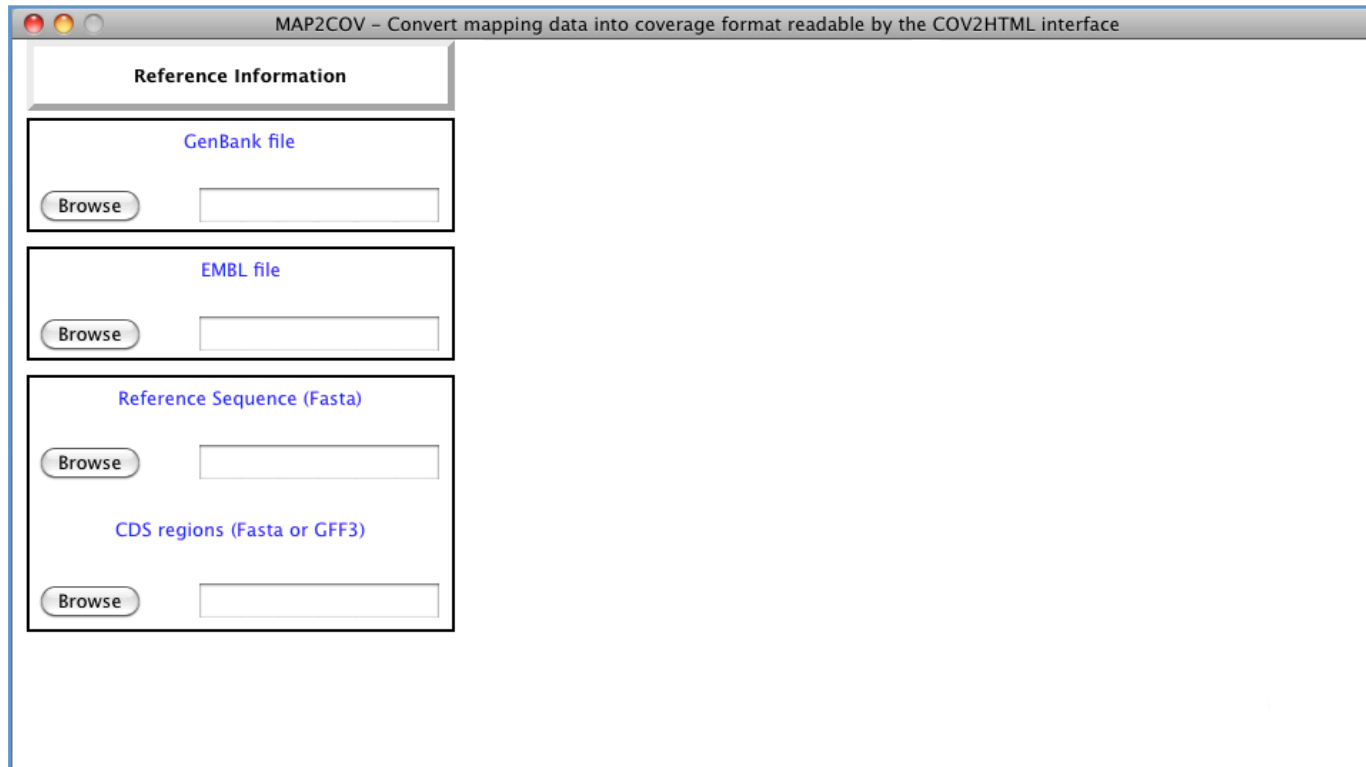


MacOSX

Command line graphical interface Tcl/Tk



Linux



The screenshot shows a web browser window titled "MAP2COV - Convert mapping data into coverage format readable by the COV2HTML interface". The main content area is titled "Reference Information" and contains four distinct input sections, each with a "Browse" button and a text input field:

- GenBank file**: A section for uploading a GenBank file.
- EMBL file**: A section for uploading an EMBL file.
- Reference Sequence (Fasta)**: A section for uploading a reference sequence in Fasta format.
- CDS regions (Fasta or GFF3)**: A section for uploading CDS regions in either Fasta or GFF3 format.

Reference Information

A file containing the annotated reference sequence previously used for the mapping assembly, it can be in [GenBank](#), [EMBL](#) format or two files, a file containing the [reference sequence](#) in Fasta format associated with a file containing [CDS regions](#) annotations in gff3 format or features nucleotide sequence in fasta format.

The screenshot shows a web browser window titled "MAP2COV - Convert mapping data into coverage format readable by the COV2HTML interface". The main content area is titled "Alignment File" and contains four stacked sections for file selection:

- SAM/BAM file:** A "Browse" button followed by an empty text input field.
- ELAND file:** A "Browse" button followed by an empty text input field.
- WIG file:** A "Browse" button followed by an empty text input field.
- Data type:** Four radio button options: DNA, RNA, TSS, and ChIP.

Alignment File

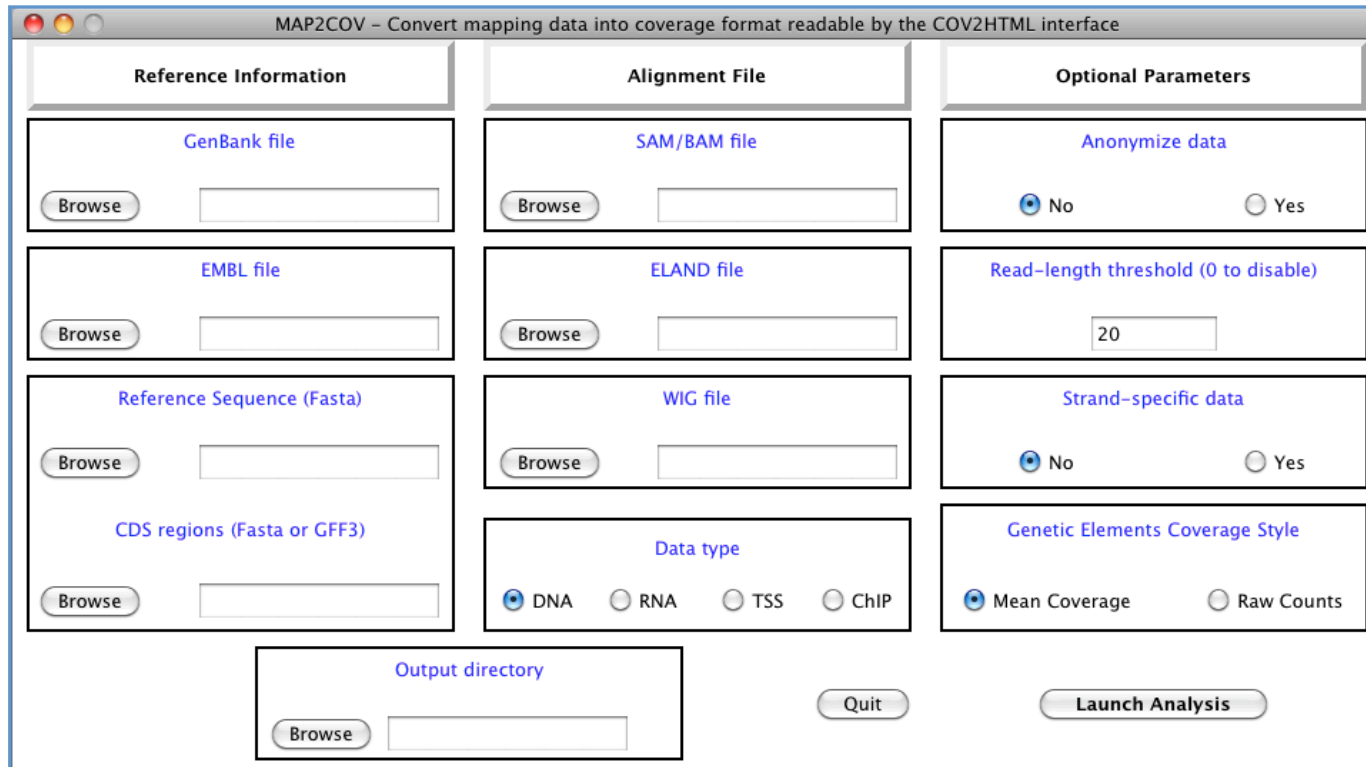
An alignment map file in 'SAM'/'BAM', 'ELAND' or 'WIG' format. Then users have to select the **data type** contained in the alignment file, '**DNA**' (DNA-seq), '**RNA**' (RNA-seq), '**TSS**' (Transcriptional Start Site) or **ChIP** (Chromatine Immunoprecipitation).

The screenshot shows a web browser window titled "MAP2COV - Convert mapping data into coverage format readable by the COV2HTML interface". The main content area is empty. On the right side, there is a panel titled "Optional Parameters" containing four sections:

- Anonymize data**: A radio button labeled "No" is selected, and a radio button labeled "Yes" is unselected.
- Read-length threshold (0 to disable)**: A text input field contains the value "20".
- Strand-specific data**: A radio button labeled "No" is selected, and a radio button labeled "Yes" is unselected.
- Genetic Elements Coverage Style**: A radio button labeled "Mean Coverage" is selected, and a radio button labeled "Raw Counts" is unselected.

Optional Parameters

Anonymize data (default: **No**): replace ID of genes with unique identifiers numbered from the origin and remove their description. **Read-length threshold** (default: **20** bp): remove reads from the alignment file shorter than the threshold. **Strand-specific data** (default: **No**): generate two strand-specific files from the alignment. **Genetic Elements Coverage Style** (default: Mean Coverage): coverage of genes and intergenic regions is calculated either as the **Mean coverage** or as the number of read that match on them (**Raw Counts**).



MAP2COV Tcl/Tk graphical interface.

Reference information: GenBank, EMBL file or Genome and Annotation files.

Alignment File: SAM/BAM, Eland or Wig files. Data type: DNA, RNA, TSS, ChIP.

Optional Parameters: Anonymize, Read-length, Strand-specific or Genetic Elements Coverage Style.