genotypst: A bioinformatics Typst package for sequence analysis and visualization

`genotypst` is a bioinformatics package for Typst that enables analysis and visualization of biological data. It provides functionality for parsing FASTA and Newick files and generating publication-ready visualizations, including multiple sequence alignments, sequence logos, genome maps, and phylogenetic trees.

Contents

Working with sequence data

`genotypst` provides functions to parse sequence data and produce different visualizations.

Loading data

The `parse-fasta` function reads FASTA data and returns a dictionary mapping sequence identifiers to their corresponding sequences.

```
#let sequences = parse-fasta(read("/docs/data/dna.fna"))
```

```
(
  seq_1: "AAGGGACACTGATTTTCTCCCACAGCTGGGCCGTGGACCGTAGTGTTTCAAGAAGCCCACACAC",
  seq_2: "GCAATGGAGACAACATAGCCAACTACCTACTAGATGGCCTAGATCTGCCGCA",
  seq_3: "GGAACTGGCGTTACAGACAGTTGTGAGCCACCACATGGGCCTGGGATTTAAATATTATAAAGCTCCTC",
)
```

FASTA rendering

Use `render-fasta` to display sequences in the standard FASTA format.

```
#render-fasta(sequences, max-width: 50)
```

```
>seq_1
AAGGGACACTGATTTTCTCCCACAGCTGGGCCGTGGACCGTAGTGTTTCA
AGAAGCCCACACAC
>seq_2
GCAATGGAGACAACATAGCCAACTACCTACTAGATGGCCTAGATCTGCCG
CA
>seq_3
GGAACTGGCGTTACAGACAGTTGTGAGCCACCACATGGGCCTGGGATTTA
AATATTATAAAGCTCCTC
```

In this example, `max-width` controls how many characters appear per line (default is 60).

Multiple sequence alignments

The `render-msa` function displays multiple sequence alignments with optional residue coloring and conservation bars.

In the example below:

- `colors: true` enables residue coloring based on biochemical properties.
- `conservation: true` adds conservation bars above the alignment.
- `start: 100` and `end: 160` limit the display to a specific region of interest (residues 100 to 160).

```
#let protein_msa = parse-fasta(read("/docs/data/msa.afa"))

#render-msa(
  protein_msa,
  start: 100,
  end: 160,
  colors: true,
  conservation: true,
)
```

Figure 1. MSA visualization for positions 100–160, with residue coloring and conservation bars enabled.

Residue coloring represents amino acid physicochemical properties. The sequence alphabet (amino acid, DNA, or RNA) is determined automatically and a suitable color palette is applied.

The bars above the alignment indicate the degree of conservation at each column.

Sequence logos

Sequence logos[1] summarize conservation patterns within a sequence alignment and are commonly used to visualize binding sites, motifs, and functional domains. In a sequence logo, the total height of each stack represents the information content (in bits) at that position, while the height of individual letters reflects their relative frequencies.

In the example below, we visualize the same region as the MSA of the previous section (positions 100 to 160).

```
#render-sequence-logo(protein_msa, start: 100, end: 160)
```

Figure 2. Sequence logo for positions 100–160, showing conservation and residue frequency.

Like `render-msa`, `render-sequence-logo` automatically applies the appropriate color palette based on the sequence alphabet.

Color palettes

`genotypst` uses predefined color palettes to assign colors to sequence residues.

Amino acid palette

Amino acids are colored according to their physicochemical properties. Grouping residues by color helps reveal the chemical nature of conserved positions (e.g., whether a position is consistently hydrophobic or charged), which is often important for understanding protein structure, function, and evolution.

Hydrophobic

Alanine	Ala	A	#4d78ff
Histidine	His	H	#4d78ff
Isoleucine	Ile	I	#4d78ff
Leucine	Leu	L	#4d78ff
Methionine	Met	M	#4d78ff
Valine	Val	V	#4d78ff

Polar

Serine	Ser	S	#00c990
Threonine	Thr	T	#00c990
Glutamine	Gln	Q	#00c990
Asparagine	Asn	N	#00c990

Aromatic

Phenylalanine	Phe	F	#bac1d2
Tryptophan	Trp	W	#bac1d2
Tyrosine	Tyr	Y	#bac1d2

Negatively charged

Aspartic acid	Asp	D	#ff07b8
Glutamic acid	Glu	E	#ff07b8

Positively charged

Lysine	Lys	K	#e51f3e
Arginine	Arg	R	#e51f3e

Cysteine

Cysteine	Cys	C	#494e5b

Glycine

Glycine	Gly	G	#f59116

Proline

Proline	Pro	P	#dce100

Nucleic acid palettes

The DNA and RNA palettes assign a distinct color to each nucleotide.

DNA palette			RNA palette		
Adenine	A	#00c990	Adenine	A	#00c990
Cytosine	C	#4d78ff	Cytosine	C	#4d78ff
Guanine	G	#ff07b8	Guanine	G	#ff07b8
Thymine	T	#f59116	Uracil	U	#f59116

Visualizing genomic loci with genome maps

Genome maps enable visualization of the genes and other genomic elements within a locus, highlighting their order, orientation, and length. `genotypst` provides a `render-genome-map` function that produces a genome map from an array of dictionaries, each representing a genomic feature that will be plotted:

- `start` (required): Start coordinate.
- `end` (required): End coordinate.
- `strand`: Feature orientation (`1` or `"+"` for the positive strand, `-1` or `"-"` for the negative strand). `none` draws an undirected block.
- `label`: Feature label
- `color`: Fill color.

```
#let f_plasmid_locus = (
  (start: 65556, end: 66065, strand: -1, label: [_ygfA_]),
  (start: 66118, end: 66407, label: [_oriT_], color: rgb("#696975")),
  (start: 66479, end: 66862, strand: 1, label: [_traM_], color: rgb("#62B9F2")),
  (start: 66977, end: 67055, strand: -1, label: [_finP_]),
  (start: 67049, end: 67738, strand: 1, label: [_traJ_], color: rgb("#F7ED6C")),
  (start: 67837, end: 68232, strand: 1, label: [_traY_]),
  (start: 68265, end: 68630, strand: 1, label: [_traA_]),
  (start: 68645, end: 68956, strand: 1, label: [ _traL_]),
  (start: 68978, end: 69544, strand: 1, label: [_traE_]),
)

#render-genome-map(
  f_plasmid_locus,
  coordinate-axis: true,
  unit: "bp",
)
```

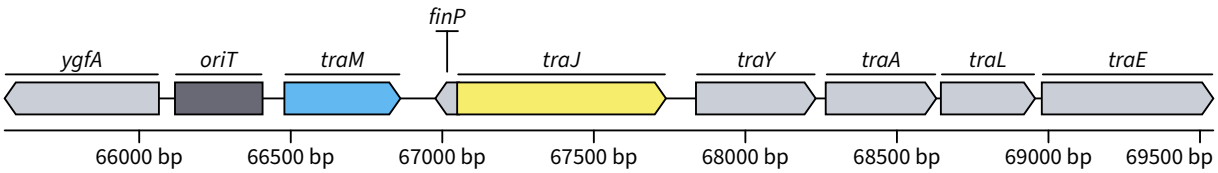


Figure 3. Genome map showing the genes within the 65,556–69,544 bp region of the F plasmid of *Escherichia coli* K-12 (GenBank: AP001918.1).

Working with phylogenetic trees

`genotypst` includes functions to parse and render phylogenetic trees. Trees can be created by parsing Newick-formatted strings with `parse-newick` or by manually constructing nested dictionary structures.

```
#let parsed_newick_tree = parse-newick(
  "(('Leaf A':0.2,'Leaf B':0.1)'Internal node':0.3,'Leaf C':0.6)Root;"
)

#let manual_tree = (
  rooted: true,
  name: "Root",
  length: none,
  children: (
    (
      name: "Internal node",
      length: 0.3,
      children: (
        (name: "Leaf A", length: 0.2, children: none),
        (name: "Leaf B", length: 0.1, children: none),
      ),
    ),
    (name: "Leaf C", length: 0.6, children: none),
  ),
)
```

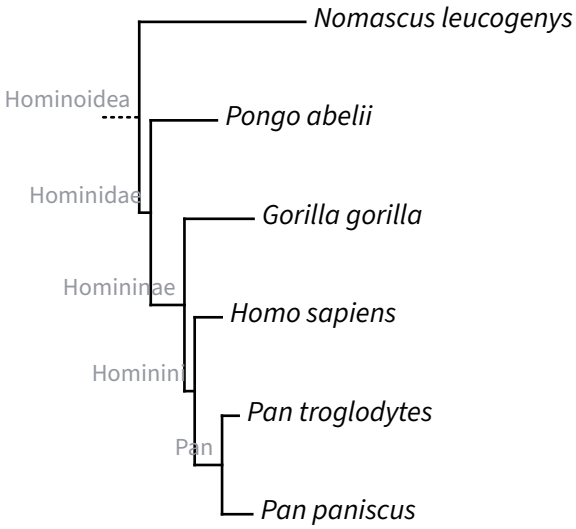
Visualizing trees

`genotypst` can produce visualizations of phylogenetic trees. To illustrate this, we will read and render a Newick file containing a phylogeny of the *Hominoidea* superfamily, which was extracted from the Ensembl Compara species tree[2].

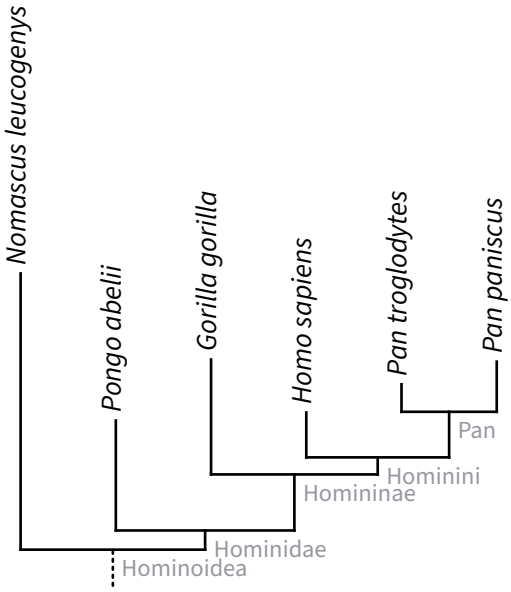
```
#let hominoidea_tree = parse-newick(read("/docs/data/hominoidea.nwk"))
```

To render the tree, use the `render-tree` function. By default, it produces a horizontal rectangular dendrogram, but a vertical layout can be specified using the `orientation: "vertical"` option.

```
#render-tree(hominoidea_tree, tip-label-italics: true, orientation:
"horizontal")
#render-tree(hominoidea_tree, tip-label-italics: true, orientation: "vertical")
```



Tree with horizontal orientation



Tree with vertical orientation

Customizing visualizations

Font selection

By default, `render-fasta` and `render-msa` inherit the monospaced font used for raw text in your document. To use a different font, wrap the rendering function in a `context` block with a custom font for raw text.

```
#let dna_msa = (
  "seq1": "AGTCTCAAGATAACTTTCGAAACAAACTTC",
  "seq2": "AGTTTCCAAGTGGATTTGGAATTGAACTTT",
  "seq3": "ACTCT-CGGATGGATTCGGATACAAACTTT",
  "seq4": "AGTCT---GATTGATGTGGATACAAACTTC",
  "seq5": "AGTCT--GGGTGGATTTGG-AACAAATTTT",
  "seq6": "CAGTGCTCCCTGGTGGTGG-ACCATCTTAC",
  "seq7": "AGTCTCAAGACGGATACTG--ATGCCCTAT",
)

#context {
  show raw: set text(font: "Maple Mono")
  render-msa(dna_msa)
}
```

```
seq1    AGTCTCAAGATAACTTTCGAAACAAACTTC
seq2    AGTTTCCAAGTGGATTTGGAATTGAACTTT
seq3    ACTCT-CGGATGGATTCGGATACAAACTTT
seq4    AGTCT---GATTGATGTGGATACAAACTTC
seq5    AGTCT--GGGTGGATTTGG-AACAAATTTT
seq6    CAGTGCTCCCTGGTGGTGG-ACCATCTTAC
seq7    AGTCTCAAGACGGATACTG--ATGCCCTAT
```

Default document font for raw text

```
seq1    AGTCTCAAGATAACTTTCGAAACAAACTTC
seq2    AGTTTCCAAGTGGATTTGGAATTGAACTTT
seq3    ACTCT-CGGATGGATTCGGATACAAACTTT
seq4    AGTCT---GATTGATGTGGATACAAACTTC
seq5    AGTCT--GGGTGGATTTGG-AACAAATTTT
seq6    CAGTGCTCCCTGGTGGTGG-ACCATCTTAC
seq7    AGTCTCAAGACGGATACTG--ATGCCCTAT
```

Custom font (Maple Mono)

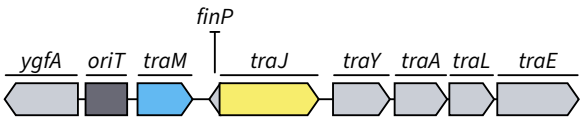
Sequence logos, genome maps, and trees are rendered using the default document font, rather than the monospaced font for raw text. To specify a custom font sequence logos and trees, use a `show text` rule instead.

```
#context {
  show text: set text(font: "Libertinus Serif")
  render-sequence-logo(dna_msa)
}
```

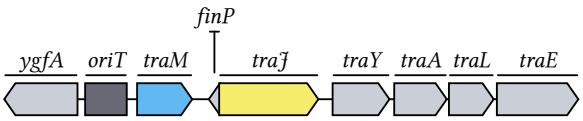
Default document font

Custom font (Libertinus Serif)

```
#context {
  show text: set text(font: "Libertinus Serif")
  render-genome-map(f_plasmid_locus)
}
```

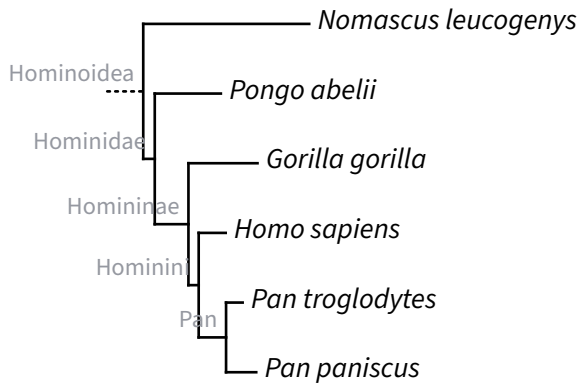


Default document font

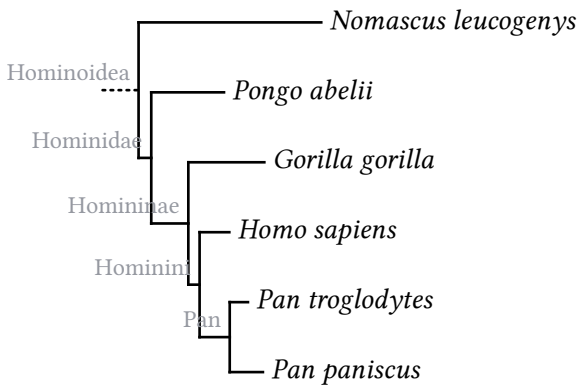


Custom font (Libertinus Serif)

```
#let hominoidea_tree = parse-newick(read("/docs/data/hominoidea.nwk"))
#context {
  show text: set text(font: "Libertinus Serif")
  #render-tree(hominoidea_tree, tip-label-italics: true)
}
```



Default document font



Custom font (Libertinus Serif)

Bibliography

1. Schneider, T. D. & Stephens, R. Sequence logos: a new way to display consensus sequences. *Nucleic Acids Research* **18,** 6097–6100 (1990).
2. Herrero, J. *et al.* Ensembl comparative genomics resources. *Database* **2016,** bav96 (2016).