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, and phylogenetic trees.

Contents

Working with sequence data

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

Loading data

The `parse-fasta-file` function reads FASTA files 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

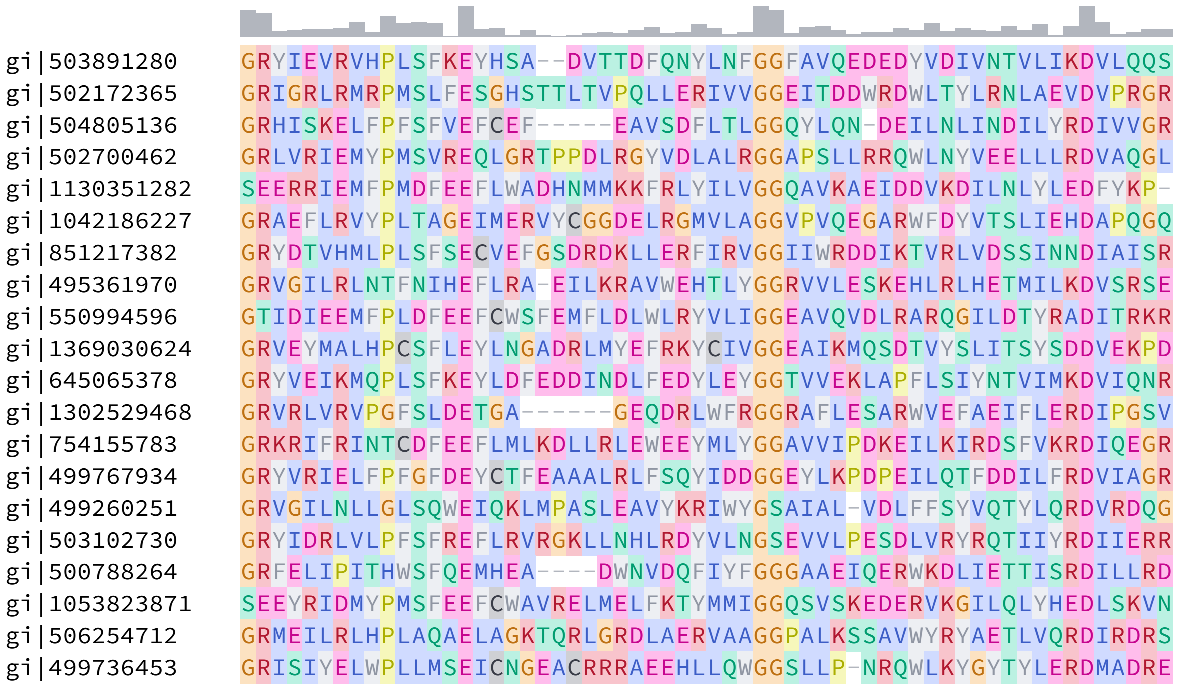
The `render-msa` function displays multiple sequence alignments with optional residue coloring and conservation bars.

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,
)
```



```
gi|503891280    GRYIEVRVHPLSFKEYHSA--DVTTDFQNYLNFGGFAVQEDEDYVDIVNTVLIKDVLQQS
gi|502172365    GRIGRLRMRPMSLFESGHSTTLTVPQLLERIVVGGEITDDWRDWLTYLRNLAEVDVPRGR
gi|504805136    GRHISKELFPFSFVEFCEF-----EAVSDFLTLGGQYLQN-DEILNLINDILYRDIVVGR
gi|502700462    GRLVRIEMYPMSVREQLGRTPPDLRGYVDLALRGGAPSLLRRQWLNYVEELLLRDVAQGL
gi|1130351282   SEERRIEMFPMDFEEFLWADHNMMKKFRLYILVGGQAVKAEIDDVKDILNLYLEDFYKP-
gi|1042186227   GRAEFLRVYPLTAGEIMERVYCGGDELRGMVLAGGVPVQEGARWFDYVTSLIEHDAPQGQ
gi|851217382    GRYDTVHMLPLSFSECVEFGSDRDKLLERFIRVGGIIWRDDIKTVRLVDSSINNDIAISR
gi|495361970    GRVGILRLNTFNIHEFLRA-EILKRAVWEHTLYGGRVVLESKEHLRLHETMILKDVSRSE
gi|550994596    GTIDIEEMFPLDFEEFCWSFEMFLDLWLRYVLIGGEAVQVDLRARQGILDTYRADITRKR
gi|1369030624   GRVEYMALHPCSFLEYLNGADRLMYEFRKYCIVGGEAIKMQSDTVYSLITSYSDDVEKPD
gi|645065378    GRYVEIKMQPLSFKEYLDFEDDINDLFEDYLEYGGTVVEKLAPFLSIYNTVIMKDVIQNR
gi|1302529468   GRVRLVRVPGFSLDETGA------GEQDRLWFRGGRAFLESARWVEFAEIFLERDIPGSV
gi|754155783    GRKRIFRINTCDFEEFLMLKDLLRLEWEEYMLYGGAVVIPDKEILKIRDSFVKRDIQEGR
gi|499767934    GRYVRIELFPFGFDEYCTFEAAALRLFSQYIDDGGEYLKPDPEILQTFDDILFRDVIAGR
gi|499260251    GRVGILNLLGLSQWEIQKLMPASLEAVYKRIWYGSAIAL-VDLFFSYVQTYLQRDVRDQG
gi|503102730    GRYIDRLVLPFSFREFLRVRGKLLNHLRDYVLNGSEVVLPESDLVRYRQTIIYRDIIERR
gi|500788264    GRFELIPITHWSFQEMHEA----DWNVDQFIYFGGGAAEIQERWKDLIETTISRDILLRD
gi|1053823871   SEEYRIDMYPMSFEEFCWAVRELMELFKTYMMIGGQSVSKEDERVKGILQLYHEDLSKVN
gi|506254712    GRMEILRLHPLAQAELAGKTQRLGRDLAERVAAGGPALKSSAVWYRYAETLVQRDIRDRS
gi|499736453    GRISIYELWPLLMSEICNGEACRRRAEEHLLQWGGSLLP-NRQWLKYGYTYLERDMADRE
```

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)
```

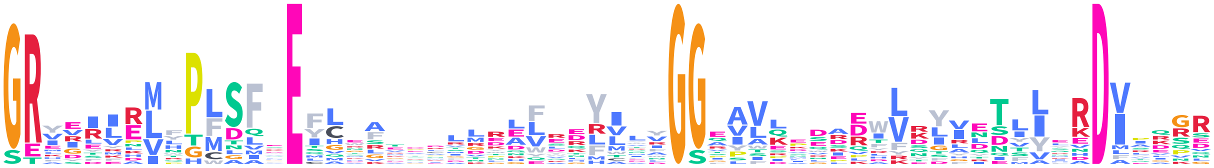


Figure 2. Sequence logo for positions 100–160, showing conservation and residue frequency.

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

Adenine	A	#00c990
Cytosine	C	#4d78ff
Guanine	G	#ff07b8
Thymine	T	#f59116

RNA palette

Adenine	A	#00c990
Cytosine	C	#4d78ff
Guanine	G	#ff07b8
Uracil	U	#f59116

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),
  ),
)
```

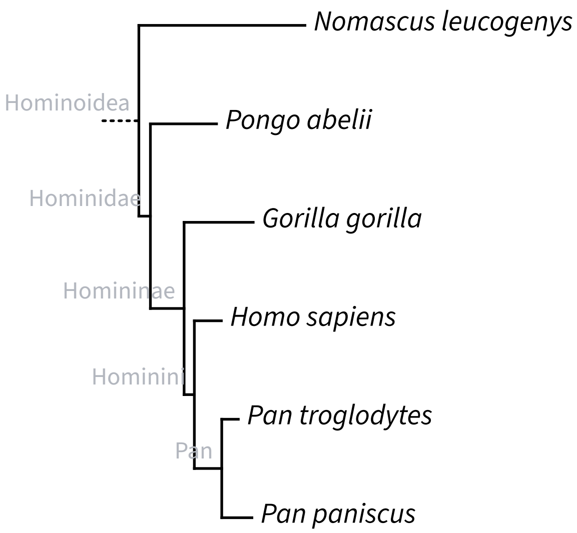
Visualizing trees

`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].

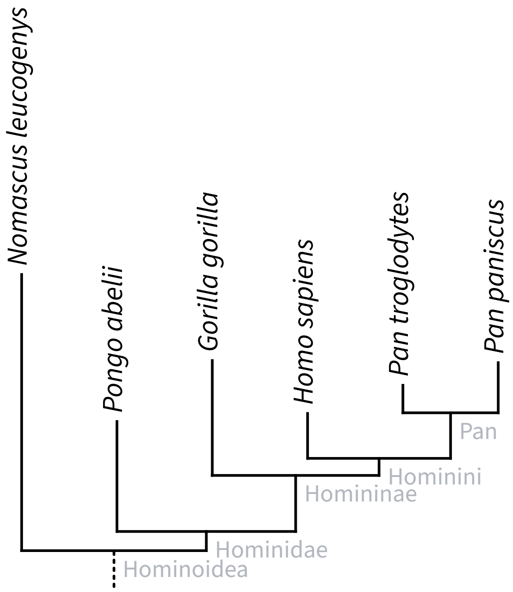
```
#let hominoidea_tree = parse-newick(read("/docs/data/hominoidea.nwk"))
```

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
```

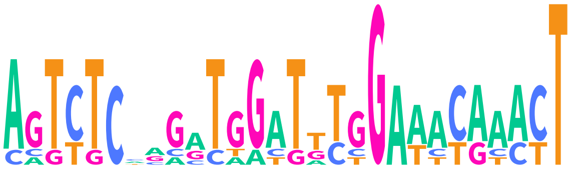
Default document font for raw text

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

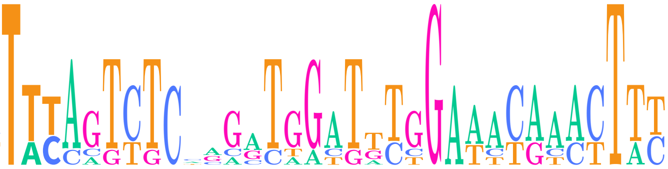
Custom font (Maple Mono)

Sequence logos 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: "New Computer Modern")
  render-sequence-logo(dna_msa)
}
```

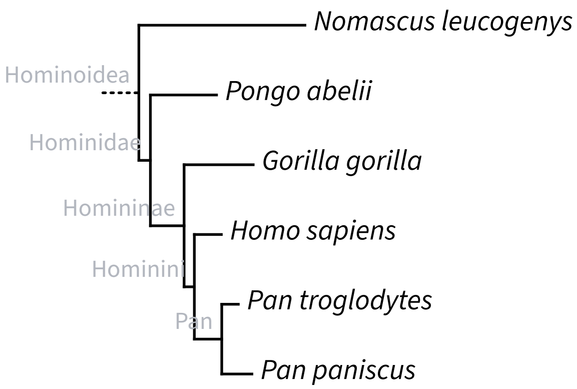


Default document font

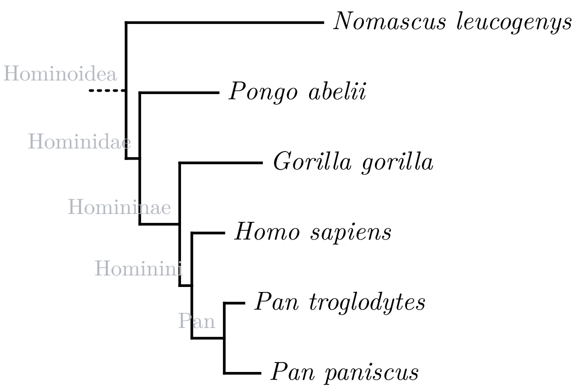


Custom font (New Computer Modern)

```
#let hominoidea_tree = parse-newick(read("/docs/data/hominoidea.nwk"))
#context {
  show text: set text(font: "New Computer Modern", size: 0.9em)
  #render-tree(hominoidea_tree, tip-label-italics: true)
}
```



Default document font



Custom font (New Computer Modern)

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).