# Command-line options

## --no-best-position-introns

abbildung der aenderung

## PDB-options

## Taxonomy

-add taxonomy line to std-output? (all introns common to some taxa)

Supply: --taxonomy --taxonomy-to-fasta --taxonomy-common-to

Supply optional also: --[no-]exclusively-in-taxa

-add output with introns present in each last common ancestor?

Supply: --taxonomy --taxonomy-to-fasta --introns-per-taxon

## Statistics

-add taxonomy?

Supply: --taxonomy example/taxdump.tar.gz --taxonomy-to-fasta example/fastaheaders2species.txt --statistics

# Options

GenePainter – Optionen

-i, --input <path\_to\_alignment> Path to fasta-formatted multiple sequence alignment

-p <path\_to\_genestructures>, Path to folder containing gene structures in YAML or GFF format

--path

Options:

Text-based output format:

--intron-phase Mark introns by their phase instead of '|'

--phylo Mark exons by '0' and introns by '1'

--spaces Mark exons by space (' ') instead of '-'

--no-standard-output Specify to skip standard output format.

--alignment Output the alignment file with additional lines containing intron phases

Graphical output format:

--svg H,W Drawn SVG of size height x width

--svg-format FORMAT FORMAT: ["normal", "reduced"]

'normal' draws details of aligned exons and introns [default]

'reduced' focuses on common introns only

--pdb FILE Mark consensus or merged gene structure in pdb FILE

Consenus gene structure contains introns conserved in N % of all genes

Specify N with option --consensus N; [default: 80%]

Two scripts for execution in PyMol are provided:

'color\_exons.py' to mark consensus exons

'color\_splicesites.py' to mark splice junctions of consensus exons

--pdb-chain CHAIN Mark gene structures for chain CHAIN

[Default: Use chain A]

--pdb-ref-prot PROT Use protein PROT as reference for alignment with pdb sequence

[Default: First protein in alignment]

--pdb-ref-prot-struct Color only intron positions occuring in the reference protein structure.

Meta information and statistics:

--consensus N Introns conserved in N % genes.

Specify N as decimal number between 0 and 1

--merge Merge all introns into a single exon intron pattern

--statistics Output additional file with statistics about common introns

To include information about taxomony, specify '--taxomony' and '--taxonomy-to-fasta' options

Taxonomy:

--taxonomy FILE Mark introns by taxonomy

NCBI taxonomy database dump file FILE

--taxonomy-to-fasta FILE Text-based file mapping fasta header to species names

Gene1[,Gene2]:Species

--taxonomy-common-to x,y,z Mark introns common to taxa x,y,z

List can consist of one taxon only

--[no-]exclusively-in-taxa Mark introns occuring (not) exclusivley in listed taxa

--introns-per-taxon Newly gained introns for every inner node in taxonomy

General options:

-o, --outfile <file\_name> Name of the output file

--range START,STOP Restrict genes to range START-STOP in alignment

--[no-]delete-range (Not) Delete specified range

--keep-common-gaps Keep common gaps in alignment

--no-best-position-introns Plot introns always onto beginning of a gap

Default: Align introns if their position differs by alignment gaps only

-h, --help Show this message