src/abichromatogram

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Contents

This module provides functionality to generate SVG chromatograms from ABIF trace files. It renders the four fluorescence channels with base calls in a visual format that resembles the output of DNA sequencing instruments. Command-line usage:

```
abichromatogram <trace_file.ab1> [options]
```

Options:

`-o, --output FILE`	Output SVG file (default: chromatogram.svg)
`-w, --width WIDTH`	SVG width in pixels (default: 1200)
`--height HEIGHT`	SVG height in pixels (default: 600)
`-s, --start POS`	Start position (default: 0)
`-e, --end POS`	End position (default: whole trace)
`-d, --downsample`	FACTOR Downsample factor for visualization (default: 1)
`--hide-bases`	Hide base calls
`--debug`	Show debug information
`-h, --help`	Show this help message and exit
`-v, --version`	Show version information and exit

Example usage:

```
# Generate a chromatogram from a trace file
abichromatogram input.ab1 -o output.svg

# Generate a zoomed view of a specific region with downsampling
abichromatogram input.ab1 -s 500 -e 1000 -d 5
```

1 Imports

abif

2 Types

```
Channel = enum
  A = "A", C = "C", G = "G", T = "T"
```

The four channels used in capillary electrophoresis

```
TraceData = object
  points*: seq[TraceDataPoint] ## Processed trace data points
  baseOrder*: string           ## Order of bases in channels (e.g., "ACGT")
  peaks*: seq[int]             ## Base call peak positions
  sequence*: string            ## Called sequence
  traceLen*: int               ## Total length of trace in data points
  baseColors*: Table[Channel, string] ## Color mapping for each nucleotide base
```

Processed trace data ready for visualization

```
TraceDataPoint = object
  position*: int              ## X position (scan number)
  values*: Table[Channel, int] ## Intensity value for each channel (scaled 0-1000)
```

A single data point in the trace with values for each channel