## src/abichromatogram

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## Contents

## 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