alignments: summary

Building an alignment takes two steps. `alignSequences()` aligns the hits chosen by a logical `subset` column of the `polyBlast()` monolist, with `mode` set to nucleotide, amino-acid or codon alignment. `analyzeAlignment()` then profiles each column for gaps and conservation, lets us tune the trimming thresholds interactively, and writes the trimmed alignment to `<alignment_in_path>_trimmed`, ready for tree building.

Function	What it does	Arguments students vary
`readMonolist()`	reads the hit-list CSV written by `polyBlast()`	the CSV path
`alignSequences()`	aligns the monolist rows where the `subset` column is TRUE and writes an aligned FASTA	`subset`, `input_sequence_type` (`"nucl"`, `"amin"`), `mode` (`"nucl_align"`, `"amin_align"`, `"codon_align"`, `"fragment_align"` with `base_fragment`), `alignment_out_path`, `sequences_of_interest_directory_path`
`analyzeAlignment()`	Shiny app for trimming gap-heavy or poorly conserved columns, returning the trimmed alignment	`alignment_in_path`, `type` (`"DNA"`, `"AA"`), `jupyter` (TRUE in Jupyter)