kdm-snakemake-helpers Documentation

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To use these, `pip install` this package **in the same python environment as snakemake**, then use `from kdmsnakemake import *` in the top of your Snakefile.

CHAPTER 1

Helper functions

`kdmsnakemake.`**`make_regions`**(*rdict*, *window=1000000.0*)

Splits a reference into *window* sized windows.

Makes a list of regions for each reference in a dict of {refname: refpath: entries.

Parameters

- **`rdict`** – dict of {refname: refpath, . . . }
- **`window`** – Size of windows

Returns dict of {refname: {region: coordinates, . . . }, . . . }

`kdmsnakemake.`**`make_chromosomes`**(*rdict*, *chrom_regex='^chr'*)

Splits a reference into chromosome chunks

Makes a list of regions for each reference in a dict of {refname: refpath} entries. Sequences matching *chrom_regex* appear as their own entires, all other sequences appear under a "scaffols" pseudo-chromosome.

Parameters

- **`rdict`** – dict of {refname: refpath, . . . }
- **`chrom_regex`** – Regular expression that (case-insensitively) matches proper chromosomes.

Returns dict of {refname: {chromosome_set: [refseq_name, . . .]}, . . . }

CHAPTER 2

Indices and tables

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