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# **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

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## Helper functions

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`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

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### Indices and tables

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- `genindex`
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**k**

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## K

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## M

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