vipertools

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CONTENTS:

PARSE

Contains functions to parse imaging data into a usable formats for downstream pipelines.

vipertools.parse.**parse_phenix**(*phenix_dir*, *flatfield_exported=True*, *parallel=False*)
    Function to automatically rename TIFS exported from Harmony into a format where row and well ID as well as Tile position are indicated in the file name. Example of an exported file name: "Row{#}_Well{#}_{channel}_zstack{#}_r{#}_c{#}.tif"

    Parameters

- **phenix_dir** – Path indicating the exported harmony files to parse.

- **flatfield_exported** – boolean indicating if the data was exported from harmony with or without flatfield correction.

- **parallel** – boolean value indicating if the data parsing should be performed with parallelization or without (CURRENTLY NOT FUNCTIONAL ONLY USE AS FALSE)

PYTHON MODULE INDEX

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