## **Experiments using opentrons** hydra metadata file wormsorter file source plates file robot log info about drugs or other summary info about summary info about all C.elegans and bacteria in the experimental runs content in each well in each each imaging plate: in a tracking day: source plate. Examples: info about shuffling between instument name worm strain days in diapause imaging plate id drug type / bacteria source plates and imaging date bleached run number plates type date refed run time drug concentration bacteria strain temperature units media type humidity solvent repeat for every tracking day get day metadata shuffling log source plates file wormsorter file merge robot metadata: populate\_96WP: create dataframe with information create dataframe with basic about the source-plate content metadata for each well in that went into each well in each each imaging plate imaging plate source metadata for basic imaging plate metadata imaging plates plate\_metadata source\_metadata merge\_robot\_wormsorter: merge the basic and source metadata complete imaging plate metadata complete\_plate\_metadata get\_day\_metadata: get the metadata for every hydra metadata file recording of every run in a single day of experiments complete metadata for one tracking day day\_metadata concatenate metadata from all tracking days complete metadata **Experiments without plate shuffling** wormsorter file hydra metadata file source plates file imaging2source plates file summary info about summary info about all info about drugs or other the experimental runs C.elegans and bacteria in content in each well in each source plate. each imaging plate: in a tracking day: Examples: worm strain instument name mapping between source days in diapause imaging plate id drug type / bacteria plates and imaging plates date bleached run number type date refed run time drug concentration temperature units bacteria strain media type humidity solvent repeat for every tracking day get day metadata imaging2source source plates file plates file wormsorter file get\_source\_metadata: populate\_96WP: create dataframe with information create dataframe with basic about the source-plate content metadata for each well in that went into each well in each each imaging plate imaging plate basic imaging plate source metadata for imaging plates metadata source\_metadata plate\_metadata merge\_basic\_and\_drug\_meta: merge the basic and source metadata complete imaging plate metadata complete\_plate\_metadata <u>get\_day\_metadata</u>: get the metadata for every hydra metadata file recording of every run in a single day of experiments complete metadata for one tracking day day\_metadata concatenate metadata from all tracking days complete metadata **Experiments without source plates** wormsorter file hydra metadata file summary info about summary info about all C.elegans and bacteria in the experimental runs each imaging plate: in a tracking day: worm strain instument name imaging plate id days in diapause date bleached run number date refed run time bacteria strain temperature media type humidity get day metadata -repeat for every tracking day wormsorter file populate\_96WP: create dataframe with basic metadata for each well in each imaging plate basic imaging plate metadata plate\_metadata get\_day\_metadata: get the metadata for every manual metadata file recording of every run in a single day of experiments complete metadata for one tracking day day\_metadata concatenate\_days\_metadata: concatenate metadata from all

tracking days

complete metadata