

## STEP 1

load\_sample()



load\_population()



load\_taxonomies()

Must at least use get\_validity()

## STEP 2

get\_lineages()



get\_validity()



get\_status()



term\_conversion()

get\_inconsistencies()



## STEP 3

prepare\_rank\_dist()



prepare\_comparable\_rank\_dist()

## STEP 4

plot\_mdb()



Indicates workflow prohibition



Indicates end of workflow