

embedding\_termfreq  ${\bf embedding\_autocorrelation}$ **→ input → input** data/red\_transcriptome\_human.csv data/red\_transcriptome\_human.csv data/words.csv output → postprocessing/DNADCC.csv postprocessing/termfreq.csv

random\_weighting

data/red\_transcriptome\_human.csv

output →

output →

**→ input** 

data/TF\_IDF.csv

data/words.csv

data/seq2vec\_ids.csv

data/seq2vec\_weights.csv

 $embedding\_random$ 

data/red\_transcriptome\_human.csv

postprocessing/random.csv

output →

**→ input** 

seq2vec\_weighting

data/red\_transcriptome\_human.csv

output →

**→ input** 

data/TF\_IDF.csv

data/words.csv

data/seq2vec\_ids.csv

data/seq2vec\_weights.csv

embedding\_seq2vec

data/red\_transcriptome\_human.csv

output →

**→ input** 

data/words.csv

data/seq2vec\_ids.csv

data/seq2vec\_weights.csv

output →

**→ input** 

embedding\_pseudoDNC

output →

data/red\_transcriptome\_human.csv

postprocessing/DNAPse.csv