Command line input: src/scripts/regression.py --input data/preprocessed/HIV_maccs.csv -c src/configs/config_regression_hiv.py --output tmp/ --feature maccs
Parameters: batch_size: 128, activation: sigmoid, optimizer: Adam, loss: binary_crossentropy, learning_rate: 0.1, momentum: 0, init_mode: he_uniform, metrics: [accuracy]
Score: 0.137
Accuracy: 0.968
Score for positive data only: 2.967
Accuracy for positive data only: 0.128
Score for negative data only: 0.036
Accuracy for negative data only: 0.998
Started at: 2017-08-23 03:28:00.533672
Time required: 0:00:09.583517
Host name: lab