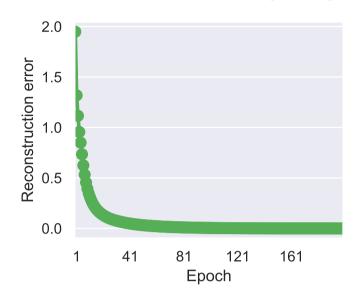
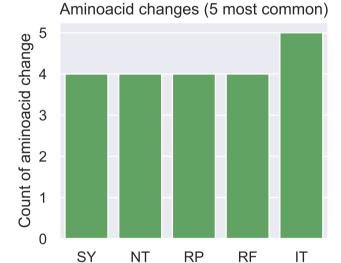
## Reconstruction error during training

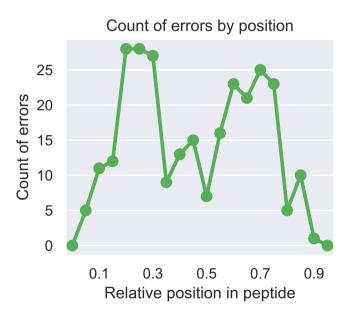




Aminoacid change

RF

NT



Average reconstruction error on test set: CELoss: 0.01479

From 7057 sequences with right seq len:7053

	precision		all f1-s	core si	upport
ACCEFGHIKLNNPGRSTVVY	1.0 1.0 1.0 1.0 1.0 1.0 0.9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	00 1.0 00 1.0 00 0.0 00 1.0 00 1.0 99 0.9 99 0.9 99 0.0 00 1.0 99 0.0 99 0.0 99 0.0 99 0.0 99 0.0	00 1. 00 1. 99 1. 00 1. 00 1. 00 1. 99 0. 98 0. 97 0. 99 0. 99 0. 00 1. 99 0. 00 1. 99 0. 99 0. 90	00 10 .00 7 .00 2 .00 5 .00 10 .99 1 .99 13 .98 6 .99 2 .99 2 .00 6 .99 3 .00 15 .00 15 .00 6 .99 1	0581 083 881 975 0826 0221 108 611 667 306 383 961 898 6639 195 5912 551 823 684
accur macro weighted	avg	0.99 1.00	1.0 0.99 1.00	00 102 0.99 1.00	2029 102029 102029

