Accuracy of input is: 0.8755265548856034

Model trained on 0.9 and above of noiseless added to training

Epoch 0

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9268191955067316

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.2026100602956967

Average good changes per sequence : 0.5294457751713885

Average bad changes per sequence: 0.003221276947220616

Average failure to change per sequence: 0.1993887833484761

Error per base: 0.0008074981121069413

Error per sequence: 0.2026100602956967

Epoch 1

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9394565127612126

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.1838605765259767

Average good changes per sequence : 0.5481952589411084

Average bad changes per sequence: 0.003221276947220616

Average failure to change per sequence: 0.1806392995787561

Error per base: 0.0007327724409091119

Error per sequence: 0.1838605765259767

Epoch 2

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9443297266044437

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.17477492359791855

Average good changes per sequence : 0.5594284298339803

Average bad changes per sequence: 0.00536879491203436

Average failure to change per sequence: 0.1694061286858842

Error per base: 0.0006965617632361549

Error per sequence: 0.17477492359791855

Epoch 3

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9425951928636326

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.17163624349549847

Average good changes per sequence : 0.5721483439332617

Average bad changes per sequence: 0.01495002890889568

Average failure to change per sequence: 0.15668621458660278

Error per base: 0.0006840526200400424

Error per sequence: 0.17163624349549847

Epoch 4

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9550673164285124

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.15775997356900967

Average good changes per sequence : 0.5757000082596845

Average bad changes per sequence: 0.0046254233088296026

Average failure to change per sequence: 0.15313455026018005

Error per base: 0.0006287490395940717

Error per sequence: 0.15775997356900967

Epoch 5

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9574626249277277

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.15462129346658957

Average good changes per sequence : 0.5793342694309077

Average bad changes per sequence: 0.005121004377632774

Average failure to change per sequence: 0.1495002890889568

Error per base: 0.0006162398963979593

Error per sequence: 0.15462129346658957

Epoch 6

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9585363839101346

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.15247377550177582

Average good changes per sequence : 0.5819773684645246

Average bad changes per sequence: 0.005616585446435946

Average failure to change per sequence: 0.1468571900553399

Error per base: 0.0006076810089479876

Error per sequence: 0.15247377550177582

Epoch 7

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9606013050301478

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.1486743206409515

Average good changes per sequence : 0.5866853886181548

Average bad changes per sequence: 0.006525150739241761

Average failure to change per sequence: 0.14214916990170975

Error per base: 0.0005925383619211147

Error per sequence: 0.1486743206409515

Epoch 8

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9620880482365574

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.14619641529693567

Average good changes per sequence : 0.5892458908069712

Average bad changes per sequence: 0.00660774758404229

Average failure to change per sequence: 0.13958866771289336

Error per base: 0.0005826627225557628

Error per sequence: 0.14619641529693567

Epoch 9

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9619228545469563

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.14652680267613777

Average good changes per sequence : 0.5889981002725696

Average bad changes per sequence: 0.006690344428842818

Average failure to change per sequence: 0.13983645824729496

Error per base: 0.000583979474471143

Error per sequence: 0.14652680267613777

Epoch 10

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9634095977533659

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.14446188155612455

Average good changes per sequence : 0.5916411993061865

Average bad changes per sequence: 0.0072685223424465185

Average failure to change per sequence: 0.13719335921367803

Error per base: 0.0005757497750000165

Error per sequence: 0.14446188155612455

Epoch 11

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9619228545469563

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.14330552572891717

Average good changes per sequence : 0.5919715866853886

Average bad changes per sequence: 0.006442553894441232

Average failure to change per sequence: 0.13686297183447593

Error per base: 0.0005711411432961855

Error per sequence: 0.14330552572891717

Epoch 12

Using accuracy as number of completely correct (noiseless) sequences divided by total number of sequences:

Accuracy of model is: 0.9632444040637648

Baseline error(num mismatched nucleotides between target and input average per sequence): 0.7288345585198646

Prediction error(num mismatched nucleotides between target and prediction average per sequence): 0.14330552572891717

Average good changes per sequence : 0.5919715866853886

Average bad changes per sequence: 0.006442553894441232

Average failure to change per sequence: 0.13686297183447593

Error per base: 0.0005711411432961855

Error per sequence: 0.14330552572891717