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Size of chromosome: 42

Capacity of population: 100

Epoch: 100

With mutation 15%

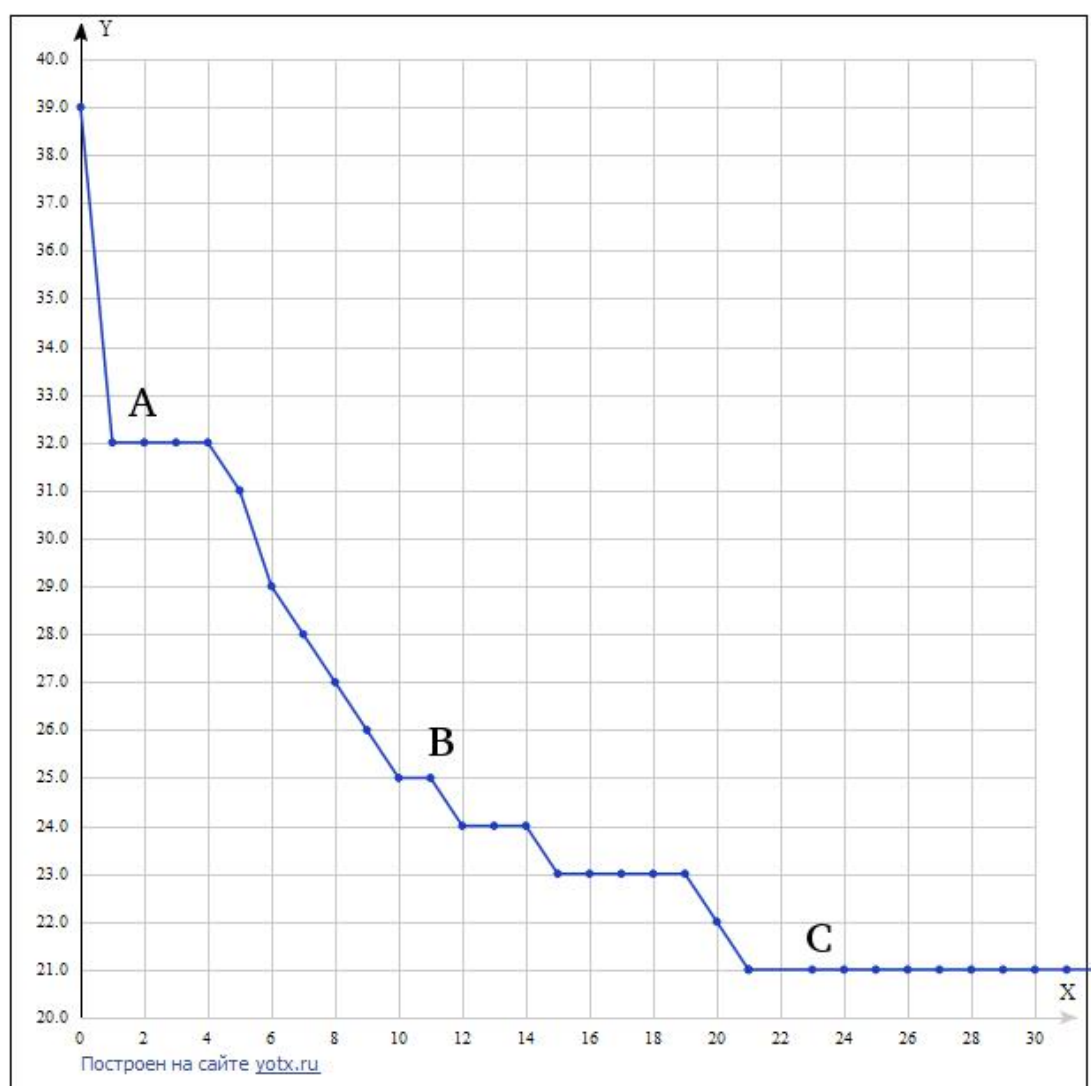
Onepoint crossover

Truncate selection

Evolution:

X - epoch

Y - Error (misses). Maximum 64, minimum 0. The lowest the best



For 100 epoch:

(0;39) (1;32) (2;32) (3;32) (4;32) (5;31) (6;29) (7;28) (8;27) (9;26) (10;25) (11;25) (12;24) (13;24) (14;24) (15;23) (16;23) (17;23) (18;23) (19;23) (20;22) (21;21) (21;21) (23;21) (24;21) (25;21) (26;21)

(27;21) (28;21) (29;21) (30;21) (31;21) (32;21) (33;21) (34;21) (35;21) (36;21) (37;21) (38;21) (39;21)
(40;21) (41;21) (42;21) (43;21) (44;21) (45;21) (46;21) (47;21) (48;21) (49;21) (50;21) (51;21) (52;21)
(53;21) (54;21) (55;21) (56;21) (57;21) (58;21) (59;21) (60;21) (61;21) (62;21) (63;21) (64;21) (65;21)
(66;21) (67;21) (68;21) (69;21) (70;21) (71;21) (72;21) (73;21) (74;21) (75;21) (76;21) (77;21) (78;21)
(79;21) (80;21) (81;21) (82;21) (83;21) (84;21) (85;21) (86;21) (87;21) (88;21) (89;21) (90;21) (91;21)
(92;21) (93;21) (94;21) (95;21) (96;21) (97;21) (98;21) (99;21)

Point A

0.004245162 0.08754581 0.37957603 0.36770684 0.5778013 0.07725388 0.14192855 0.7543234
0.42969728 0.17503065 0.42685878 0.3071699 0.17578715 0.3659436 0.75706375 0.97458124
0.85807246 0.47447425 0.19501913 0.1976096 0.43215084 0.5598304 0.715094 0.19540817
0.3007388 0.19147402 0.5548215 0.62097657 0.6440255 0.44789517 0.92192554 0.9732774
0.028865397 0.18767267 0.33827305 0.6195456 0.26375097 0.6724794 0.89487356 0.6629467
0.7851216 0.21195334

Point B

0.8751986 0.033119917 0.73026574 0.58937746 0.8135171 0.48040628 0.9484121 0.19210583
0.061212182 0.9244324 0.59333897 0.0076673627 0.9500237 0.8432017 0.6217603 0.40738833
0.7209009 0.31805164 0.79173535 0.85162294 0.74586654 0.2949344 0.9671813 0.24793327
0.95141006 0.85089016 0.59230137 0.36596107 0.90872407 0.5133424 0.89559484 0.74186224
0.6055385 0.7311639 0.6468245 0.27063346 0.691351 0.54994255 0.10828096 0.7082432
0.8684708 0.3809595

Pint C (final best result)

First 36

0.5320507 0.3858598 0.21637619 0.5086662 0.86583084 0.05435121 0.33201706 0.6123477
0.295375 0.57253164 0.98317593 0.037694633 0.39461106 0.85863614 0.30541158 0.30779827
0.594807 0.40282744 0.5604942 0.011066675 0.674144 0.121821105 0.2916584 0.7030977
0.059620082 0.09843016 0.93465763 0.8380325 0.18338889 0.35547692 0.59128684 0.5074554
0.661581 0.70974874 0.31215125 0.21463263

Second 6:

0.9568468 0.27174288 0.5929145 0.89609176 0.8066547 0.07917625

Conclusion: Algorithm could achieve only 67,2% accuracy. In generation 50 all chromosomes had the same genes, so make more then 50 epoch it for nothing even if you use mutation. 43 right answers is my best result.