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1: #include "NelderMead.h"
2:
3: NelderMead::NelderMead(SegmentData &segment)
4: {
5:     generateSimplex();
6:     countAllMetrics(segment);
7:     sort();
8:     calculate(segment);
9: }
10:
11: void NelderMead::calculate(SegmentData &segment){
12:     double current_best_metric = DBL_MAX;
13:     double Xg_p = 0, Xg_cg = 0, Xg_c = 0, Xg_dt = 0, Xg_h = 0, Xg_k = 0;
14:     int size_without_last = _simplex.size() - 1;
15:     int last_simplex_index = size_without_last;
16:
17:     for (int x = 0; x < ITERATIONS; x++){
18:         //set new best metric
19:         current_best_metric = min(current_best_metric, _simplex[0].getMetric());
20:
21:         // Termination criteria
22:         if (current_best_metric < METRIC_EPSILON) {
23:             cout << "Found metric " << current_best_metric << " less than epsilon " <<
METRIC_EPSILON << endl;
24:             break;
25:         }
26:
27:         // -- REFLECTION -- //
28:         for (int z = 0; z < size_without_last; z++){ //Xg - součet všech a na
poslední (nejhorší)
29:             Xg_p += _simplex[z].getP();
30:             Xg_cg += _simplex[z].getCg();
31:             Xg_c += _simplex[z].getC();
32:             Xg_dt += _simplex[z].getDt();
33:             Xg_h += _simplex[z].getH();
34:             Xg_k += _simplex[z].getK();
35:         }
36:         // Xg //
37:         Xg_p /= size_without_last;
38:         Xg_cg /= size_without_last;
39:         Xg_c /= size_without_last;
40:         Xg_dt /= size_without_last;
41:         Xg_h /= size_without_last;
42:         Xg_k /= size_without_last;
43:         // Xr //
44:         EquationData Xr(
45:             (A*(Xg_p - _simplex[last_simplex_index].getP())) +
46:             _simplex[last_simplex_index].getP(),
47:             (A*(Xg_cg - _simplex[last_simplex_index].getCg())) +
48:             _simplex[last_simplex_index].getCg(),
49:             (A*(Xg_c - _simplex[last_simplex_index].getC())) +
50:             _simplex[last_simplex_index].getC(),
51:             (A*(Xg_dt - _simplex[last_simplex_index].getDt())) +
52:             _simplex[last_simplex_index].getDt(),
53:             (A*(Xg_h - _simplex[last_simplex_index].getH())) +
54:             _simplex[last_simplex_index].getH(),
55:             (A*(Xg_k - _simplex[last_simplex_index].getK())) +
56:             _simplex[last_simplex_index].getK()
57:         );
58:         Xr.setMetric(countMetrics(Xr, segment));
59:         // Reflection condition: YES => update the worst parameters; NO =>
contraction or expansion //
60:         if (_simplex[0].getMetric() < Xr.getMetric() && Xr.getMetric() <
_simplex[last_simplex_index - 1].getMetric()){

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55:         _simplex[last_simplex_index] = Xr;
56:     }
57: // Contraction/Expansion condition: YES => Contraction; NO => Expansion //
58: else if (_simplex[0].getMetric() < Xr.getMetric()){
59:     // -- CONTRACTION -- //
60:     // Xc //
61:     EquationData Xc(
62:         (G*(_simplex[last_simplex_index].getP() - Xg_p)) + Xg_p,
63:         (G*(_simplex[last_simplex_index].getCg() - Xg_cg)) + Xg_cg,
64:         (G*(_simplex[last_simplex_index].getC() - Xg_c)) + Xg_c,
65:         (G*(_simplex[last_simplex_index].getDt() - Xg_dt)) + Xg_dt,
66:         (G*(_simplex[last_simplex_index].getH() - Xg_h)) + Xg_h,
67:         (G*(_simplex[last_simplex_index].getK() - Xg_k)) + Xg_k
68:     );
69:     Xc.setMetric(countMetrics(Xc, segment));
70:     // Contraction condition: YES => update the worst parameters; NO =>
multiple contraction //
71:     if (Xc.getMetric() < _simplex[last_simplex_index].getMetric()){
72:         _simplex[last_simplex_index] = Xc;
73:     }
74:     else {
75:         // -- MULTIPLE CONTRACTION-- //
76:         EquationData tmp_eq;
77:         for (int size = _simplex.size(), k = 1; k < size; k++){ // contraction
all sets of parameters without the best one
78:             tmp_eq.setAllParameters(
79:                 (H*(_simplex[k].getP() - _simplex[0].getP())) + _simplex[0].getP(),
80:                 (H*(_simplex[k].getCg() - _simplex[0].getCg())) +
_simplex[0].getCg(),
81:                     (H*(_simplex[k].getC() - _simplex[0].getC())) + _simplex[0].getC(),
82:                     (H*(_simplex[k].getDt() - _simplex[0].getDt())) + _simplex[0].getP(),
83:                     (H*(_simplex[k].getH() - _simplex[0].getH())) + _simplex[0].getH(),
84:                     (H*(_simplex[k].getK() - _simplex[0].getK())) + _simplex[0].getK()
85:                 );
86:                 _simplex[k] = tmp_eq;
87:             }
88:         }
89:     }
90:     else {
91:         // -- EXPANSION -- //
92:         // Xe //
93:         EquationData Xe(
94:             (B*(Xr.getP() - Xg_p)) + Xr.getP(),
95:             (B*(Xr.getCg() - Xg_cg)) + Xr.getCg(),
96:             (B*(Xr.getC() - Xg_c)) + Xr.getC(),
97:             (B*(Xr.getDt() - Xg_dt)) + Xr.getDt(),
98:             (B*(Xr.getH() - Xg_h)) + Xr.getH(),
99:             (B*(Xr.getK() - Xg_k)) + Xr.getK()
100:         );
101:         Xe.setMetric(countMetrics(Xe, segment));
102:         // Expansion condition: ALWAYS => update the worst parameters; YES =>
update by Xe; NO => update by Xr //
103:         if (Xe.getMetric() < Xr.getMetric()){
104:             _simplex[last_simplex_index] = Xe;
105:         }
106:         else {
107:             _simplex[last_simplex_index] = Xr;
108:         }
109:     }
110:     sort();
111: }
112: // Save the best parameters into segment //
113: segment.setResult(_simplex[0]);
114: }

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115:
116: void NelderMead::generateSimplex(){
117:     default_random_engine rnd((unsigned)
118:         chrono::system_clock::now().time_since_epoch().count());
119:     uniform_real_distribution<double> gen_p(EquationBounds::pmin,
120:         EquationBounds::pmax);
121:     uniform_real_distribution<double> gen_cg(EquationBounds::cgmin,
122:         EquationBounds::cgmax);
123:     uniform_real_distribution<double> gen_c(EquationBounds::cmin,
124:         EquationBounds::cmax);
125:     uniform_real_distribution<double> gen_dt(EquationBounds::dtmin,
126:         EquationBounds::dtmax);
127:     uniform_real_distribution<double> gen_h(EquationBounds::hmin,
128:         EquationBounds::hmax);
129:     uniform_real_distribution<double> gen_k(EquationBounds::kmin,
130:         EquationBounds::kmax);
131:     if (!_simplex.empty()){
132:         cout << "Clear simplex before generate new one..." << endl;
133:         _simplex.clear();
134:     }
135: }
136: }
137:
138: void NelderMead::countAllMetrics(SegmentData &segment){
139:     double metric;
140:     bool least_one_good = false;
141:     for (int size = _simplex.size(), i = 0; i < size; i++){
142:         metric = countMetrics(_simplex[i], segment);
143:         _simplex[i].setMetric(metric);
144:         if (metric != DBL_MAX){
145:             least_one_good = true;
146:         }
147:     }
148:     if (!least_one_good){
149:         cout << "Any metric isn't good => generate new simplex..." << endl;
150:         generateSimplex();
151:         countAllMetrics(segment);
152:     }
153: }
154:
155: double NelderMead::countMetrics(EquationData &params, SegmentData &segment){
156:     double current_blood_time;
157:     double eq_fi, eq_alfa, eq_beta, eq_gama, eq_D, eq_b;
158:     double relative_error, total_relative_error, sum_relative_error = 0, deviation
159: = 0, sum_deviation = 0;
160:     int blood_values_count = segment.getBloodValues().size();
161:     int total_count_metrics_values = blood_values_count;
162:     for (int i = 0; i < blood_values_count; i++){
163:         current_blood_time = segment.getBloodValues()[i].getDate();
164:         eq_fi = current_blood_time + params.getD() + (params.getK() *
165:             ((segment.getInterpolationIst(current_blood_time) -
166:                 segment.getInterpolationIst(current_blood_time - params.getH())) /
167:                 params.getH()));
168:         if (eq_fi < segment.getMinDate() || eq_fi > segment.getMaxDate()){
169:             total_count_metrics_values--;

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167:     continue;
168: }
169: eq_alfa = params.getG();
170: eq_beta = params.getP() - (eq_alfa *
    segment.getInterpolationIst(current_blood_time));
171: eq_gama = params.getG() - segment.getInterpolationIst(eq_fi);
172: eq_D = pow(eq_beta, 2) - (4 * eq_alfa * eq_gama);
173: if (eq_D < 0.0) eq_D = 0.0;
174: eq_b = (-eq_beta + sqrt(eq_D)) / (2 * eq_alfa);
175:
176: relative_error = abs(segment.getBloodValues()[i].getBlood() - eq_b) /
    segment.getBloodValues()[i].getBlood();
177: sum_relative_error += relative_error;
178: sum_deviation += pow(relative_error, 2);
179: }
180:
181:
182: if (total_count_metrics_values == 0){
183:     return DBL_MAX;
184: }
185: else {
186:     total_relative_error = sum_relative_error / total_count_metrics_values;
187:     deviation = sqrt((sum_deviation / total_count_metrics_values) -
    pow(total_relative_error, 2));
188:     return total_relative_error + deviation;
189: }
190: }
191:
192: void NelderMead::sort(){
193:     std::sort(_simplex.begin(), _simplex.end());
194: }
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