Application of aging chain model on demographical data of the Czech Republic

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Abstract. Paper deals with the design of dynamic aging chain model of Czech Republic. Population aging chains are necessary for different kinds of system dynamics models that focus on socioeconomic problems. Aging chain structure commonly consists of stock variables for age cohorts and flow variables for aging, births, deaths and migration. The basis of such computer simulation model that is based on system dynamics methodology is the system of nonlinear first-order differential equation.

In the first part, we will present three different aging chains quantified on the basis of current demographical data. Each chain is divided into two separate chains, one for each gender. Chains differ in the level of age groups aggregation and in the type of delay that is used to model the aging between age cohorts. Also two different approaches to represent changes in childbearing are explained. In second part, each simulation run is compared with official demographical data of the Czech Statistical Office and thus the best approach is identified on the basis of the accuracy of simulation.

Keywords: system dynamics, aging chain, population, fertility rate, delay.

JEL Classification: C63, C44, J12
AMS Classification: 91D20, 93C15

1 Introduction

Paper deals with the design of dynamic aging chain model of Czech Republic. Population aging chains are necessary for different kinds of system dynamics models that focus on socioeconomic problems. Aging chain structure commonly consists of stock variables for age cohorts and flow variables for aging, births, deaths and migration [1]. The core of such computer simulation model that is based on system dynamics methodology is the system of nonlinear first-order differential equation.

The aging chain structure is useful for non-human population simulation e.g. for housing [8] or capital in general [16]. Moreover similar structure to aging chain is possible use for model of persons' fluctuation between cohorts that are distinguished on basis of some more qualitative indicator e.g. work position promotion [12]. Nevertheless, we focused on human aging chain. Such chains are commonly used for macro models of whole world [13, 14] or country [17]. At the beginning, we set the goal to design versatile aging chain of Czech Republic population, which can serve as a molecule for more complex models [11]. The versatility should be ensured by disaggregation of age cohorts.

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2 Materials and methods

Aging chain is designed in Vensim DSS 5.10e. For parameters quantification the official demographical data from Czech Statistical Office were used. For fertility and initial stock values we used Czech demographic hand book [2], Demographic yearbooks of the Czech Republic [3, 4], for mortality parameters the life tables were necessary [5, 7].

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Population model is divided according to gender, thus model contains two aging chains. Figure 1 present general stock and flow of aging chain, index i is age, index s stands for sex identification (M or F), box variables represent stock variables, pipes with arrow and faucet represent flow variables and simple arrows are causal links with polarity.

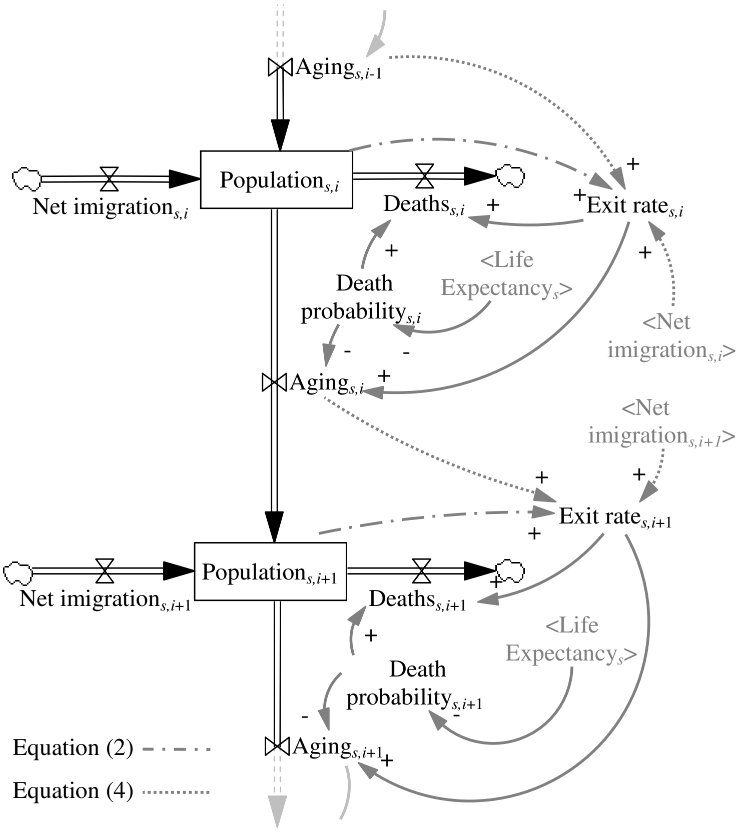

Figure 1 Simple stock and flow diagram of aging chain

In equation (1) stock variable population $P_{s,i}$ has two inflows and two outflows. $A_{s,i}$ is aging (maturation) from age cohort i to i+1 (thus inflow from previous cohort and outflow to following one), $I_{s,i}$ is net immigration and $D_{s,i}$, is outflow of deaths from population $P_{s,i}$. T is current time, initial time is T_0 and t is any time between T and T_0.

$$P_{s,i}(T)=\int_{T_0}^{T}\left(A_{s,i-1}(t)-A_{s,i}(t)+I_{s,i}(t)-D_{s,i}(t)\right)dt+P_{s,i}(T_0) \tag{1}$$

First aging chain in [11] used disaggregation into twelve age groups (i=0 was for age between 0–14 years, i=1, …, 10 is for of five-year groups, the last group i=11 is the population in the age of 65 and older). Next models used 72 age cohorts, one year cohorts until age of 70, then i=71 is for age 71 and more [10].

There are two possible ways to express exit rate $E_{s,i}$ (total outflow from population $P_{s,i}$). That is the reason why the causal link to exit rate missing in figure 2. Equation (2) is first order delay where $a_{s,i}$ is average time in cohort, thus in case with one year cohorts the equation (3) was used. First order delay generates exponential decay and assumes perfect mixing entities in stock [15].

$$E_{s,i}=\frac{P_{s,i}}{a_{s,i}} \tag{2}$$

$$E_{s,i}=P_{s,i} \tag{3}$$

Second possible approach is fixed delay. In this case the equation (4) express exit rate from $P_{i,s}$. Total output from population is total input to same population delayed by fixed time.

$$E_{s,i}(T)=A_{s,i-1}(T-a_{s,i})+I_{s,i}(T-a_{s,i}) \tag{4}$$

The first approach in equation (3) is suitable in “situations where cohorts are defined not by age but by membership in category” [15] but in referred cases [13, 14, 17] it is used instead of equation (4) despite the cohorts are defined by age. Both types of delays were tested for exit rate in our models and appropriate causal links are shown in figure 1.

Anyhow the exit rate is defined; outflows of deaths and aging are obtained from equations (5) and (6). Death probability $DP_{s,i}$ is function of exogenous life expectancy, which is specified for both genders separately. We applied ordinary least square method on data from life tables [5, 7], the lowest value of determination coefficient R^2 is obtained for cohorts i=0, …, 15, it is always more than 0.75; for i=30, …, 71 R^2 is more than 0.9. In case of 12 age cohorts the R^2 is more than 0.9 for all cohorts.

$$D_{s,i} = E_{s,i} \cdot DP_{s,i} \tag{5}$$

$$A_{s,i} = E_{s,i} \cdot \left(1 - DP_{s,i}\right) \tag{6}$$

Official data on fertility focus only on females of age between 15 and 49 years (marginal cohorts are assumed to be 15 or less and 49 and more). The average age of mothers in the Czech Republic grew by more than two years in the first decade of 21st century. Thus, it was necessary to dynamise cohorts’ fertility. We tested two approaches. In [10] we used equation (7) to calculate births B, FI_i is cohort fertility index and TF is total fertility rate. Again, the ordinary least square method was used; R^2 does not drop below 0.9. We used 20-year average ratio of male and female births, which means 51.4% of births are the inflow to male aging chain.

$$B = \sum_{i=15}^{49} P_{F,i} \cdot TF \cdot FI_i \tag{7}$$

Second approach uses density function of normal distribution. We defined standard deviation as function of average mothers’ age with R^2 higher than 0.97. For extrapolation of exogenous variables we used estimates from [6]. In case of net immigration we used average age structure from years 2003-2010. Starting point of simulation is T_0 is 2003.5, i.e. 1st July 2003, fourth order Runge-Kutta integration with time step 0.03125 was used.

3 Results and discussion

The smallest model has more than 190 variables, the biggest more than eight hundred (144 stock variables, 432 flow variables of deaths, aging, migration and births, other variables are parameters – fertility indices, death probabilities, life expectancy etc.). We tested all mentioned combinations: five x one year cohorts, first order x fixed delay, fertility indices x normal distribution approximation.

Mean Absolute Percent Error was calculated for years 2004-2010, always for first of July. The worst results were obtained from aging chain with five year cohorts, first order delay and fertility calculated by (7). MAPE was 0.24 for whole population but it grows to more than 8.2 for female cohort of 30-34, which is very important for correct births estimation. Models with one year age cohorts produced better result. At first we tested aging chains that used (7). For both types of exit rate the worst results were for youngest age cohorts and showed possible improvement in estimation of fertility. The best results were obtained from aging chain that used fixed delay for exit rate (4) and normal distribution for fertility. Just 5 age cohorts has worse MAPE than the second best model with exit rate from (2) and also normal distribution approximation for fertility. Table 1 shows values of the mean absolute percent error MAPE for whole population, each gender and age cohorts.

System of demographic structure has high inertia, thus it is not surprising the MAPE for total population reaches always very good results for such short period. But the indicator doesn’t fall if we use shorter period. More important is MAPE for specific age cohorts and, in this case, especially first six that are result of fertility modeling.

Age	Total	Male	Female	Age	Total	Male	Female	Age	Total	Male	Female
Total	0.164	0.132	0.194	**24**	0.340	0.515	0.157	**48**	0.475	0.597	0.350
0	0.979	1.233	0.714	**25**	0.515	0.573	0.452	**49**	0.358	0.479	0.234
1	0.500	0.376	0.658	**26**	0.613	0.723	0.495	**50**	0.354	0.433	0.273
2	0.636	0.533	0.744	**27**	0.431	0.468	0.393	**51**	0.290	0.314	0.297
3	0.519	0.483	0.557	**28**	0.462	0.394	0.534	**52**	0.273	0.321	0.225
4	0.488	0.530	0.443	**29**	0.469	0.447	0.494	**53**	0.161	0.184	0.162
5	0.330	0.408	0.270	**30**	0.589	0.646	0.529	**54**	0.144	0.164	0.164
6	0.220	0.219	0.221	**31**	0.507	0.537	0.474	**55**	0.128	0.149	0.108
7	0.175	0.235	0.152	**32**	0.490	0.536	0.442	**56**	0.110	0.152	0.085

8	0.181	0.168	0.195	**33**	0.338	0.365	0.310	**57**	0.101	0.131	0.073
9	0.091	0.108	0.107	**34**	0.447	0.543	0.346	**58**	0.058	0.075	0.061
10	0.106	0.097	0.135	**35**	0.365	0.387	0.341	**59**	0.107	0.164	0.055
11	0.067	0.065	0.085	**36**	0.404	0.490	0.314	**60**	0.088	0.163	0.05
12	0.141	0.143	0.157	**37**	0.455	0.571	0.332	**61**	0.169	0.252	0.094
13	0.078	0.103	0.101	**38**	0.522	0.579	0.463	**62**	0.139	0.235	0.062
14	0.086	0.077	0.112	**39**	0.379	0.442	0.313	**63**	0.258	0.403	0.132
15	0.158	0.134	0.183	**40**	0.410	0.528	0.286	**64**	0.217	0.354	0.105
16	0.145	0.135	0.154	**41**	0.185	0.308	0.079	**65**	0.346	0.453	0.256
17	0.468	0.371	0.581	**42**	0.304	0.410	0.192	**66**	0.217	0.303	0.184
18	1.239	1.404	1.067	**43**	0.244	0.329	0.155	**67**	0.302	0.378	0.241
19	1.900	2.371	1.408	**44**	0.357	0.397	0.316	**68**	0.226	0.253	0.238
20	1.911	2.380	1.459	**45**	0.279	0.436	0.125	**69**	0.377	0.460	0.314
21	1.098	1.558	0.648	**46**	0.352	0.439	0.262	**70**	0.359	0.421	0.312
22	0.615	0.834	0.397	**47**	0.312	0.474	0.148	**71+**	0.695	0.620	0.739
23	0.403	0.525	0.273								

Table 1 Mean Absolute Percent Error for best aging chain (%)

Figure 2 compares extrapolations from Eurostat [9], three extrapolations from the Czech statistical office [6] and results from most accurate aging chain model with fixed delay for aging and normal distribution for fertility. The presented result from modeled aging chain used low extrapolation of CZSO for exogenous variables, (i.e. total net immigration is 15,000 persons, LEF = 86.4 LEM = 81.6 in 2050) and middle extrapolation for fertility parameters (average mothers' age grows to 31 years in 2050 and total fertility grows to 1.72 in same year).

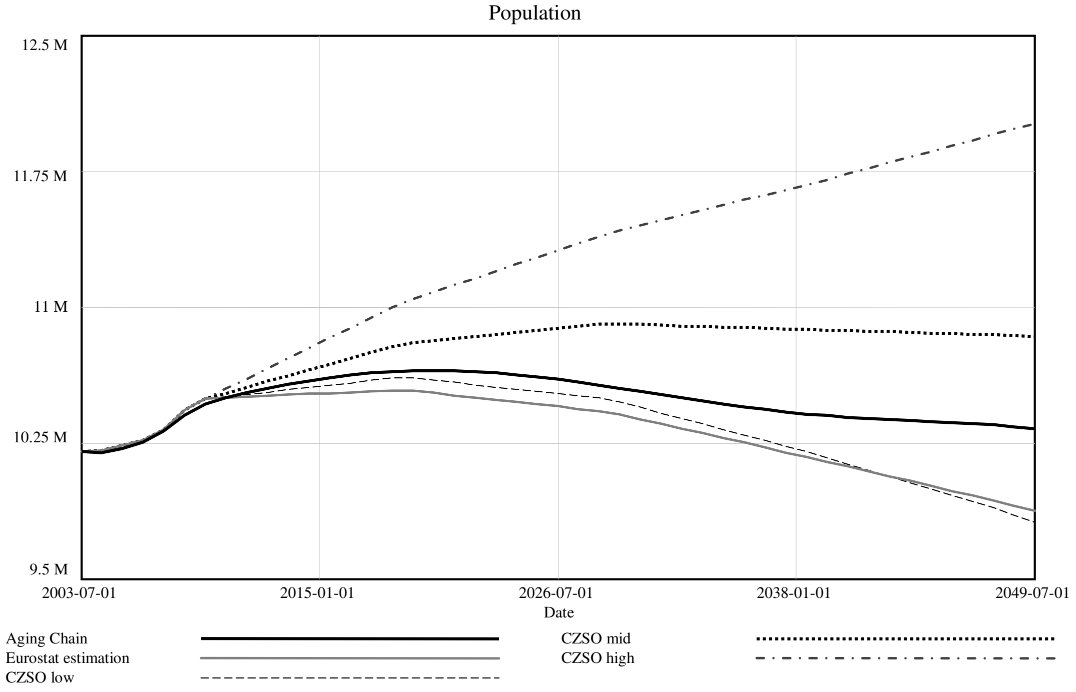

Figure 2 Simple stock and flow diagram of aging chain

The results shown that one-year cohorts are always better than five-year. Also the normal distribution approximation for fertility led to better results. Furthermore, the approximation simplifies the model construction (fertility indices require regression for every appropriate age cohort). Better results from fixed delay exit rate probably rise from highly non-uniform Czech population age structure, see figure 3 for comparison (cohort 71+ was excluded from the picture). On the left the structure is from second best model with first order delay like in [14] or [17], which smoothes the structure, on the right is the result from best model with fixed delay. The structure at 2003 is surveyed [2] and is same for both aging chains.

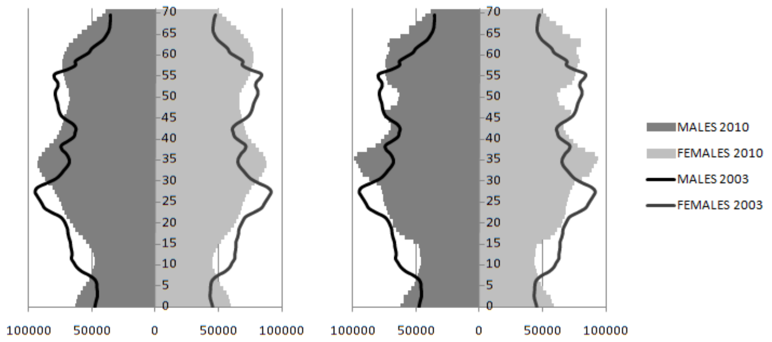

Figure 3 Comparison of age structure from different aging chains

4 Conclusions

We compared eight variants of aging chain with different age cohorts, different form of outflow from these cohorts and different approximation of fertility distribution. The best model used one year age cohorts, normal distribution approximation for fertility and fixed delay for outflow from age cohorts. The last is different from aging chains used in more complex models [14, 17], which rises from specific age structure of Czech population.

The presented aging chain is prepared for implementation into more complex system dynamics models. And we can provide it to any author for testing or implementation into their own model. Although it isn't constructed for purely predictive purposes it is also possible to use it this way.

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