Economics Letters 113 (2011) 269–272

Contents lists available at SciVerse ScienceDirect

Economics Letters

journal homepage: www.elsevier.com/locate/ecolet

Disease and development: The role of life expectancy reconsidered☆

Matteo Cervellati [a,b], Uwe Sunde [c,b,d,*]

[a] University of Bologna, Italy
[b] IZA, Bonn, Germany
[c] University of St. Gallen, Switzerland
[d] CEPR, London, United Kingdom

ARTICLE INFO

Article history:
Received 3 February 2011
Received in revised form
12 August 2011
Accepted 17 August 2011
Available online 24 August 2011

JEL classification:
J10
J13
N30
O10
O40
E10

Keywords:
Life expectancy
Demographic transition
Epidemiological revolution
Heterogeneous treatment effects
Finite mixture models

ABSTRACT

This note estimates the causal effect of life expectancy on per capita income and tests the hypothesis of a non-monotonic effect using finite mixture models. The results confirm the hypothesis and qualify recent evidence for a negative effect by Acemoglu and Johnson (2007).

1. Introduction

In their influential paper, Acemoglu and Johnson (2007) (AJ) investigate the effect of life expectancy on economic growth, exploiting within-country variation on the exogenous reduction in mortality that followed the epidemiological revolution of mid-20th Century. Contrary to previous evidence based on cross-country variation, see, e.g., Lorentzen et al. (2008), their results indicate that (instrumented) life expectancy had a positive effect on population growth but a negative effect on income per capita. The surprising conclusion is that better health does not have a positive effect on economic growth.

This note revisits the analysis in view of the non-monotonic relationship between life expectancy and population that is predicted from standard demographic transition theory. In light of the widely documented stylized facts, the standard representation of the "demographic transition" begins with an initial drop of mortality, DT, which is followed by a drop in fertility, FT (Chesnais, 1992) or (Livi-Bacci, 1992). The time delay between DT and FT induces a hump-shaped population growth, which initially accelerates due to the lower mortality but eventually slows down due to reduced fertility. In the presence of Malthusian effects, GDP per capita may be affected negatively by life expectancy in response to the increase in population growth, but the effect should be positive in countries after the fertility transition.[1] The non-monotonic effect of life expectancy on population growth should therefore be associated with non-monotonic effects on GDP per capita, as illustrated in Fig. 1.

This note replicates the analysis of AJ using their data and identification strategy, but relaxes the constraint that the effect should

☆ We thank Martin Huber, Davide Raggi, Rudi Stracke, Anthony Strittmatter, and Thomas Vischer for helpful comments.

* Correspondence to: University of St. Gallen, SEW-HSG, Varnbuelstr. 14, CH-9000 St. Gallen, Switzerland. Tel.: +41 71 224 2309; fax: +41 71 224 2302.
E-mail address: uwe.sunde@unisg.ch (U. Sunde).

[1] For studies predicting these dynamics see, e.g., Kalemli-Ozcan (2002), Soares (2005), Boucekkine et al. (2008), and Cervellati and Sunde (2007, 2011), among others.

0165-1765/$ – see front matter © 2011 Published by Elsevier B.V.
doi:10.1016/j.econlet.2011.08.008

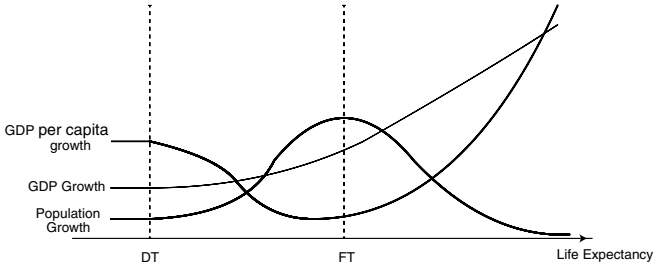

Fig. 1. Life expectancy, population and income growth.

be the same in all countries since estimating the causal effect of life expectancy on income per capita growth without accounting for its inherent non-monotonicity may deliver misleading results. This is done using finite mixture models (FMM) that account for possible non-monotonic causal effects of life expectancy on growth.

2. Empirical framework, data and identification

The dependent variable is growth in log GDP per capita, the central explanatory variable is the change in life expectancy at birth.[2] The causal effect of changes in (instrumented) life expectancy, $\Delta\widehat{\ln T_i}$, in country i on growth in income per capita, $\Delta \ln y_i$, is estimated by AJ in a log-linear specification,

$$\Delta \ln y_i = C + \pi \Delta\widehat{\ln T_i} + u_i$$

using a long panel of 47 countries with two observations per country (1940 and 1980). The instrument for the change in life expectancy in a country is the drop in mortality from the 15 most important infectious diseases due to the epidemiological revolution. This reduction in mortality is exogenous since there were no effective treatments or vaccines for these diseases available by 1940. All of the diseases could be treated and even be prevented everywhere by 1980, independently of the level of economic development thanks to the advances in medical knowledge, drugs, prevention technologies (such as DDT for the eradication of malaria transmitting vectors) and through their world-wide dissemination by international organizations like WHO or UNICEF. Hence, the identifying assumption is that mortality from the respective diseases is exogenous in 1940 for lack of appropriate medical treatments, and unrelated to economic development in 1980 due to the world-wide dissemination of innovations in the medical sector after World War II.[3] As described in AJ, the predicted mortality change has a strong effect on changes in life expectancy, and countries with initially low life expectancy benefitted relatively more since mortality from the main killers was higher.

Demographers have used different criteria to characterize countries in terms of whether they passed the critical turning point of the demographic dynamics depicted in Fig. 1. The conventional criteria are (Chesnais, 1992, p. 19):

1. *Life expectancy at birth exceeds* 50;
2. *Fertility or the crude birth rate has exhibited a sustained decline*;
3. *The crude birth rate has fallen below a given threshold* (30/1000 *or* 25/1000).

The application of each criterion allows us to classify countries into two groups. In the sample of 47 countries studied by AJ there are 25, 28 and 31 countries that do not fulfil each of respective criteria by 1940. We call these countries pre-transitional, while the countries fulfilling the criteria are called post-transitional.[4] The simplest test of the hypothesis that the effect of life expectancy depends on the stage of the demographic transition is to exploit information on the pre-treatment status of countries in 1940 and to allow for a heterogeneous effect of life expectancy by splitting the sample. This strategy, which has been applied by Cervellati and Sunde (2011), has the advantage of closely reflecting the demographic transition theory, but has the disadvantage of relying on an exogenously imposed country classification.

An alternative, more flexible, way to account for the potential heterogeneous effect of the effect of life expectancy on growth countries is to estimate the effect of life expectancy and the probability of being in one of two distinct growth regimes jointly without imposing any ex-ante classification. This can be done by estimating the growth process as a finite mixture model with two latent components.[5] This approach has the advantage of being entirely data driven, and allows for a parametric estimation of the regime probabilities. In this case, the density function of observed growth rates conditional on the latent regime $j = pre, post$ is given by

$$p(\Delta \ln y|\Delta \ln T; \boldsymbol{\pi}, \mathbf{w}) = w^{pre}(X)p(\Delta \ln y_i|\Delta \ln T; \pi^{pre}) + w^{post}(X)p(\Delta \ln y_i|\Delta \ln T; \pi^{post}),$$

where π^j are the coefficients of interest that are supposed to differ across regimes, and w^j are weights that take values between 0 and 1. The weights are parameterized as a logit of the form

$$w^{pre}(X) = \frac{1}{1+\exp(\gamma^{post}X)} \quad \text{and}$$

$$w^{post}(X) = \frac{\exp(\gamma^{post}X)}{1+\exp(\gamma^{post}X)},$$

with covariates X as determinants of regime membership, and γ^j being parameters to be estimated that capture the effect of the covariates X on the probability of being in either regime. The covariate X can be generically specified as a constant, or using variables that are potential determinants of the latent growth regime in 1940. We assume a normal distribution with standard deviation σ and estimate the parameters on the basis of $N = 47$ observations in long differences by maximizing the log likelihood function

$$\max_{\pi^{pre},\pi^{post},w^{pre},w^{post}} L = \prod_{i=1}^{N} \left(\ln\left(w^{pre}(X)p(\Delta \ln y_i \mid \Delta \ln T; \pi^{pre}) + w^{post}(X)p(\Delta \ln y_i \mid \Delta \ln T; \pi^{post})\right)\right),$$

where

$$p(\Delta \ln y_i|\Delta \ln T; \pi^j) = \frac{1}{\sqrt{2\pi(\sigma^j)^2}} \exp\left(-\frac{(\ln y_i - \ln T_i\pi^j)^2}{2(\sigma^j)^2}\right)$$

for $j = pre, post$.

The analysis below presents results for intention to treat (reduced form) models, using the predicted mortality instrument as regressor. This helps avoiding potential endogeneity problems associated with life expectancy and allows inference using standard tests.[6]

[2] The data sources are the *United Nations Demographic Yearbook* and Maddison (2003).

[3] See Acemoglu and Johnson (2007) for details.

[4] The first criterion delivers the same classification as the third one for a threshold of 30/1000. The second criterion follows Reher (2004) by considering if a country has entered a falling trend of crude birth rates by the year 1935 using 5-year averages. The third criterion with a threshold of 25/1000 refers to advanced stages of the transition and is the most restrictive. See Cervellati and Sunde (2011) for a detailed discussion of the different classifications.

[5] See Frühwirth-Schnatter (2006) for a detailed account of finite mixture models, and Owen et al. (2009) for an application to growth regressions.

[6] From the discussion in AJ the relationship between predicted mortality reductions and increases in life expectancy is negative and approximately linear.