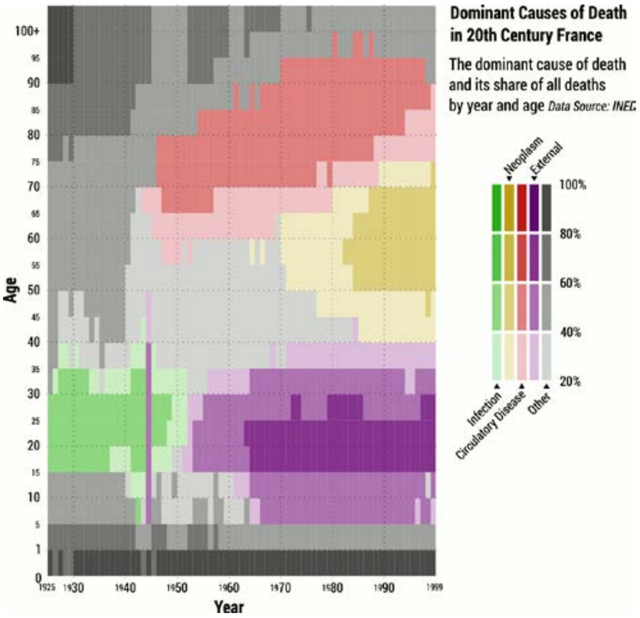
UNIVERSITY OF SOUTHERN DENMARK

MaxO Max-Planck Odense Center on the Biodemography of Aging

MAX-PLANCK-GESELLSCHAFT

Max-Planck Odense Center on the Biodemography of Aging

ANNUAL REPORT 2015



Dominant Causes of Death in 20th Century France

The dominant cause of death and its share of all deaths by year and age *Data Source: INE*

Max-Planck Odense Center on the Biodemography of Aging
http://www.sdu.dk/maxo

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People affiliated with MaxO

Leadership:

James W. Vaupel, Professor, Public Health, Director
Kaare Christensen, Professor, Public Health, Deputy Director
Donald Canfield, Professor, Biology, Deputy Director
Annette Baudisch, Professor MSO of Biodemography, Biology
Rune Lindahl-Jacobsen, Associate Professor, Deputy Head, Public Health
Hal Caswell, Adjunct Professor, Biology

Research staff:

Vladimir Canudas-Romo, Associate Professor, Public Health
Jim Oeppen, Associate Professor, Public Health
Ulrich Steiner, Associate Professor, Biology

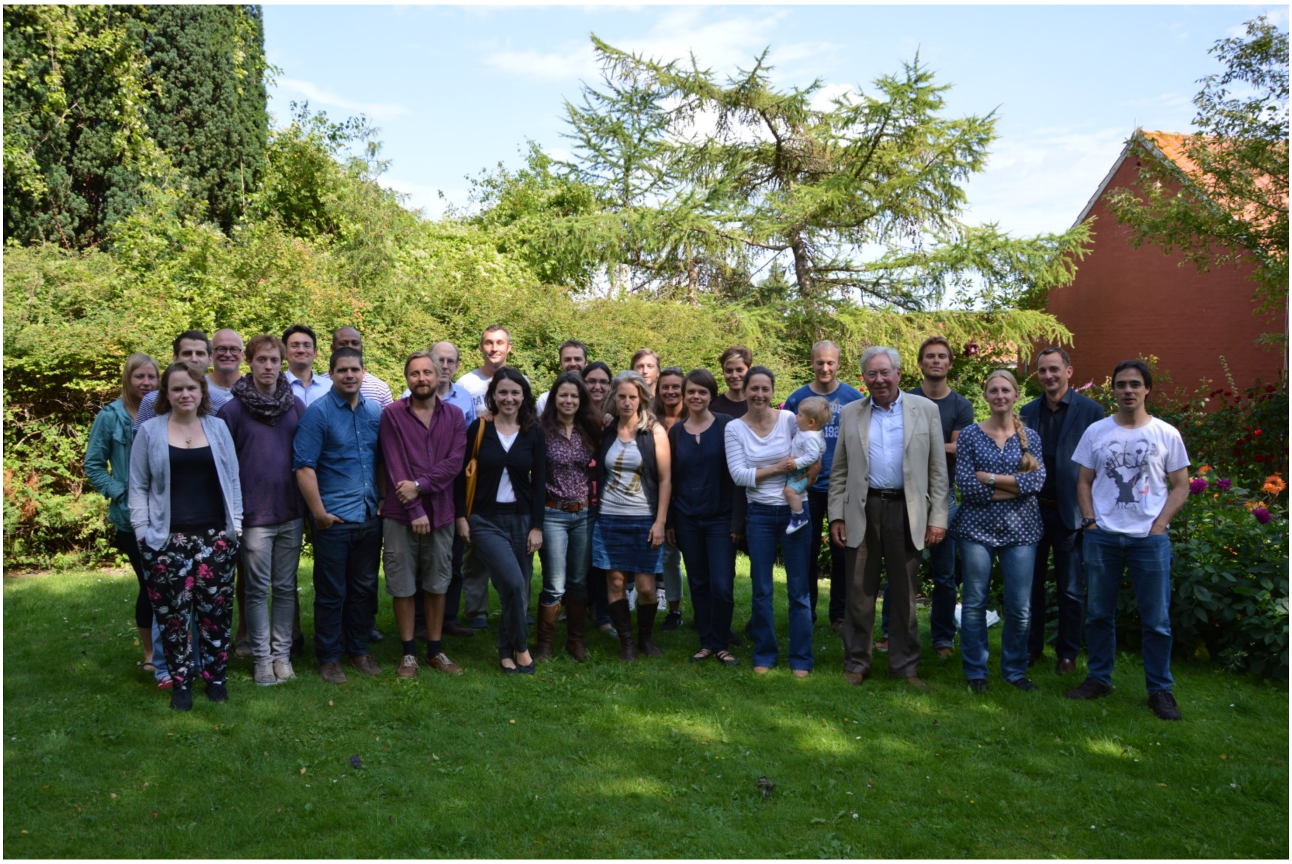
Fernando Colchero, Assistant Professor, Mathematics
Dalia Amor Conde, Assistant Professor, Biology
Johan Dahlgren, Assistant Professor, Biology
Owen Jones, Assistant Professor, Biology
Maarten Wensink, Assistant Professor, Public Health
John E. Fa, Visiting Professor, Biology

Julia Barthold, Post Doc, Public Health
Lionel Jouvet, Post Doc, Biology
Adam Lenart, Post Doc, Public Health
Jonas Wastesson, Post Doc, Public Health
Virginia Zarulli, Post Doc, Public Health (on maternity leave)
Mikael Thinggaard, Post Doc, Public Health

Marie-Pier Bergeron Boucher, PhD student , Public Health
Josephine Goldstein, PhD student, Biology
Lars Kumala, PhD student, Biology
Marius Pascariu, PhD student, Public Health
Danielle Sherman, PhD student, Biology
Johanna Stärk, PhD student, Biology
Francisco Villavicencio, PhD student, IMADA

Maria Baden, Research Assistant, Biology
Søren Kjærgaard, Research Assistant, Public Health
Anthony Medford, Research assistant, Public Health
Silvia Rizzi, Research Assistant, Public Health

Jonas Schöley, Research assistant, Public Health
Catalina Torres, Research assistant, Public Health
Lucia Zanotto, visiting researcher, Public Health
Vibeke Jensen, Secretary, Biology



Please note that this report focusses on the Research Staff of MaxO. For information about the leadership of MaxO, please see:

James Vaupel: http://user.demogr.mpg.de/jwv/

Kaare Christensen: http://www.sdu.dk/staff/kchristensen

Donald Canfield: http://www.sdu.dk/staff/dec

Annette Baudisch: www.sdu.dk/staff/baudisch

Rune Lindahl-Jacobsen: www.sdu.dk/staff/rjacobsen

Hal Caswell: http://www.uva.nl/en/about-the-uva/organisation/staff-members/content/c/a/h.caswell/h.caswell.html

Demography of MaxO 2015

Arrivals to the group in 2015

Mikael Thinggaard, Post Doc, Public Health
Jonas Wastesson, Post Doc, Public Health
Francisco Villavicencio, PhD student, IMADA (Mathematics and Computer Science)
Maarten Wensink, Assistant Professor, Public Health
Søren Kjærgaard, Research Assistant, Public Health
Silvia Rizzi, Research Assistant, Public Health
Jonas Schöley, Research Assistant, Public Health
Catalina Torres, Research Assistant, Public Health
John E. Fa, Visiting Professor, Biology
Lucia Zanotto, visiting researcher, Public Health

Babies born in 2015

Ulrich Steiner had a baby boy in April 2015
Virginia Zarulli and Adam Lenart had a baby girl in July 2015

People who left the group in 2015

Daniel Levitis, Assistant Professor, Biology
Paul Dunn, Post Doc, Biology
Raisa Hernandez-Pacheco, visiting post doc, Biology
Kim Lundgreen, Academic Assistant, Biology

Research staff highlights

Jim Oeppen, Associate Professor, Public Health

Main research interest

"Forecasting Mortality by Cause of Death"

Forecasting mortality is a difficult problem that is undertaken by many international, government, and financial institutions. It would be useful to disaggregate these forecasts by cause of death because that would allow policy makers to identify target areas for future reductions in mortality. In addition, the ultimate cause of death may be a good guide to the period of ill health that precedes most deaths and help to indicate its cost to society. At the moment, very few institutions try to forecast mortality by cause of death because of the technical difficulties.

One of the reasons it is more difficult is that even though the average age at death is generally rising, each person must die, so if the forecast suggests that a cause will become less important in the future , one or more of the other causes has to absorb extra deaths and not necessarily at the same age. A second problem arises because we would like the sum of the forecasts for each cause to match the existing forecasts that do not separate the causes of death. This project undertakes basic research to explore new statistical methods that are explicitly designed to address these problems.

Ongoing work

"Forecasting Mortality by Cause of Death"

Planners in public and private institutions would like coherent forecasts of the components of age-specific mortality, such as causes of death. This has been difficult to achieve because making a separate forecast for each cause, or group of causes, has proved inadequate. The relative values of the separate forecast components often fail to behave in a way that is coherent with historical experience. In addition, when the individual forecasts are combined the result is often incompatible with an all-groups forecast. It has been shown that cause-specific mortality forecasts are pessimistic when combined and compared with all-cause forecasts.

This research abandons the conventional approach of forecasting separate time-series of log mortality rates for each cause and forecasts the cause-specific density of deaths d(x) in a single model of a time-series of multiple-decrement life tables. Demographers have given a little theoretical attention to "life-saving" models that treat survival improvement as a perturbation of the density of the death distribution by age d(x), but there have been no previous attempts to define such models for forecasting in a single- or multiple-decrement context.

"Medical Intervention and the Demography of Years Gained"

Demographers have considerable expertise in analysing how changes in mortality rates affect life expectancy at the aggregate level, but for the last 50 years they seem to have made no contribution to analysing the effectiveness of individual medical interventions. This research is concerned with methods for calculating the number of person–years needed–to–treat in order to add one year of life expectancy. Some specific calculations suggest that the treatment time required to add one year may be many multiples of an individual's expected remaining lifetime. The issues of the proper measure of the effectiveness of a treatment, and how to communicate this correctly to the patient and the doctor, are important topics in medicine and epidemiology.

Publication highlights

Cohort–Specific Mortality Response in the 1918 Influenza Pandemic.

The Influenza pandemic of 1918 was the worst in statistical history, but the adaptive immune system is thought to have protected older cohorts through prior exposure to a similar virus. Its unique lethality amongst young adults is unexplained. The objective was to investigate the hypothesis that excess mortality risk in 1918 can be understood as an interaction between the new virus and cohort-specific immunological experience. A multi-national, cohort study using a population-level, epidemiological method was applied to data from the Human Mortality Database. We estimated the effect of the virus on each female birth cohort in 1918, after controlling for age, by comparing the pandemic mortality rate and the "normal" rate from 1913 to 1917 for women of the same age. There is a clear association between the severity of relative risk in 1918 and the cohorts born around the time of the previous pandemic of 1891, although the reasons are unclear. The results show that analyses of aggregate mortality can be used to supplement the laboratory analysis of the legacy of earlier exposure to other influenza viruses and confirm the importance of assessing unusual cohort-specific mortality when evaluating the threat of a new virus.

Vladimir Canudas-Romo, Associate Professor, Public Health

Main research interest

My main research interests are

- Formal demography or the mathematical relations between demographic measures is at the core of my interests: I continue to develop new demographic measures and methods that help explicate observed population phenomena.

- Causes of death modeling and forecasting remain among my deepest interests. I believe the future rise in life expectancy will still be heavily dependent on public health interventions, as it was in the past (sanitation, living standards, clean water, health-education, etc.). However, medical innovations will also play a central part in this change. Demography, and more specifically the study of mortality by causes of death, will be at the center of this debate helping experts from other fields disentangle the contribution of the new advances in both public health and clinical practices.

- Demography has a central role in the public debate because it informs about existent "Disparities" in populations. In the study of mortality/health disparities by causes of death mentioned above I would also like to study the experience of cohorts, as opposed to period studies on causes of deaths.

- Using individual-level register data from Denmark, I would be interested to study the life span of couples. Previously, a strong association has been noted between wives and husbands with regard to their achieved level of education, socioeconomic status, religion, lifestyle, and other social and behavioral factors. Associations between spouses' specific causes of death have also been identified, e.g. smoking related causes of death, HIV/AIDS and tuberculosis. Nevertheless, correlations between couples' ages at death as well as between their causes of death when all causes are considered remain to be addressed. It would be interesting to further expand this project to other Scandinavian countries, twin-register partners and US data.

Publication highlights

Canudas-Romo, V., M. Guillot. 2015. "A Measure for Comparing the Mortality History of Cohorts: TCAL." Population Studies 69:2, 147-159, doi: 10.1080/00324728.2015.1019955.

Period life expectancies are commonly used to compare populations, but these correspond to simple juxtapositions of current mortality levels. In order to construct life expectancies for cohorts, a complete historical series of mortality rates is needed, and these are available for only a subset of developed countries. The Truncated Cross-sectional Average Length of Life (TCAL) is a new measure that captures historical information about all cohorts present at a given moment and is not limited to countries with complete cohort mortality data. The value of TCAL depends on the rates used to complete the cohort series, but differences between TCALs of two populations remain similar irrespective of the data used to complete the cohort series. This result is illustrated by a comparison of TCALs for the United States of America with those for Denmark, Japan, and other high-longevity countries. Specific cohorts that account for most of the disparity in mortality between the populations are identified.

Canudas-Romo, V., A. Lenart. 2015. “Mortality of the Oldest-Old.” In: James D. Wright (editor-in-chief), International Encyclopedia of the Social & Behavioral Sciences, 2nd edition, Vol 15. Oxford: Elsevier. pp. 863–867

“An 80-year-old is as healthy today as a 70-year-old yesterday,” such phrases are not uncommon, and we can actually observe that the probability of death of an 80-year-old in Japan in 2009 corresponds to the mortality of a 70-year-old in 1959. This significant change in the mortality level of the oldest-old population, i.e., people 80 years and older, is the focus of this article. Among other topics, we concentrate on the age patterns, time changes, and population variation in mortality among the oldest age groups of the population.

Roberts ET, DuGoff EH, Heins SE, Swedler DI, Castillo RC, Feldman DR, Wegener ST, Canudas-Romo V, Anderson GF. Evaluating Clinical Practice Guidelines Based on Their Association with Return to Work in Administrative Claims Data. Health Serv Res. 2015 Sep 14. doi: 10.1111/1475-6773.12360.

Objective. To examine the association between non-adherence to clinical practice guidelines (CPGs) and time to return to work (RTW) for patients with workplace injuries.

Data Sources/Study Setting. Secondary analysis of medical billing and disability data for 148,199 shoulder and back injuries from a workers’ compensation insurer.

Study Design. Cox proportional hazard regression is used to estimate the association between time to RTW and receipt of guideline-discordant care. We test the robustness of our findings to an omitted confounding variable.

Principal Findings. Receiving guideline-discordant care was associated with slower RTW for only some guidelines. Early receipt of care, and getting less than the recommended amount of care, were correlated with faster RTW. Excessive physical therapy, bracing, and injections were associated with slower RTW.

Conclusions. There is not a consistent relationship between performance on CPGs and RTW. The association between performance on CPG and RTW is difficult to measure in observational data, because analysts cannot control for omitted variables that affect a patient’s treatment and outcomes. CPGs supported by observational studies or randomized trials may have a more certain relationship to health outcomes.

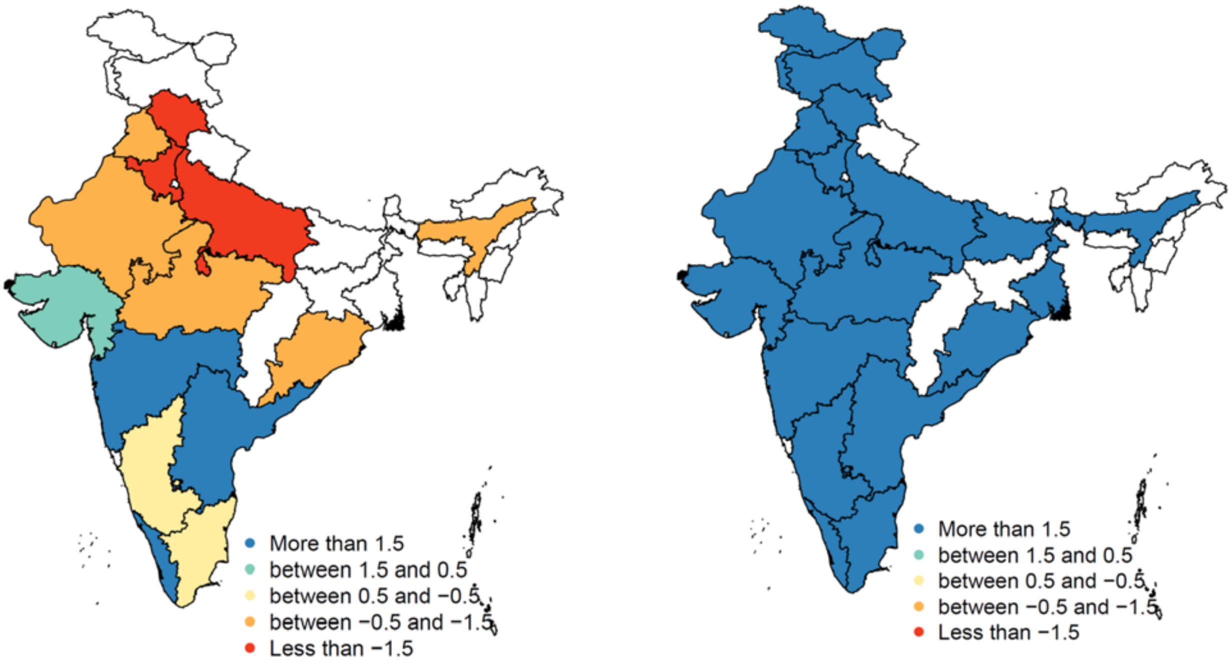
Ongoing work

“Aburto, J.M., H. Beltrán-Sánchez, V.M. García-Guerrero, V. Canudas-Romo. (in press). “The lost decade at the turn of the century: health disparities and heterogeneity among states in Mexico.” Health Affairs”

After more than six decades of sustained improvements in life expectancy, Mexico experienced stagnation in 2000-2010. This decade was characterized by the enactment of a major health care reform (Seguro Popular) that aimed at providing coverage for the entire Mexican population, and by an unexpected increase in homicide mortality. We assessed the impact on life expectancy of conditions amenable to medical service, sensitive to public health policies and behaviors, homicides, and diabetes by analysing mortality trends at the state level. We find life expectancy deterioration among males in 2005-2010 relative to improvements made in 2000-2005. Opposing this trend, females in most states experienced small gains in life expectancy by 2010. The unprecedented rise in homicides after 2005 lead to a reversal in life expectancy among males and a slowdown among females in most states in the first decade of the 21st century.

“Canudas-Romo, V., N. Saikia, N. Diamond-Smith. (in press). “The contribution of age-specific mortality towards male and female life expectancy differentials in India and selected States, 1970-2013.” Asia-Pacific Population Journal”

Most research on mortality differentials by sex in India focusses on disparities among children under 5 years of age. In this paper, we assess the changing age and cause patterns of mortality by sex in India and selected states using survey data and including mortality trends over the life span. Since the 1970s, the gap between female and male mortality in India has increased to females’ advantage. This occurred despite persisting higher female mortality below age 5, a disadvantage masked by the large gap favoring women at adult and older ages. This paper finds that the life expectancy gap between females and males in the second half of the 1990s can be attributed mainly to non-communicable diseases and external causes of death. While more developed states (primarily in the South) already showed higher female longevity in the 1970s, the states that lagged behind displayed similar mortality levels for females and males up until the turn of the century.



Maps of the state distribution of the female to male life expectancy at birth gap (female-male), India, 1970-75(panel-a) and 2009-13 (panel-b).

New grants awarded

1) Title: “Why do Hong Kong live so long?” Description: To study the extremely long life of the population from Hong Kong. Agency: Hong Kong Research Grant Council. Role: Consultant (5% Effort Time)

Starting: January 2016

2) Visiting fellow Australian National University award. To be used for travel and accommodation in January 2016.

Ongoing grants

I closed my European Research Council starting grant in the summer of this year.

Rune Lindahl-Jacobsen, Associate Professor, Deputy Head, Public Health

Main research interest

A special research area of interest is sex differences in mortality and health with focus on 'The male-female health survival paradox' (e.g. why men die whereas women suffer). Its determinants have been studied in both animal and human populations and this research may provide additional clues on why women outlive men in all human populations World Wide. Trends in life expectancy and mortality and explanations for these trends at a population level have been one of my important research areas with the aim of pointing towards possible factors explaining these trends. That these factors could act both in time and on specific generations, and developing methods for examining this, have been a part of my research through time. One factor I have studied with particular interest is the effect of smoking and the smoking epidemic on mortality patterns of various populations.

On the developmental part, fertility patterns and its associations with reproductive hazards, increased mortality and diseases is a part of my research field with studies ranging from trends in assisted reproductive techniques and childlessness to analysis of life expectancy depending on semen quality.

Publication highlights

Ahrenfeldt L.J., Skytthe A., Möller S., Czene K., Adami H.O., Mucci L.A., Kaprio J., Petersen I., Christensen K., Lindahl-Jacobsen R. Risk of Sex-Specific Cancers in Opposite-Sex and Same-Sex Twins in Denmark and Sweden. Cancer Epidemiol Biomarkers Prev. 2015 Oct;24(10):1622-8.

Increasing evidence shows that some cancers originate in utero. It is hypothesized that elevated exposure to some steroid hormones might increase cancer risk and that hormone transfer between twin fetuses could result in different prenatal exposure to testosterone.

This large-scale prospective twin study compared opposite-sex (OS) and same-sex (SS) twins to test the impact of intrauterine exposures on cancer risk. On the basis of the Danish and Swedish twin and cancer registries, we calculated incidence rate ratios for OS and SS twins, whereas standardized incidence ratios (SIR) with 95% confidence intervals (CI) were calculated for OS/SS twins compared with the general population.

No significant differences were observed between OS and SS twins, neither for the sex-specific cancers nor for cancer at all sites. All-cause cancer was slightly reduced for OS and SS twins compared with the general population, significant for OS males (SIR, 0.95; 95% CI, 0.92-0.98) and for SS males and females (SIR, 0.97; 95% CI, 0.94-0.99).

Having a male co-twin - which may entail higher exposure to prenatal testosterone - does not increase the risk of sex-specific cancers in OS females.

Ongoing work

"Effects of smoking on the male-female Health survival paradox "

The smoking epidemic during the last century when first men took up smoking followed by women, has had a tremendous influence on the mortality patterns seen in many Western populations. The differential onset of taking up smoking and the influence on later mortality is a factor that influences the sex differences seen in life expectancy in these populations. In these studies we aim to quantify the influence of smoking on the sex differences in life expectancy seen in the populations of Denmark, Sweden and Utah. Using lung cancer death rates from the extensive Danish, Swedish and Utah population registers on causes of death we will be able to calculate the smoking component of the age specific deaths responsible for the sex differential mortality. The method to be used is the revised version for estimating smoking-attributable mortality by Preston, Glei, and Wilmoth (the PGW-R method). Using the Utah population will further make us able to address the applicability of the PGW-R method as causes of death are available by religious setting, including Mormons where smoking is not allowed.

Conferences/activities

Reviewer for the Swedish Research Council on 2015 applications: 1) Health Care science 2) Distinguished professors

Ulrich Steiner, Associate Professor, Biology

Main research interest

I am interested in variability among individuals in their life courses, what influences such variability and how it evolves and is maintained. In particular I am interested in decomposing stochastic, environmental and evolutionary drivers of individual differences. My approach is based on developing age-stage structured models rooted within Markov chain theories. I confront these theories with empirical data collected on a microfluidic device that records individual level demographic information for thousands of bacteria.

Publication highlights

"Constraints on the evolution of phenotypic plasticity: limits and costs of phenotype and plasticity "

Phenotypic plasticity is ubiquitous and a key mechanism for enabling organisms to survive in the face of environmental change. Because no organism is infinitely or ideally plastic, theory suggests that there must be limits to the evolution of phenotypic plasticity, or that plasticity may have inherently significant costs. Yet numerous experimental studies have not detected widespread costs. Explicitly differentiating plasticity costs from phenotype costs, we re-evaluate fundamental questions of the limits to the evolution of plasticity and of generalists vs specialists. We advocate the view that relaxed selection and variable selection intensities are likely to be more important constraints on the evolution of plasticity than the costs of plasticity. In addition, we examine opportunities to offset costs of phenotypes through ontogeny, amelioration of phenotypic costs across environments, and the condition-dependent hypothesis. We propose avenues of further inquiry on the limits of plasticity using new and classic methods of ecological parameterization, phylogenetics and omics in the context of answering questions on the constraints of plasticity. Given plasticity's key role in coping with environmental change, approaches spanning the spectrum from applied to basic will greatly enrich our understanding of the evolution of plasticity and resolve our understanding of its limits.

Ongoing work

"Stochastic processes rather than age shape diverse senescence patterns in a single-cell organism"

Senescence patterns are thought to be universal and directional, but a diversity of patterns across species is observed. Here we report on diverse senescence patterns even within one species. We report on isogenic Escherichia coli bacteria that exhibit classical senescence patterns even in controlled, homogeneous environment. While daughters produced early in a mother's life reveal classical senescence pattern resembling those of humans, late daughters do not senescence. Senescence is thus mostly unpredictable and not age-driven. Rather, it results from stochastic processes underlying an individual's life course. This is in contrast to evolution theory's postulates that base their reasoning on age-specific action of alleles, or similar epigenetically motivated arguments. Our results call for a shift of focus of aging research towards such stochastic processes in simple organisms and beyond.

"Drivers of diversification in individual life courses"

Heterogeneity among individuals influences the speed of adaptive and neutral evolutionary processes, but it is less clear how biotic and abiotic environmental fluctuations influence variability among individuals. Such variability is reflected in individual life courses, defined as the sequence of stages experienced during an individual's life. To determine its principal drivers for stage-structured populations we quantify this heterogeneity by a measure of entropy. This measure quantifies the rate of diversification of individual life courses and is determined by stage-dependent vital rates in any year. We investigate the influence of population density, cohorts and time periods on entropy. Using 40 years of individual data on a free-ranging primate population we show that changes in population density drive individuals into a certain stage, rather than the alternative of forcing individuals to explore new niches by diversifying life courses. High population density reduces heterogeneity in individual life courses. This finding is independent of stage-specific survival, cohort, or period effects. Our results suggest that populations under density-dependent regulation experience both a reduction in individual heterogeneity and in population growth rate. To this end the variability in life courses that selection can act upon is reduced under the more stressful high density scenario.

Ongoing grants

AXA research dissemination fund

Conferences/activities

Keynote speaker International CRC 973 Symposium “Bridging Ecology and Molecular Biology: Organismic Responses to Recurring Stress”, 18-20.2.2015, Berlin, Germany

NESCent working group meeting ”Cryptic Genetic Variation and the Evolution of Reaction Norms in Novel Environments”, 23-25.2. 2015, Durham, NC, US

Workshop “Individual heterogeneity”, 13.10. 2015, Tromsø, Norway

Evolutionary Demography meeting, 5.-7. 10. 2015, Lunteren, Netherlands

Fernando Colchero, Assistant Professor, Mathematics

Main research interest

I work on linking mathematics, statistics and demography to understand what shapes demographic rates and spatial processes in wild populations. My projects include the development and application of hierarchical Bayesian models to estimate age-specific demographic rates when age is unknown (e.g. R package BaSTA), and to understand animal population dynamics with incomplete count data. I am particularly interested in understanding how age, heterogeneity and environmental factors affect mortality and fertility in wild populations, and how these may determine age-specific demographic rates, ageing rates, and population growth.

Publication highlights

Colchero, F. and R. Schaible (2014) Mortality as a bivariate function of age and size in indeterminate growers. Ecosphere 5(12): 161

Mortality in organisms that grow indefinitely, known as indeterminate growers, is thought to be driven primarily by size. However, a number of ageing mechanisms also act as functions of age. Thus, to explain mortality in these species, both size and age need to be explicitly modeled. We developed a mathematical framework that treats age- and size-specific mortality as a bivariate process, which facilitates the exploration of the underlying (unobserved) contributions of age and size to mortality. We then embed the model into a Bayesian inference framework, which we first applied to simulated data, and then used it to test hypotheses regarding the effects of age and size on mortality on published datasets. We show how this method can help to improve the demographic models commonly applied to a vast number of species of commercial and conservation importance such as fish, trees, or bivalves, for which both age and size are relevant. In addition, the application of these methods can help to shed light on the existence of processes such as negative senescence, and contribute to our understanding of the evolutionary mechanisms of senescence in species that do not fit the established theories.

Ongoing work

“Unravelling the effect of individual heterogeneity and environment on demographic rates”

Recent studies have revealed that there is a striking diversity of age-specific trajectories of demographic rates in nature. Although some of these trends in mortality over age have been described theoretically, current statistical methods cannot yet reproduce the astonishing variety of age-specific trajectories of mortality–and the unobserved processes that produce them–for populations under natural conditions. My current research is motivated by the urgent need to develop state of the art statistical methods to understand how demographic rates, and in particular mortality, are regulated by environmental factors; what is the role that individual differences in frailty (i.e. heterogeneity) play in shaping them; and how the environment and individual heterogeneity interact to govern demographic rates. I am combining the latest advances in Bayesian inference, state-space modelling and multidisciplinary biodemographic approaches to make a substantial leap forward in our understanding of ageing and its underlying mechanisms. Such improvement in our capacity to model and understand these processes will allow us and other researchers to find answers to fundamental questions about the processes that govern ageing, their relation to longevity, and how they could have evolved.

New grants awarded

E-science PhD support.

Conferences/activities

Workshop: BaSTA. BES annual Symposium “Demography Beyond the Population,” University of Sheffield, UK, 23 March. ***Lecturer***

Conference: Colchero, F. and R. Schaible *Mortality as a bivariate function of age and size in indeterminate growers*. Statistics in Ecology and Environmental Monitoring, SEEM 2015 conference, University of Otago, Queenstown, New Zealand, June 2015.

Workshop: Evolutionary Ecology of Primate Life Histories. National Evolutionary Synthesis Center (NESCent). Duke University, Durham, North Carolina, May 7-10, 2015.

Workshop: The Era of Big Data Hits Conservation Science. Centre of Excellence for Environmental Decisions (CEED) University of Queensland, Australia, 15-19 June 2015

Dalia A. Conde, Assistant Professor, Biology

Main research interest

My work focusses mainly on the field of conservation demography. In the MPIDR I started the conservation research section, and now I continue developing this research at MaxO. I am particularly interested in exploring ways to incorporate methods from formal demography and population biology to manage species that are at risk of extinction. However, there is a lack of reliable demographic data for most taxa. Therefore my work focusses on developing indexes of data availability and knowledge at the species level for demographic analyses, finding gaps in data and exploring alternative ways to parameterize models for species with little or no demographic data, and expanding on demographic and environmental data collection using bio-robotic technology and a citizen science approach (this is mainly towards working with school children). I strongly collaborate with different institutions including zoos to i) develop state of the art research on applying biodemography towards advancing the field of biodiversity conservation, ii) developing research that promotes the integration with the Danish community based on working with school kids and nature with the goal to collect demographic data through education, and iii) improve the decision making process of conservation investment using Decision Analyses.

Publication highlights

Conde D.A., Colchero F., Güneralp B., Gusset M., Skolnik B., Parr M., Byers O., Johnson K., Young G., Flesness N., Possingham H., Fa J.E.. 2015. Opportunities and costs for preventing vertebrate extinctions. Current Biology. 2015 March; 25(6): R219-R221

Despite an increase in policy and management responses to the global biodiversity crisis, implementation of the 20 Aichi Biodiversity Targets still shows insufficient progress. These targets, defined by the United Nations Convention on Biological Diversity (CBD), partially address this issue by establishing protected areas and preventing species extinctions. Here we focus on Alliance for Zero Extinction (AZE) species, which are arguably the most irreplaceable category of important biodiversity areas. Effective conservation of AZE sites is essential, as the loss of any of these sites would certainly result in the global extinction of at least one species. However, averting human-induced species extinctions requires enhanced planning tools to increase the chances of success. Here, we developed a conservation opportunity index (COI) that includes social and biological indicators and costs, to quantify the possibility of achieving a species successful conservation in its natural habitat (COIh) and by securing populations in zoos. We show that the total annual costs for effectively managing all AZE vertebrates in their natural habitat are US$ 1.18 billion and that ~39% of the species had high opportunities for habitat conservation. However there are 15 species with low opportunities for habitat and zoo conservation.

Ongoing work

“Demographic Index of Species Knowledge“

Extinction is in principle a demographic process. When populations’ fertility rates cannot offset their mortality rates, populations collapse and subsequently the species become extinct. Therefore, data on species survival and fertility are crucial to manage threatened species. Despite this fact, we still do not have a single repository of demographic data. This is the case even for vertebrates; the best studied group on the planet. As a result we have no idea of the breadth of knowledge available to develop species management plans. In this project we derived a Demographic Index of Species Knowledge (DISKo) for each of the worlds described mammals, birds, reptiles and amphibians. DISKo is a data miner that standardizes the taxonomy and demographic ontology across 27 databases and contains more than 4 million records for more than 24 000 species. We will use DISKo to develop a decision framework on how to better increase the quantity of Demographic Knowledge. Another aim is to obtain the funding to launch DISKo as a meta-database for public use.

Ongoing grants

Principal Investigator, VELUX Visiting Professor Programme. € 48 691.45.

Media highlights

Artensterben: Die Tiere mit den geringsten Überlebenschancen, Holger Dambeck, Spiegel Online Wissenschaft: http://www.spiegel.de/wissenschaft/natur/artensterben-15-tiere-mit-den-geringsten-ueberlebenschancen-a-1025076.html

$1.34 BILLION PER YEAR COULD SAVE 841 ENDANGERED SPECIES, Conservation Magazine: http://conservationmagazine.org/2015/03/1-34-billion-per-year-could-save-841-endangered-species/

Pris for at bevare verdens mest truede dyr: 9,14 mia. kroner, Videnskab dk http://videnskab.dk/miljo-naturvidenskab/pris-bevare-verdens-mest-truede-dyr-914-mia-kroner

Les 15 espèces qui ont le moins de chances de survivre dans le monde.http://www.lemonde.fr/biodiversite/article/2015/03/18/les-15-especes-qui-ont-le-moins-de-chances-de-survivre-dans-le-monde_4596190_1652692.html#KhzOwJAwiZ1U2qD8.99

Johan Dahlgren, Assistant Professor, Biology

Main research interest

I conduct plant demographic research with two major focus areas. The first is aging in plants. A gradual physiological deterioration occurs over high ages in all mammals and many other animals, with an associated increased risk of mortality and a lowered fertility with age. However, whether plants in general age and, if they do how aging progresses, is still unknown. One major reason for this lack of knowledge is simply a lack of data on the age-dependence of plant demographic rates. I am addressing this in two ways. First, I collaborate with field biologists who are collecting long-term monitoring data, and use that data to determine age trajectories of demographic rates for plants. In addition I am combining neglected age-determination techniques based on root anatomy with field monitoring to collect new data.

My second main research interest is to elucidate how the environment drives the demography of plants. This gets right at the heart of the main ecological goal of understanding the distribution and abundance of species. I analyse existing data on plant demographic rates, physical environment, interacting species and population density. I also collect new such data, primarily for the forest herb *Actaea spicata* (Baneberry), on which I also conduct field experiments, manipulating environmental conditions and density. I fit statistical models of the effects of environmental drivers on individual mortality, fertility and growth, and analyse the combined effects of these demographic rates on populations using Integral Projection Models (IPMs).

Publication highlights

The demography of climate-driven and density-regulated population dynamics in a perennial plant. Dahlgren et al. Ecology. http://www.esajournals.org/doi/pdf/10.1890/15-0804.1

This publication reports results from a study showing how climate variation drives the density-dependent demography of the Eurasian dwarf shrub *Fumana procumbens* (Sprawling Needle Sunrose), based on observations of individuals over twenty annual transitions. Identifying the internal and external drivers of demographic rates and population dynamics is a key objective in ecology, currently accentuated by the need to forecast the effects of climate change on species distributions and abundances. Here we show that environment-specific size-structured population projection models can accurately forecast plant population dynamics if density dependence is correctly accounted for. We also show how expected climate change will likely have limited effects on *Fumana* population sizes, because density regulation will dampen otherwise detrimental environmental effects. We also conducted simulations showing that implicitly assuming variation in demographic rates to be driven solely by the environment can overestimate extinction risks if there is density dependence. This is a crucial insight for population viability analyses (PVAs) of threatened species, where current methods confound effects of intrinsic regulation with effects of environmental variation.

Ongoing work

“Age structures of Greenlandic dwarf shrubs“

In cooperation with experts on dendrochronology at the Swiss Federal Research Institute WSL, and with Silvia Rizzi of MaxO, I am testing hypotheses on demographic senescence in long-lived dwarf shrubs by analysing their age distributions. We have excavated plants and determined the ages of individuals based on sections at their “root collars”, the oldest part of the plant. About 100 individuals have been sampled from each of nine species, ranging in age from 10 to 217 years. Age distributions for each species have then been determined using a penalized composite link model. In agreement with our hypotheses, tails of the age distributions are remarkably log-linear, suggesting not only stable population growth in very stable environments, but also that mortality is roughly constant with age, and thus that these species show negligible actuarial senescence.

Owen Jones, Assistant Professor, Biology

Main research interest

The variety of life histories displayed by the world's animals and plants has fascinated scientists for centuries. One of the oldest and most fundamental life history questions is that of why some animals live a long time, while others only live a short time. Demography is at the core of this question and my research focusses on understanding the diversity of demographic behaviour in species across the tree of life. I address the topic at three hierarchical levels (1) the single population level, for example using tools such as Bayesian Survival Trajectory Analysis; (2) the species level where I take a 'macro demographic' approach and study multiple populations of the same species separated spatially; and (3), a comparative level where I conduct comparative analyses of demographic traits across multiple species to gain a deeper understanding of the evolution of aging. This work requires the development and use of sophisticated analytical approaches to confront demographic and phylogenetic data. Therefore, in addition to working to address the evolution of demography I spend time contributing to statistical approaches and building demographic databases.

Publication highlights

Salguero-Gómez, R., Jones, O.R.* et al. (accepted) COMADRE: a global database of animal demography. Journal of Animal Ecology. * Joint first authors*

The open data philosophy is being widely adopted and promotes scientific progress. Open-databases exist on migration, distribution, conservation status, etc.. However, a gap exists for data on population dynamics in the animal kingdom. This information is fundamental to our understanding of the conditions that have shaped variation in animal life histories and their relationships with the environment.

Matrix population models (MPMs) are among the most widely used demographic tools and project population dynamics based on the reproduction, survival, and development of individuals in a population over their life cycle. Outputs from MPMs have direct biological interpretations, facilitating comparisons among animal species as different as Caenorhabditis elegans, Loxodonta africana and Homo sapiens.

Thousands of animal demographic data exist in the form of MPMs, but are dispersed throughout the literature, rendering comparative analyses difficult. Here, we introduce the COMADRE Animal Matrix Database which contains data on hundreds of species worldwide. COMADRE also contains ancillary information (e.g. ecoregion and taxonomy) that facilitates interpretation of the numerous metrics that can be derived from MPMs.

Through future frequent updates of COMADRE, and its integration with other online resources, we encourage researchers to tackle global ecological and evolutionary questions with unprecedented sample size.

Ongoing work

"Life history evolution in animals and plants"

Age- and stage-based matrix projection models (MPMs) capture major components of life history strategy. These strategies include the balances of trade-offs among demographic components throughout the life-cycle and mould mortality and fertility trajectories. Species' life history strategies have been shaped by millions of years of adaptive and neutral evolution over their shared evolutionary history. One might expect closely related species to share similar traits. Traits where this is observed are said to have high phylogenetic signal, but signal strength depends on factors including the amount of selection acting on the trait (i.e. adaptation), the degree of environmental canalization, and measurement error. I am exploring these relationships using MPMs from the COMPADRE and COMADRE Plant and Animal Matrix Databases and elsewhere. I am particularly interested in how these relationships may affect the concept of "borrowing strength" whereby unknown values for some species can be inferred if traits of relatives elsewhere in the phylogeny are known. This is potentially of great interest to workers in population management and conservation fields.

"Demographic trade-offs in parasitic plants"

The demography of parasitic plants is understudied, even though they are excellent models to explore ecological trade-offs. These plants use their hosts for support, and resource provisioning. They thus partially escape several costs that non-parasites endure. With colleagues Roberto Salguero-Gomez (University of Queensland) and Sydne Record (Smith College), I am exploring the significance of this "cheating" strategy using European mistletoe (Viscum album), an iconic species across much of Europe. Like other parasitic species, mistletoe derives much of its nutrients by stealing resources from the trees on which they live. We are collecting data on establishment, survival, growth, and reproduction of the species, and building demographic models to estimate the relative importance of various demographic processes. In particular, we are focussing on the role of trade-offs between those vital rates in explaining the species' success.

Ongoing grants

British Ecological Society.

Maarten Wensink, Assistant Professor, Public Health

Main research interest

As a medical doctor with a good understanding of mathematics and statistics I try to connect the mechanisms of ageing and cancer with (relatively simple) biodemographic models. Realistic restrictions on mathematical models need to be derived from an understanding of biomedical principles. For instance, it is mathematically straightforward to calculate the demographic and evolutionary consequences of 70-year-olds becoming biological 3-year-olds the next year. Biologically, however, this is clearly problematic. Mathematical implications of biological mechanisms are not always as straightforward as in this example, and require better theory formation. The biological mechanisms in evolutionary theories of ageing are often just defined as “genes”, or “resource allocation” without further specification, and are therefore not very informative. In contrast, biologically inspired models are not always analysed deeply enough to extract all the information. I try to work on the problem from both sides, hoping to make ends better meet.

Recently I have taken an increased interest in cancer research, in particular the relationship between size, longevity, and cancer incidence across species and across tissues. Commonly, research on this topic fatally lacks standard demographic concepts, such as age structure. Results that may seem plausible turn out to be far from straightforward when taking into account the demographics. Similarly, mathematical models can yield more and more interesting conclusions when analysed demographically. By creating better theory I hope to advance the science of ageing and cancer.

Publication highlights

“Intrinsic and extrinsic mortality reunited” Koopman, J.J.E., Wensink, M.J., Rozing, M.P., van Bodegom, D., Westendorp, R.G.J.. *Experimental Gerontology* 2015; 67: 48-53

Intrinsic and extrinsic mortality are often separated in order to understand and measure aging. Intrinsic mortality is assumed to be a result of aging and to increase over age, whereas extrinsic mortality is assumed to be a result of environmental hazards and be constant over age. However, allegedly intrinsic and extrinsic mortality have an exponentially increasing age pattern in common. Theories of aging assert that a combination of intrinsic and extrinsic stressors underlies the increasing risk of death. Epidemiological and biological data support the notion that the control of intrinsic as well as extrinsic stressors can alleviate the aging process. We argue that aging and death can be better explained by the interaction of intrinsic and extrinsic stressors than by classifying mortality itself as being either intrinsic or extrinsic. Recognition of the tight interaction between intrinsic and extrinsic stressors in the causation of aging leads to the recognition that aging is not inevitable, but malleable through the environment.

Ongoing work

“Size, longevity, and cancer incidence”

Multicellular organisms have to keep their cells from proliferating in an uncontrolled way, i.e. keep them from carcinogenesis. To do so, a number of checks and balances are in place. A cell that escapes all these checks and balances can become a cancer cell. Thus, healthy cells need to take a number of ‘hits’, which may arise entirely at random during cell division, to become a cancer (the multihit or multistage model of cancer).

This work introduces standard demographic concepts in the study of the relationship between size, longevity and cancer incidence. From this viewpoint it reassesses Peto’s paradox (which turns out to be logically flawed), a simple mathematical model of cancer incidence under the multihit model (which has been published before, but has never been fully analysed), and a recent high profile result that found a statistical correlation between lifetime cancer risk and the lifetime number of cell divisions (Tomasetti and Vogelstein 2015).

Conclusions that can be drawn from this work include the observation that lifetime cancer risk is an inappropriate measure in this context, that the introduction of extra ‘hits’ is more effective in larger organisms, and that the result of Tomasetti and Vogelstein should be discarded unless it can be given an interpretation that includes age structure.

Lionel Jouvet, Post Doc, Biology

Main research interest

At the frontier of applied and fundamental sciences, I am passionate about the development of new tools to accurately and precisely answer my research questions in ecology and evolution.

In our research group, I study the biodemographic parameters of the bacteria Escherichia coli in a highly controlled experimental setup. Variability is the key in evolutionary processes. A precise control of the environment and genetics of the bacteria allows us to quantify and identify the origin of this variability. In a state-of-the-art experimental setup (microfluidics, fluorescence microscopy, image analysis), I aim to understand how fundamental aspects of aging and biodemographic parameters are impacted by the environment (temperature, food availability, temperature/food availability variation, antibiotics).

Before joining the MaxO team, I worked for the biotechnology company Partec GmbH developing new instruments and applications for the fields of research, health, and industry. I visited a large array of laboratories from Lithuania to Saudi Arabia, where I trained researchers and engineers, and participated in numerous conferences. From the close collaborations with researchers, health specialists, and industry partners, I acquired a broader view of biology and its applications. In my university research projects, I developed numerous new techniques and procedures to investigate several ecological systems in collaboration with ecologists, biologists and physicists.

Ongoing work

“Lifespan and reproduction of E.coli in different environments”

Lifespan and reproduction are key fitness components, both of which are influenced by genetics and the environment. Tracking large numbers of genotypically known individuals throughout their lives in known environments has been challenging. We study isogenic individual E. coli bacteria under controlled environments and how the demographic parameters and distributions of reproduction and survival change across environments. We achieve this by using a microfluidic device that traps thousands of individual E. coli cells and tracks their division (reproduction) over their lifespan. Our results show substantial variation of lifespan and reproduction within the same environment, and significant shifts in mean and variance in lifespan and reproduction between environments. Both variance and mean lifespan and reproduction decrease with increased temperature, but the ratio between the two remains surprisingly constant. The environmental dependency of neutral variability among individuals suggests different adaptive paces across environments.

Adam Lenart, Post Doc, Public Health

Main research interest

My research is motivated by the application of probability theory in demography. In addition to a general treatment of probability theory in demography, I concentrate on forecasting methods and compositional data analysis. As I see it, many demographers already use probability theory implicitly by calculating age-specific rates and probabilities or expected values such as life expectancy or mean age at childbearing. More recently, demographers became interested in the standard deviation or variance of indicators as well. Population biologists started to measure the pace and shape of similar processes. However, all of these approaches could be unified using a formal treatment of demographic measures based on probability theory. Moreover, by applying probability theory to distributions describing the schedules of death, it is possible to calculate the minimal failure time of vital systems of an organism. It fascinates me that demographic methods might help to answer profound questions such as the biological processes leading to death. In the field of mortality forecasting, currently used methods can be too conservative in projecting the level of old age mortality. However, forecasting the moments of the distribution of deaths themselves can open new ways in projecting mortality. Compositional data analysis, a method recently introduced to demography concentrates on the proper analysis of data with a constant sum. Demography is teeming with such data, for example, the age structure of the population or relatedly, dependency ratios.

Publication highlights

"DNA methylation age is associated with mortality in a longitudinal Danish twin study"

An epigenetic profile defining the DNA methylation age (DNAm age) of an individual has been suggested as a biomarker of aging, possibly providing a tool for assessment of health and mortality. We estimated the DNAm age of 378 Danish twins, and included a 10-year longitudinal study of the 86 oldest-old twins, who subsequently were followed for mortality over 8 years. We found that the DNAm age is highly correlated with chronological age across all age groups, but that the rate of change of DNAm age decreases with age. The results may in part be explained by selective mortality of those with a high DNAm age. This hypothesis was supported by a classical survival analysis showing a 35% increased mortality risk for each 5-year increase in the DNAm age vs. chronological age. Furthermore, intrapair twin analysis revealed a more-than-double mortality risk for the DNAm oldest twin compared to the co-twin and a 'dose–response pattern' with the odds of dying first increasing 3.2 times per 5-year DNAm age difference within twin pairs, showing a stronger association of DNAm age with mortality in the oldest-old when controlling for familial factors.

Ongoing work

"Compositional data in demography"

Compositional data analysis concentrates on the proper analysis of non-negative data with a constant sum. It offers a fresh view on lifesaving models as well. If lives are saved at a given age, they are going to be lost at a higher one. Similarly, if lives are saved from one cause of death, they are simply redistributed to another cause. Compositional data analysis offers advantages in other fields of demography and its related topics as well, where the analysed quantities always sum up to a constant, such as the age structure of the population, number of hours spent on different activities in time use surveys, or factors of gross domestic product measured in percentages.

Jonas Wastesson, Post Doc, Public Health

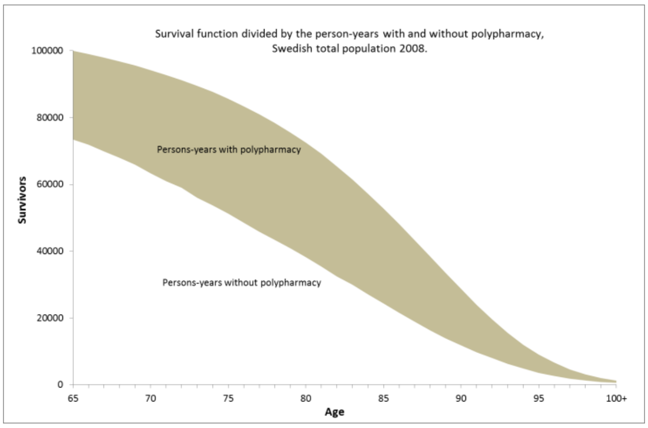
Main research interest

Older people live longer today than earlier, but it is unclear how different aspects of health and health care have changed during this period of increased longevity. My research focusses mostly on how the use of medications changes with age and over time. Medications contribute to better health and longevity in the population. However, at older ages medications can also cause considerable harm, as medication use becomes excessive and increasingly complex. At the core of my research is the question about how to balance the beneficial effects of medication treatment with the risk of unwarranted side-effects in a population with increasing life expectancy and heterogeneous health.

Publication highlights

Wastesson, J. W., Canudas-Romo, V., Lindahl-Jacobsen, R., & Johnell, K. Remaining life expectancy with and without polypharmacy: A register-based study of swedes aged 65 years and older. J Am Med Dir Assoc, [Epub ahead of print] Doi. http://dx.doi.org/10.1016/j.jamda.2015.1007.1015

Women live longer than men, but spend more years, and a larger proportion of life, exposed to polypharmacy (the use of 5 or more medications). This suggests that women have higher levels of morbidity. It is also a cause for concern as polypharmacy increase the risk of having adverse effects from the medications. A 65 year old can expect to live 20 more years and, of these, eight years will be spent with polypharmacy.



Ongoing work

“Increasing drug use and polypharmacy after the age of 90”

Results from cross-sectional studies have suggested that people use fewer drugs and have lower levels of polypharmacy after the age of 90 than at younger old ages. However, few have studied this with longitudinal data. By using the longitudinal Danish 1905 cohort, we find that people continue to increase their use of drug as they age from 92 to 100 years on an individual level. The decreasing use of drugs found in earlier cross-sectional studies can possibly be explained by selective high mortality among extensive drug users at these ages.

Julia Barthold, Post Doc, Public Health

Main research interest

Social species, as for example great apes or elephants, seem to have longer lifespans than non-social species. In these long-lived social species, individuals form permanent social units and cooperate to achieve tasks. My research focusses on the role that the evolution of cooperation and sociality plays in the evolution of long lifespans. Together with my collaborators, we are approaching the topic from two perspectives. Firstly, we study the demographic underpinnings of the evolution of cooperation. We put forth the hypothesis that two idiosyncrasies of species-specific mortality influence the evolution of cooperation: the average length that an individual can expect to live, and the proportion of an individual's life that it can expect to overlap with a birth-cohort peer. In order to be able to test this hypothesis, we are currently studying the relationship between these two quantities for a wide range of species, including many human populations. Secondly, we are testing whether the positive relationship between sociality and lifespans holds when analyses control for shared evolutionary history between species. After all, social primates may live long because they are all social or because they are all primates. These projects will help unveil one important biological factor in the evolution of ageing and life span.

Ongoing work

“Novel Bayesian method provides first mortality estimates for male African lions for future use in population management”

The global population size of African lions is plummeting, and many small fragmented populations face local extinction. Extinction risks are amplified through the common practice of trophy hunting for males, which makes setting sustainable hunting quotas a vital task. Various demographic models evaluate consequences of hunting on lion population growth. However, none of these models use unbiased estimates of male age-specific mortality because such estimates do not exist. Until now, estimating mortality from re-sighting records of marked males has been impossible due to the uncertain fates of disappeared individuals: whether dispersal or death. In this project, we developed a new method and inferred mortality for male and female lions from two populations that are typical with respect to their experienced levels of human impact. We found that mortality of both sexes differed between the populations and that males had higher mortality in both populations. Our mortality estimates can be used to improve lion population management and, in addition, the mortality model itself has potential applications in demographically-informed approaches to the conservation of species with sex-biased dispersal.

Non-peer reviewed publication

Barthold, J.A. (2015) A demographic perspective on trait heritability and sex differences in life history (Doctoral dissertation, publication embargoed). University of Oxford, UK. http://ora.ox.ac.uk/objects/uuid:94f04aac-182f-466b-a267-179d68db398f

Mikael Thinggaard, Post Doc, Public Health

Main research interest

My main interest is within aging research. The average lifespan has increased greatly over the last 150 years and the age group 85 years and older has been the fastest growing age segment for the last 50 years. Not only has the increase in the oldest old population been remarkable, but their mortality rates have also been cut in half over the last 60 years. However, there is also a large variation in mortality among the oldest old and I am interested in investigating what predicts this variation in nonagenarians and centenarians.

Another interest is to investigate whether this decline in mortality is due to overtreatment of the most disabled giving rise to a large proportion of oldest old who will be in very poor health and have very low life satisfaction, which has been called the failure of success hypothesis. Studies have generally shown that in more recent cohorts the young elderly (ages 65-85 years) have more diseases but also better physical and cognitive functioning. My interest is to investigate whether this improvement will continue for more recent cohorts of nonagenarians and centenarians.

In aging research there are a lot of challenges with missing data, which is mainly due to the use of proxy participants. Hence, another of my interests is to apply methods in the analysis that can take the missing data into account, and thereby obtain less biased results compared to complete case analysis.

Publication highlights

Survival Prognosis in Very Old Adults

Thinggaard, M., McGue, M., Jeune, B., Osler, M., Vaupel, J. W., & Christensen, K.

Over the last 50 years there has been an almost seven-fold increase in nonagenarians in the high-income countries accompanied by a decreasing ageism with regard to treatment. Considering the average short survival prognosis in very old adults, there is a general concern of overtreatment. However, there is a large variation in survival, and the aim of this study is to determine whether simple functional indicators are predictors of survival prognosis in very old adults. We found that men and women aged 93 had an overall 6.0% and 11.4% chance of surviving to 100 years, respectively. Being able to rise without use of hands combined with a Mini-Mental State Examination (MMSE) scores from 28 to 30, increased the chances for men to 21.7% (95% CI = 11.5-31.9) and for women to 34.2% (95% CI = 24.8-43.5). This indicated that chair stand score combined with MMSE score is an easy way to estimate overall chance of survival in very old adults, which is particularly relevant when treatment with potential side effects for non-acute diseases is considered.

Physical and mental decline and yet rather happy? A study of Danes aged 45 and older

Vestergaard, S., Thinggaard, M., Jeune, B., Vaupel, J. W., McGue, M., & Christensen, K.

Little is known about whether the feeling of happiness follows the age-related decline in physical and mental functioning. The objective of this study was to analyse differences by age in physical and mental functions and in the feeling of happiness among Danes aged 45 years and older. Overall, successively older age groups performed worse than the youngest age group (45-49 years) on all three dimensions. When comparing the oldest age group (90+ years) with the youngest, the T-score differences were found to be the largest for the mobility score (men: 40.2, women: 41.4), followed by the cognitive function (men: 22.0, women: 24.9), and the total depression symptomatology score (men: 15.5, women: 17.4). Conversely, the T-score difference in happiness was small (men: 5.6, women: 6.0). The conclusion was that despite markedly poorer physical and mental functions with increasing age, in this Danish sample age did not seem to affect happiness to a similarly notable extent.

Ongoing work

"Are Advances in Survival among the Oldest Old Seen across the Spectrum of Health and Functioning?"

Thinggaard, M., McGue, M., Jeune, B., Osler, M., Vaupel, J. W., & Christensen, K.

For every ten years since 1950, 20-40% more of a birth cohort survive into their tenth decade in most high-income countries, and the mortality rates have been reduced by half over the last 60 years for nonagenarians, and progress is continuing. However, there is concern that the basis for the better survival is overtreatment of severely physically and cognitively disabled individuals. The chance of surviving to age 95 was approximately 30% higher for people born in 1915 than for people born in 1905, and survival remained significantly better in the 1915 Cohort through a 4.3-year follow-up period (median survival increase of 2 months) corresponding to 29% surviving to age 99 in the 1915 Cohort compared to 26% in the 1905 Cohort. This advance was seen across different levels of activity of daily living, physical performance, cognitive functioning, self-rated health and life satisfaction for both men and women. This suggests that advances in survival among the oldest old are not due to better survival of the most disabled alone, but seen across the spectrum of health and functioning.

"Improvements in cognition, self-rated health and life satisfaction among the very old"

Thinggaard, M., McGue, M., Jeune, B., Pedersen, P. B., Vaupel, J. W., & Christensen, K.

The aim of this study is to investigate whether cognition, self-rated health, life satisfaction and the CAMDEX depression scale has changed between two birth cohorts of 93-95 year olds born 10 years apart. We found that the 1915 Cohort did significantly better compared to the 1905 Cohort in cognition (MMSE 23-30: 60% vs 52%, P-value<0.001), self-rated health (excellent/good: 68% vs 55%, P-value<0.001) and life satisfaction (always/almost: 85% vs 74%, P-value<0.001). Hence, there were clear improvements in cognition, self-rated health and life satisfaction over a 10-year period among nonagenarians. Despite these improvements there was no difference in the CAMDEX depression scale. However, investigation of each item of the CAMDEX showed some interesting patterns, which will be investigated further.

Marie-Pier Bergeron Boucher, PhD student, Public Health

Main research interest

My main research interests include the study of human mortality, longevity and ageing, with a particular interest in exploring new demographic methods to help understand and forecast population health and mortality in industrialized societies. My interests can be summarized into three broad groups:

- Forecasting the future of mortality and longevity, using in particular Compositional Data Analysis
- Understanding mortality changes, via life table analysis and decomposition
- Changes in causes of death structure

Publication highlights

Bergeron-Boucher, M.P., Ebeling, M., Canudas-Romo, V.. Decomposing changes in life expectancy: Compression versus shifting mortality. Demographic Research 33: 391-424

In most developed countries, mortality reductions in the first half of the 20th century were strongly associated with changes in lifespan disparities. In the second half of the 20th century, changes in mortality are best described by a shift in the mortality schedule, with lifespan variability remaining nearly constant. These successive mortality dynamics are known as compression and shifting mortality, respectively. To understand the effect of compression and shifting dynamics on mortality changes, we quantify the gains in life expectancy due to changes in lifespan variability and changes in the mortality schedule, respectively. We introduce a decomposition method using newly developed parametric expressions of the force of mortality that include the modal age at death as one of their parameters. Our approach allows us to differentiate between the two underlying processes in mortality and their dynamics. An application of our methodology to the mortality of Swedish females shows that, since the mid-1960s, shifts in the mortality schedule were responsible for more than 70% of the increase in life expectancy.

Ongoing work

“Coherent Forecasts of Mortality with Compositional Data Analysis”

Mortality forecasts have failed in many cases to offer coherent forecasts among their subpopulations, e.g. countries in a region or provinces in a country. The coherence problem emerges from an inability of different forecast models to offer population-specific forecasts which are consistent with one another. We propose a forecast methodology that solves the coherence problem. We adapt the Compositional Data Analysis approach introduced by Oeppen by including a common regional trend and compare our model with other existing forecasting models. We assess which model best describes the past and future pattern of mortality in industrialized countries. We show and justify why the new proposal is an improved methodology.

Josephine Goldstein, PhD Student, Biology

Main research interest

Jellyfish have the potential for rapid somatic growth and reproduction and show large population fluctuations over a variety of temporal scales. Mass occurrence in so-called jellyfish blooms is often caused by species with complex life cycles including a sexually reproducing pelagic medusa and an asexually reproducing benthic polyp stage. My PhD project focusses on the demographic dynamics of the moon jellyfish *Aurelia aurita*, with an overall goal to identify key transitions and life-history traits that may ultimately control the booms and busts of jellyfish blooms. Combining laboratory experiments with field studies, the aim is to describe the influence of environmental stochasticity on stage-specific survival, growth and fertility.

Ongoing work

"The demographic dynamics of Aurelia aurita as a function of age/stage and size"

The moon jellyfish *Aurelia aurita* is periodically abundant in coastal waters around the world, where it can exert considerable predatory impact on prevailing food web structures. In most regions, medusae reach umbrella diameters of 10-30 cm during the summer months. In the Danish fjord system Kertinge Nor/Kerteminde Fjord, medusae of the same species are usually food-limited, restricting their own growth by high population density to a maximum umbrella diameter of a few centimeters. Size is a key variable for fertility and mortality in medusae, since sexual maturity is often followed by shrinkage ("degrowth") and morphological degradation. Both age (and/or developmental stage) and size are therefore considered in a stage and size-structured population matrix model, aiming to explain the demographic dynamics of jellyfish blooms in the context of environmental change.

"Population dynamics of the moon jellyfish Aurelia aurita as a function of water exchange in the Danish fjord-system Kertinge Nor/Kerteminde Fjord "

In the shallow cove of Kertinge Nor, located in the southern part of Kerteminde Fjord (Denmark), mass occurrence of the moon jellyfish *Aurelia aurita* (Scyphozoa, Cnidaria) is frequent in spring and summer, while the medusa population seems to disappear during the winter months. Water exchange in the fjord-system is governed by density-driven circulation created by frequent salinity changes in the adjacent Great Belt, with an approximate time scale for the residence time between one week and a few months. The present study aims to explain to what degree seasonal declines in jellyfish abundance are due to dilution by water exchange, giving an insight into the hitherto unknown mortality patterns of the local jellyfish population in Kertinge Nor.

Lars Kumala, PhD student, Biology

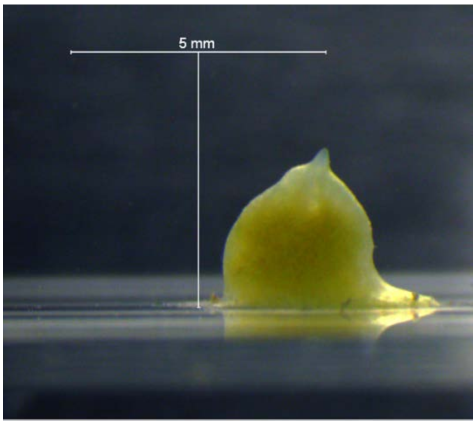
Main research interest

My research interests include the ecophysiology and biodemography of aging in basal multicellular organisms such as sponges. Sponges represent the earliest branching metazoans and feature characteristics that may facilitate non-senescence, such as the lack of a firm germ-soma distinction and the rapid renewal of the sponges' filtering choanocytes. However, the few studies on the demography of sponges still remain equivocal due to the different levels of individual organization a modular sponge may have. My PhD project focusses on sponge cell population dynamics with particular emphasis on choanocytes, which share morphological and functional characteristics with single celled choanoflagellates, and which are organized in functional construction units. I further experimentally investigate the physiological response of sponge explants propagated from cuttings of the breadcrumb sponge *Halichondria panicea*. Sponge explant colonies are cultivated in the laboratory to study growth, respiration and filtration activity of sponges under different levels of food and oxygen availability, aiming for a better understanding of basal animal physiology. Results will shed light into sponge modularity and associated properties that may minimize environmental and age-related mortality in sponges.

Ongoing work

"Using sponge explants to study basal animal physiology"

Sponge explants are colonies propagated from cuttings and provide powerful models for experimentally investigating fundamental evolutionary issues, such as the manifestation of aging or the evolutionary adaption to animal filter-feeding. In cooperation with the Marine Biological Research Center, Kerteminde, and "NordCEE", we are investigating growth, respiration and filtration of *Halichondria panicea* sponge explant colonies under different levels of food and oxygen. Recent findings indicate coordinated contractions as a behavioral response in sponge explants that lack nerves or true muscle tissue. Orchestrated contractions of the excurrent chimney and sponge body seem to strongly influence the filtration activity of sponges. This behavior has been supposed to effectively dispose waste material or to regulate oxygen within the sponge tissue and may be an early physiological adaption to prevent multicellular organisms from accumulating environmental- or age-related damage.



Marius Pascariu, PhD student, Public Health

Main research interest

- Human mortality forecasting;

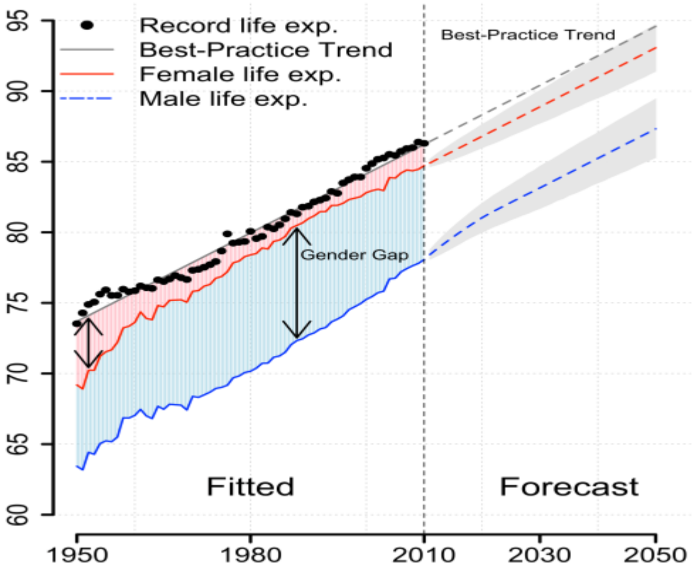
- Actuarial demography;

- Longevity risk assessment.

Ongoing work

“Forecasting mortality by making use of the best-practice life expectancy”

Human mortality is highly correlated between countries, regions and gender all over the world. The information given by these correlations could lead to the improvement of the accuracy of demographic predictions. The method studied allows the determination of joint female-male life expectancy, by forecasting the gaps between record female life expectancy in the world and country specific female life expectancy, and then the gender gap levels.



“Decomposition of life expectancy level”

Life expectancy is an aggregate measure but deeper knowledge can be obtained by converting the resulting life expectancy level into age-schedules of death rates and actuarial life tables by exploiting the regularities of age patterns of mortality. Once we have forecast life expectancy using the method presented in the previous section, we can transform it into death rates and other financial measures. Indirect estimation techniques based on model life tables and reconstruction of the empirical distribution of deaths from its statistical moments will be used.

New grants awarded

SCOR Corporate Foundation for Science.

Danielle Sherman, PhD student, Biology

Main research interest

The aim of my PhD project is to increase our understanding of life history trade-offs, and how these can affect the demography of species. The research will aim to fundamentally address topics including theoretical evolutionary biology and ecology but also applications of theory for population management and conservation biology. The methods involved include: comparative analysis of population matrix models, field data collection and analysis within on-going long-term individual-based demographic studies, and laboratory work to collect anatomical and herb-chronological data. The study organisms used will be vascular plants, where a wide range of life history strategies are documented and for which demographic field studies and experimental treatments are straightforward to undertake.

The project itself comprises two main – but interconnected parts; the first being to undertake comparative studies of demographic properties in a range of vascular plant species using the COMPADRE Plant Matrix Database. This will allow a comparative study of an unprecedented number of vascular plants. The second has been focused on collecting data on plant demography in the field and supplementing this information with measurements taken in the lab. The main study species for this type of data collection is *Borderea pyrenaica* and *Plantago lanceolata*, which are respectively a long-lived and a short-lived herbaceous species. The data will then continue to be used to study in detail the trade-offs between vital rates in these species.

Johanna Stärk, PhD student, Biology

Main research interest

My main interest is in the field of conservation demography with a focus on the development of policies to manage and conserve species at the risk of extinction. To investigate what drives extinction, I am interested in species interactions with the environment. Some questions that I am investigating are: How much mortality is driven by intrinsic or environmental factors in wild populations? How can we use data from captive populations to fill up demographic knowledge gaps of wild populations? How can zoos contribute with data and other resources to help slow down the current extinction trends? By analysing these questions I hope to overcome the problems that arise due to current data limitations that hinder conservation practices and improve the forecasting of threatened populations in the wild.

Ongoing work

"Protect your locals: Decision-making in the conservation of EU threatened species"

Nearly a quarter of European animal species are threatened with extinction. The EU targets this problem in the EU Biodiversity Strategy 2020, aiming to halt the loss of biodiversity in the EU by 2020. This target calls for different actions, ranging from the species habitat protection to securing a population in captivity. However, outcomes of alternative actions for 740 Red Listed species of EU terrestrial vertebrates are often highly uncertain. For example, there are species that are highly vulnerable to climate change for which protecting its habitat alone might not ensure the species survival or reduce its threat status. We therefore developed a decision framework to prioritize EU species and appropriate conservation actions. We incorporated data from a number of large databases, such as the species EU Red List threat status, its vulnerability to climate change, the number of individuals in a zoo, the species management experience in zoos, its evolutionary distinctiveness and the costs of investment to protect the species habitat or to secure a zoo population. We analyzed a total of 735 species under this framework to propose a mathematically rigorous decision-making process for the EU, zoo institutions and other conservation organizations. This project is being developed with funding from the Zeidler Foundation and developed together with my supervisor Dr. Dalia Conde and Dr. Hugh Possingham from the University of Queensland, as well as an extensive network of collaborators in Europe.

Francisco Villavicencio, PhD student, Mathematics

Main research interest

I am currently working on my PhD dissertation which focusses on the development of Bayesian methods to estimate age-specific survival and mortality from datasets that, due to the amount of missing information, have not been previously analysed. The main database that I am working with is the Barcelona Historical Marriage Database (BHMD), which contains information about more than 600,000 marriages celebrated in both urban and rural parishes of the Barcelona area over 450 years (1451-1905). Despite being a very rich data source, the BHMD lacks of information about ages, which justifies the use of a Bayesian approach. The method is based on the Bayesian Survival Trajectory Analysis (BaSTA), a free-open source software package that was designed to study survival in wild animals with unknown ages. While applying methods that were originally designed for biodemographic studies is challenging, it opens the possibility to adapt the model to similar demographic data from other countries and periods.

Other research interests related to ongoing projects in which I am involved are agent-based modelling and formal demography.

Publication highlights

Villavicencio, F., Jorda, J. P., & Pujadas-Mora, J. M. (2015). Reconstructing lifespans through historical marriage records of Barcelona from the sixteenth and seventeenth centuries. In Bloothooft, G., Christen, P., Mandemakers, K., & Schraagen, M. (Eds.), Population Reconstruction, Chapter 10, pp. 199–216. Springer International Publishing, Switzerland.

This chapter presents a methodology for reconstructing the lifespan of individuals through a nominal record linkage procedure using historical marriage records of Barcelona from the sixteenth and seventeenth centuries. The data are extracted from the Barcelona Historical Marriage Database (BHMD), a unique source that contains information about more than 600,000 marriages celebrated in both urban and rural parishes of the Barcelona area from over 450 years (1451--1905). We discuss the main characteristics of the database, the standardisation of the nominal information, the marriage linkage procedure, and the reconstruction of the lifespans.

Submitted (and accepted) peer-reviewed book chapter

Kashyap, R., & Villavicencio, F. An Agent-Based Model of Sex Ratio at Birth Distortions. In Van Bavel, J. & Grow, A. (eds.) Agent-Based Modelling in Population Studies: Concepts, Methods, and Applications. Springer.

Across a number of countries in Asia and the Caucasus, fertility decline in recent decades has been accompanied by an unprecedented and anomalous rise in the sex ratio at birth (SRB). Although the micro-level factors—persistent son preference within a context of fertility decline and growing access to pre-natal sex determination technology—are known, their specific levels, trends and interactions in explaining macro-level SRB trajectories are hard to discern with existing data and approaches. We present an agent-based model (ABM) that examines the contribution of each of these micro-level factors to the emergence of distorted SRBs at the macro-level. Calibrating our model to the South Korean and Indian scenarios, we show that even as son preference was declining in both settings SRB distortions emerged due to the diffusion of technology along with an increase in the probability to sex-selectively abort at lower parities as norms shifted towards smaller families. In South Korea, we find that SRBs peaked at 114 at relatively low levels of son preference of around 30% wanting one son, due to the joint effect of technology diffusion combined with steady increases in the readiness to abort, including small increases at parity 0 i.e. before the transition to first birth. In India, our model suggests that the SRB rise was less steep than South Korea's as the readiness to abort was not as high as in South Korea, due to higher fertility levels when SRBs rose and slower technology diffusion.

Ongoing work

"Symmetries between life lived and life left in finite stationary populations", F. Villavicencio and T. Riffe

The Brouard-Carey equality describes the symmetries between the age composition (life lived) and the distribution of remaining lifespans (life left) in stationary populations. This result was formally proved for populations of infinite size and continuous time, and a posterior attempt to prove it for populations of finite size turns out to be incomplete. In this paper we provide a formal mathematical proof of the Brouard-Carey equality for finite stationary populations, using basic mathematical and demographic tools, with particular attention to the Lexis diagram and an extension of the Lexis diagram that accounts for death cohorts. To our knowledge, this proof was not available in the demographic literature until now. We also discuss that the symmetries between life lived and life left in stationary populations can only be proven if time is explicitly discretized. The proof is more complex than in a continuous time framework, but provides a more realistic set-up given the data that are usually available to researchers (surveys, censuses, capture-recapture data, etc.). This result is a useful rule of thumb for the study of human and non-human populations, especially when subject ages are unknown, but individuals are followed-up until death.

"A unified framework of demographic time", T. Riffe, J. Schöley, and F. Villavicencio

Demographic thought and practice is largely conditioned by the Lexis diagram, a two-dimensional graphical representation of the identity between age, period, and birth cohort. This relationship does not account for remaining years of life or other related time measures, whose use in demographic research is both underrepresented and incompletely situated. We describe a three-dimensional relationship between six different measures of demographic time: chronological age, time to death, lifespan, time of birth, time of death, and period. We describe four identities among subsets of these six measures, and a full identity that relates the six of them. One of these identities is the age-period-cohort identity, while the other three are relatively novel. We provide a topological overview of the diagrams that pertain to these identities. The 3-D geometric representation of the full six-way identity is proposed as a coordinate system that fully describes temporal variation in demographic data. We offer this framework as an instrument to enable the discovery of yet-undescribed relationships and patterns in formal and empirical demography.

Contributions to Conferences

Ciganda, D. & Villavicencio, F. "Social feedback mechanisms in the postponement of fertility in Spain". Conference paper, Population Association of American 2015 Annual Meeting, San Diego, CA, USA, Apr 30-May 2 2015.

Kashyap, R. & Villavicencio, F. "The relative contributions of son preference, fertility decline and technology diffusion in the sex ratio transition". Poster session, Population Association of American 2015 Annual Meeting, San Diego, CA, USA, Apr 30-May 2 2015

Maria Baden, Research Assistant, Biology

Main research interest

My research interest covers topics in plant geography, community ecology, systematics, biodiversity conservation and habitat restoration. I place a high value on facilitating communication and co-operation between researchers from multi-disciplinary backgrounds. My current work focusses on generating experimental data on the role of environment in the physiology and life cycle of several local species. In particular, I explore trade-offs between growth, development, reproduction and survival in amphibians as well as perennial herbs. I am interested in a better understanding of the interplay between demographic and environmental parameters that influence distribution and population density to better predict population stability, for example for species threatened with extinction. I aim to apply my background in ecology, botany and geography to develop spatial and temporal models that include demographic, ecological and physiological data, while considering the important factors of human population pressure and climate change, in order to make realistic management plans for habitat conservation and restoration projects.

Publication highlights

Baden, M., Särkinen, T., Conde, D. A., Matthews, A., Vandrot, H., Chicas, S., Pennil, C., Bayly, D., Chance, R., Bridgewater, S. & Harris, D. 12 Nov 2015. A botanical inventory of forest on karstic limestone and metamorphic substrate in the Chiquibul Forest, Belize, with focus on woody taxa. Edinburgh Journal of Botany. 43 pages [Epub ahead of print.] doi:10.1017/S0960428615000256

The Chiquibul Forest Reserve and National Park in Belize is a priority conservation area within the "Maya Forest" in Central America. Although taxonomic data are essential for the development of conservation plans in the region, there is limited knowledge of the existing species in the area. Here we present a botanical species list of mostly woody taxa based on pressed plant samples, with particular focus on the Raspaculo watershed in the eastern part of the National Park. Within this watershed, a comparison is made between 0.1 hectare of valley floor and 0.1 hectare of hilltop vegetation, sampling trees, shrubs, palms and lianas ≥2.5 cm diameter at breast height. Additionally, a 1 ha plot was established in the Upper Raspaculo watershed. Our study shows 38 new species records for the region, and important additions to the flora of Belize. New records were obtained from forests on both metamorphic and karstic substrate, including previously overlooked hilltop forest elements. Quantitative assessment of vegetation across elevation zones shows distinct elements dominating on valley floors and hilltops. Our results show that the Chiquibul contains at least 58% of Belize's threatened plant species, and represent a source of information for the management and conservation of the area.

Särkinen, T., Baden, M., Gonzáles, P., Cueva, M., Giacomin, L. L., Spooner, D., Simon, R., Juarez, H., Nina, P., Molina, J. & Knapp, S. Apr 2015. Listado anotado de Solanum L. (Solanaceae) en el Perú. [Annotated checklist of Solanum L. (Solanaceae) for Peru.] Revista Peruana de Biologia 22 (1), pp. 3-62, DOI: http://dx.doi.org/10.15381/rpb.v22i1.11121

The genus Solanum is among the most species-rich genera both of the Peruvian flora and of the tropical Andes in general. The present revised checklist treats 275 species of Solanum L., of which 252 are native, while 23 are introduced and/or cultivated. A total of 73 Solanum species (29% of native species) are endemic to Peru. Additionally, 58 species occur only in a small number of populations outside Peru, and these species are here labelled as near-endemics to highlight the role Peru plays in their future protection. Species diversity is observed to peak between 2 500-3 000 m elevation, but endemic species diversity is highest between 3 000-3 500 m elevation. Cajamarca has the highest number of endemic (29 spp.) and total species (130 spp.), even when considering the effect of area. Centers of endemic species diversity are observed in provinces of Cajamarca (Cajamarca), Huaraz and Carhuaz (Ancash), and Canta and Huarochirí (Lima). Secondary centres of endemism with high concentrations of both endemics and near-endemics are found in San Ignacio and Cutervo (Cajamarca), Santiago de Chuco (La Libertad), Oxapampa (Pasco), and Cusco (Cusco). Current diversity patterns are highly correlated with collection densities, and further collecting is needed across all areas.

Media highlights

Fun fact: A new species of potato endemic to Peru, *Solanum mariae* Särkinen & S.Knapp was named after me early this year. You can read the taxonomic treatment here:
http://phytokeys.pensoft.net/articles.php?id=4499

Conferences/activities

Facilitator in the 27th International Congress for Conservation Biology (ICCB) & 4th European Congress for Conservation Biology (ECCB), August 2-6 2015, Montpellier – France

Participant in IUCN Red List: Using the IUCN Red List Categories and Criteria to assess extinction risk of species for the global and national Red Lists.

Participant in Marxan: Introduction to Marxan conservation planning and decision support software.

Participant in SDU workshop: Involving children in citizen science for conservation demography

Participant in SDU workshop: Gender aware teaching, learning and assessment

Anthony Medford, Research Assistant, Public Health

Main research interest

The study of lifespan can be a means to explore human longevity. In addition, one way of thinking about maximum life spans is to consider the right tail of the age at death distribution. Studies of the trends in life span as an indicator of human longevity have not been as popular as life expectancy. Age is often misreported at older ages and documentary evidence sparse or absent altogether.

Remarkably, demographers have done little research using this tail-distributional approach and when they have, the tools are often basic and lacking in statistical rigour. Extreme Value Theory (EVT) is a branch of statistical theory which examines a distribution not from the well-known perspective of central tendency, but from the extreme end points of the distribution where events are rare and data scant. My main focus is on the application of methods from Extreme Value statistical theory to the study of indicators of exceptional longevity.

Publication highlights

Medford, A. "Best Practice Life Expectancy: An Extreme Value Approach". 2015. Demographic Research. (Under review)

Whereas the rise in human life expectancy has been extensively studied, the evolution of maximum life expectancies, i.e. the rise in best practice life expectancy in a group of populations, has not been examined to the same extent. We examine best practice life expectancy more formally by using Extreme Value Theory. Extreme value distributions were fitted to time series (1900 to 2012) of maximum life expectancies at birth and age 65, for both sexes, using data from the Human Mortality Database. We show that Generalized Extreme Value distributions offer a more theoretically justified, straightforward way to model Best Practice Life expectancies and are more flexible than ARIMA time series models which assume Gaussian innovations for projections. Our findings can be useful for policymakers, insurance companies and pension funds who would like to obtain estimates and probabilities of future maximum life expectancies.

Silvia Rizzi, Research Assistant, Public Health

Main research interest

My main research focusses on the application of statistical methods in demography, biodemography and epidemiology to estimate detailed distributions from coarsely grouped count data.

Demographers and health researchers often have access to vital statistics that are less than ideal for the purpose of their research: In many instances vital statistical data are reported in coarse histograms. For example, age-specific health indices, like diseases' incidences and causes-of-death counts and rates, are habitually reported in wide age intervals, especially for older ages. With increasing longevity, more people are reaching very high ages, and traditional age classification systems become inappropriate to explore health trends among nonagenarians and centenarians. Another problem may arise when comparing age-specific health patterns across time and countries that use different age boundaries.

Parametric models and non-parametric models such as spline interpolation and kernel density estimators have long been used in the demographic literature to retrieve detailed information from grouped data. My contribution in this research area is to investigate the potentials of another method, the penalized composite link model, to smoothly estimate distributions from coarsely grouped counts.

Publication highlights

Rizzi S., Gampe J., Eilers P.H.C. 2015. Efficient Estimation of Smooth Distributions from Coarsely Grouped Data. American Journal of Epidemiology, 182(2):138-147.

Ungrouping binned data can be desirable: Bins can be too coarse to allow for accurate analysis; comparisons can be hindered when different grouping approaches are used in different histograms; and the last interval is often wide and open-ended and, thus, covers a lot of information in the tail area. Age group–specific disease incidence rates and abridged life tables are examples of binned data. In this paper we propose a versatile method for ungrouping histograms that only assumes that the underlying distribution is smooth. Because of this modest assumption, the approach is suitable for most applications. The method is based on the composite link model, with a penalty added to ensure the smoothness of the target distribution. Estimates are obtained by maximizing a penalized likelihood. This maximization is performed efficiently by a version of the iteratively reweighted least-squares algorithm. Optimal values of the smoothing parameter are chosen by minimizing Akaike's Information Criterion. The method can be extended to the estimation of rates when both the event counts and the exposures to risk are grouped. Wide, open-ended intervals can be handled properly.

Ongoing work

"Comparison of non-parametric methods for ungrouping coarsely aggregated data"

In this study we review, evaluate and compare various ungrouping techniques that are well established in the statistical literature and available to be implemented by health researchers. For the analysis we use simulated data from a Weibull distribution and detailed NORDCAN cancer data by single-year of age: Overall age-specific cancer deaths for Denmark in 2010 and numbers of age-specific testis cancer diagnoses for Denmark in years 1980, 1990, 2000 and 2010 combined. Data have been obtained from the Danish

Cancer Registry. To evaluate and compare the results between the competing ungrouping methods we compute several indicators. We find that for finer age groups, i.e. of 5-years age length, the selected methods show similar results. However for wider groups and open age intervals, our penalized link model performs best, followed by the spline interpolation with Hyman filter.

Jonas Schöley, Research Assistant, Public Health

Main research interest

My work focusses on human early life mortality and data visualization.

Biologists noticed that for humans and many other species the risk of dying decreases from birth until the onset of maturity. This phenomenon is called “ontogenescence” and various hypotheses have been put forward in an attempt to explain it.

I check these hypotheses against data on human fetal- and infant mortality, ultimately seeking to explain the phenomenon of ontogenescence for humans.

Using extensive individual level data (~70 million cases) on births, fetal- and infant deaths in the US I develop a mathematical model of early life mortality capable of answering questions such as:

- How fast does a fetus/infant adapt to life?
- How risky is the transition of birth for the child?
- How important is selection bias in explaining the aggregate age pattern of early life mortality?

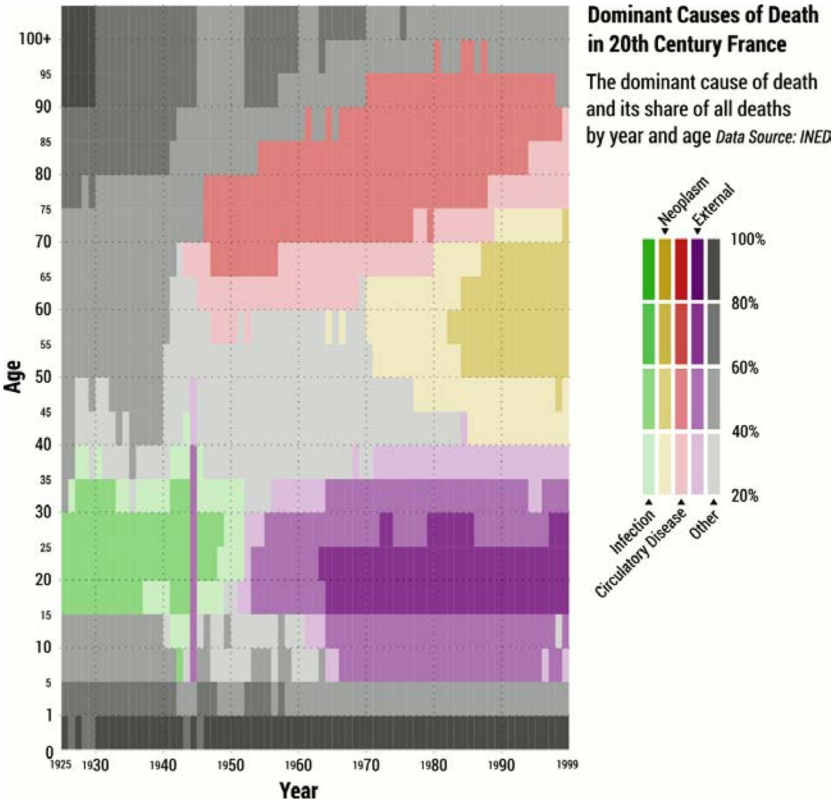
I develop new methods for visualizing demographical and biological data. Having a visual overview of the data helps to check hypotheses rapidly, understand complex relationships and – ultimately – communicate the findings to other researchers and the public. However, the visualization has to fit the question or problem to be effective. Recent visualizations I designed show,

- how the causes of death differ over age and change over time in humans,
- the amount of knowledge humans gathered on genetics and demographics of vertebrate species across the tree of life,
- the risk of death for humans across age, time, space and sex displayed in an interactive web page.

Publication highlights

Schöley, J. & Willekens, F. Visualizing compositional data on the Lexis surface PAA 2015 conference paper, 2015 (http://paa2015.princeton.edu/abstracts/151829)

The analysis of composite data is a topic inherent to demography. In recent times, due to a growing catalogue of detailed population data, it became feasible to consider populations not only structured by time, age or sex, but by any number of interesting criteria. This "inflation" of data dimensions produces challenges in visualizing the data. To aid the understanding of age-structured timelines of compositions we seek to extend the Lexis surface plot from 1-dimensional continuous data to multidimensional composite data. We apply different strategies for visualizing composite data on the Lexis surface to French death counts given by cause and compare the results for compliance with multiple desired criteria.



Dominant Causes of Death in 20th Century France

The dominant cause of death and its share of all deaths by year and age *Data Source: INED*

Ongoing work

"The Gestational Age Pattern of Human Mortality"

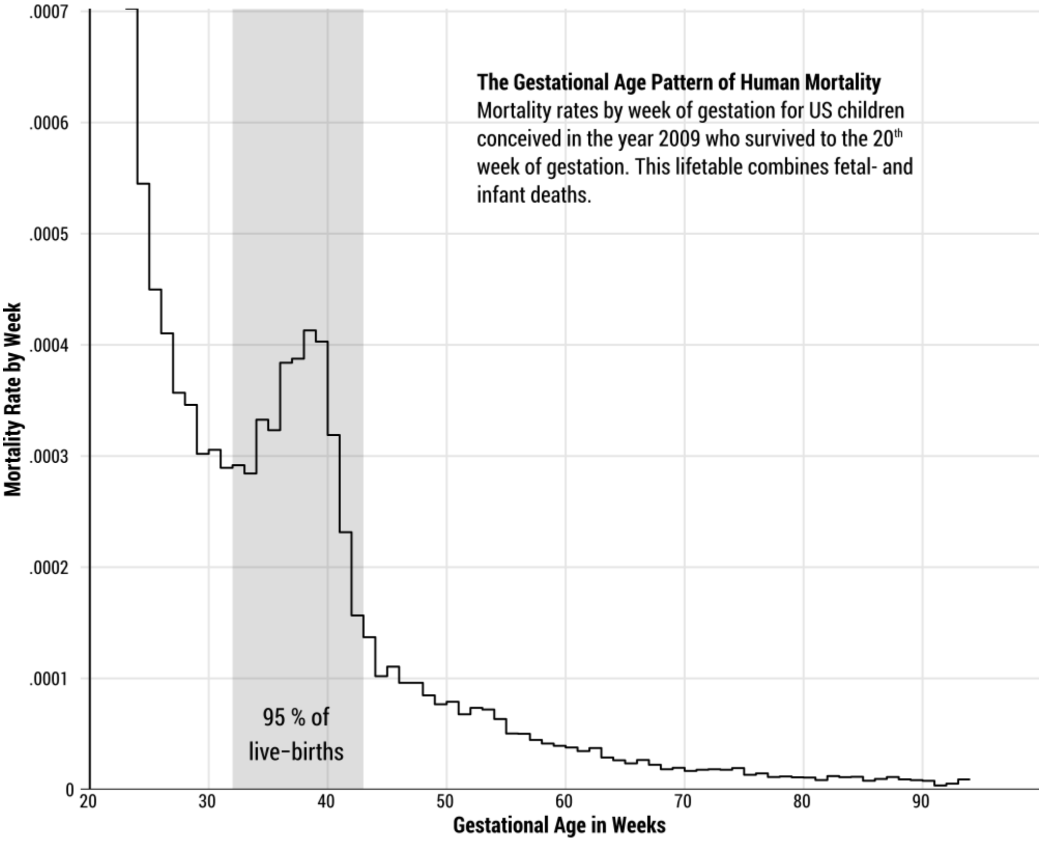
I present a lifetable by gestational age from week 23 until week 100 after the last menstrual period of the mother. The lifetable shows the pre-natal, peri-natal and post-natal mortality levels for US fetuses/infants conceived in the year 2009.

The observed age pattern of the force of mortality is consistent with three hypotheses about early mortality:

1) Adaptation: as the fetus/infant grows it becomes more resilient to death,

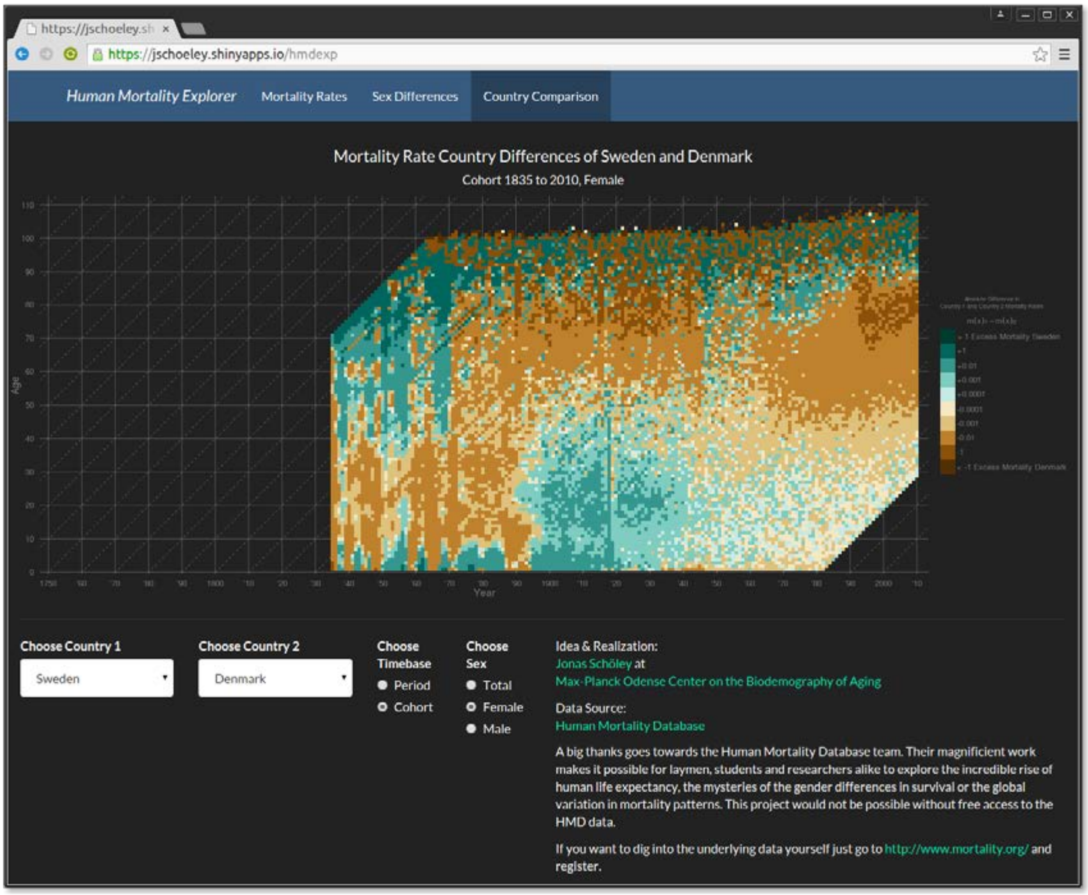
2) Transitional timing: the transition of birth is a stressful event and momentarily increases the force of mortality,
3) Mortality selection: The frailest die first, causing the mean force of mortality to decline with age.

In order to quantify the relative importance of these three processes I fit a three component mortality model against the observed force of mortality. The model describes the data with high accuracy, suggesting that the hypotheses about early mortality are correct.



“The Human Mortality Explorer”

The Human Mortality Explorer is an interactive web page for the visual exploration of the Human Mortality Database. The tool allows users from around the world to easily explore human mortality dynamics across space and time. Users select data subsets on a graphical user interface and are immediately presented with results in the form of Lexis surface plots (heatmaps over period and age). Users can toggle between a visualization of the pure mortality rates, sex differences in mortality and country comparisons. The Human Mortality Explorer is built using modern technologies that facilitate the construction of interactive web-pages without requiring expert knowledge of web-technologies.



Choose Country 1
Sweden

Choose Country 2
Denmark

Choose Timebase
● Period
◉ Cohort

Choose Sex
● Total
◉ Female
● Male

Idea & Realization:
Jonas Schöley at
Max-Planck Odense Center on the Biodemography of Aging

Data Source:
Human Mortality Database

A big thanks goes towards the Human Mortality Database team. Their magnificient work makes it possible for laymen, students and researchers alike to explore the incredible rise of human life expectancy, the mysteries of the gender differences in survival or the global variation in mortality patterns. This project would not be possible without free access to the HMD data.

If you want to dig into the underlying data yourself just go to http://www.mortality.org/ and register.

Catalina Torres, Research Assistant, Public Health

Main research interest

I am interested in the historical rise in life expectancy at birth since the early 19th century, especially in Norway and Sweden. These countries were the leaders in life expectancy at birth during most of the 19th century until the 1880s. There is uncertainty about the factors that first provoked mortality reductions in these countries, since the advances in sanitation, medicine and adequate infrastructure – which certainly accelerated the mortality decline – where not introduced until the late 19th and early 20th centuries. I am thus interested in the causes of the early decline in mortality in these Nordic countries, focussing on some aspects such as the evolution of the age-contributions to the changes in life expectancy at birth, the differences between females and males, cohort vs. the period effects, the clustering of deaths within families, and the impact of biological vs. social factors on mortality levels. With the aim of better understanding the process of the mortality decline during the early 19th century at different levels, the use of aggregate data as well as of microdata as complementary sources is of essential importance for my research. As historical data sometimes suffer from quality issues, I am also interested in methods for correcting problematic data. Finally, in order to have an idea of the factors that caused Norway and Sweden to have an advantage in survival over other neighboring Nordic and European countries, I am interested in doing comparative research, using available historical data for other countries.

Awards

From the Demography Department of the University of Montreal: Prize Jacques Henripin, for best Master's dissertation of the year (completed in 2014) about Canadian demography (prize received in 2015).

Publication highlights

Torres, C. and Dillon, L. Y., 2015, "Using the Canadian censuses of 1852 and 1881 for automatic data linkage: a case study of intergenerational social mobility". In Bloothooft, G., Christen, P., Mandemakers, K. and Schraagen, M. (eds.), Population Reconstruction, Springer, Switzerland, p 243-261.

This book chapter discusses the issues of missing and uncertain data in the Canadian census sample of 1852 within the context of automatic linkage with the complete census of 1881. The resulting linked sample from these two censuses was created to provide an opportunity to study intergenerational social mobility in Canada between fathers (in 1852) and sons (1881). We discuss the accuracy and representativeness of the automatically generated links and show how the use of marriage registers can be helpful in order to verify the results of the automatic linkage. Our verifications suggest that most of the links are accurate. However, the linked sample is not representative of some subgroups of the studied population, since some attributes favoured while others hindered the possibility of being automatically linked from 1852 to 1881. Finally, based on our efforts of manual linkage between the BALSAC marriage registers and the automatically linked census sample for the verification of the latter, we present some considerations about the great research potential of linking census and parish register data in Quebec.

Ongoing work

“The Scandinavian advantage: a comparative analysis of life expectancy at birth by sex in four European countries during the 19th century”

Record human life expectancy has increased since at least the late-18th century. During the 19th century, the first and the second places were often occupied by Scandinavian countries, in particular by Norway but also by Sweden. This advantage in survival has not been fully explored, as the research on the mortality decline during the 19th century has mainly focused on specific countries as well as on the last decades of the century. In this study I analyse the rise in life expectancy at birth during the 19th century in a broader perspective, by comparing the mortality levels between England and Wales, France, Norway, and Sweden. Using data from the Human Mortality Database, I analyse and compare the evolution of different measures related to the length of life and its variation in these four countries, by sex. Preliminary results suggest that the advantage in survival in Norway and Sweden was the result of lower and rapidly falling levels of infant mortality, which were achieved prior to the improvements in sanitation and medicine that took place during the last decades of the 19th century.

“Unequal distribution of deaths and risk families during the early 19th century: a comparative study between Sweden and France”

During the 19th century and prior to the 1880s, Norway and Sweden – which were not particularly advantaged in terms of living standards – often occupied the first and the second places in life expectancy at birth. Among the factors that may have contributed to that advantage in survival over other European countries, there are the behaviours and attitudes regarding fertility and child care, which are themselves associated with the role of the family and especially of the mother in the survival chances of infants and children. Using two reliable sources of historical microdata for different Swedish and French populations, this study aims to analyse and to compare the impact of some family variables on the survival chances of their offspring. In particular, I will examine the impact of some behaviours related to the fertility histories of females in childbearing ages on the survival chances of their infants and children. Since emphasis is put on the family as the unit of analysis, this study will also include a discussion about the definition of high risk families and mothers as well as measures of the heterogeneity in the distribution of deaths, i.e. measures of death clustering within families.

Media appearances of research staff

Print/online news

Spiegel, Le Monde, Videnskab dk, Discovery Channel, News Room America, Inovation Toronto, rtve Spain, Green Report Italy, eco Brazil, Avisen Denmark, Nordjyske Denmark, Nachhaltig leben, 24 Hodin, BIODIVN, Eurasia Review - Journal of News & Analysis, VBIO Germany, scinexx Germany, Wiener Zeitung Austria, NORDJYSKE Stiftstidende, Fyns Amts Avis, Irish Examiner, Videnskab.dk

Radio

SWR2 Tandem

TV

Interview to TV2 Funen, "The decreasing fertility rates in Denmark": http://www.tv2fyn.dk/nyheder/06-10-2015/1930/hele-udsendelsen-1930#player

Other Media

Showmeshiny.com -- A gallery of R web apps (http://www.showmeshiny.com/human-mortality-explorer/)

Teaching by research staff

The research staff of MaxO put in approximately one thousand three hundred and seventy hours of teaching in 2015 in courses and workshops both at SDU and elsewhere:

Basic Mathematics for Demographers
Statistical Modelling
Mathematics, statistics and physics for biologists and pharmacists
Multivariate analysis and chemometrics
Individual study activity - metapopulation modeling for wildlife restoration
Biodiversity Conservation and Management
Terrestrial Ecosystems
Biodemography
Workshop: University of Queensland, The Era of Big Data Hits Conservation Biology
Evidence Based and Biostatistics – Master's course for pharmaceutical students
Mathematical Demography - week course for the EDSD program
Marin- og Brakvandsøkologi
Epidemiology and Quantitative Methods in Health Science
Study Start projects, Medical Students, Epidemiology and Quantitative Methods in Health Science
Epidemiology and Registry Research, Pre-PhD course, Epidemiology and Quantitative Methods in Health Science
Probability Theory
Zoology & Evolution: Invertebrate Zoology 2014/2015 (Arthropoda: Insecta I + II)
Zoology & Evolution 2015/2016: Invertebrate Zoology (Porifera, Cnidaria, Plathelminthes, Mollusca: Gastropoda & Bivalvia)
Field Course in Terrestrial Zoology
Plants, protists and fungi
Pharmacy introductory course
Biostatistics I
Biostatistics II
Survival analysis
Mathematical demography (EDSD)
Introduction to STATA
Study-start assignments for medical students
Field course in terrestrial biology
Videnskabelig metode: Forskningsmetodologisk grundkursus
First-year student projects
MPIDR course IDEM 184 Integral Projection Models
Population biology and evolution
Introduction to biodemography
Planning and evaluation of biological studies
Evidensbaseret Lægemiddelanvendelse og Biostatistik, (E15)
Visualizing Demographic Data with ggplot
Workshop on COMADRE Animal Matrix Database at EvoDemoS conference
Workshop on COMADRE / COMPADRE Matrix Database at ESA 2015
Workshop on COMADRE / COMPADRE Matrix Database at BES 2015
Individual Study Activities in Biology (bachelor/master level)

Bachelor Project Supervision
Masters Project Supervision
First year project

Research Project I
Multivariate Analysis and Chemometrics
Mathematics, statistics and physics for biologists and pharmacists

Visitors

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Yvonne Buckley, Professor, Trinity College Dublin

David Hodgson, Associate Professor of Ecology, Centre for Ecology and Conservation, College of Life and Environmental Sciences, University of Exeter, Cornwall Campus

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Jenni Nelson Heywood, Program Director, Map Your World

Nicole Newnham, Executive Director, Map Your World

Natahalie van Vliet, CIFOR

Marcus Ebeling, University of Rostock

Francesca Sargent, University of Exeter

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Peter Harnisch, Max-Planck-Gesellschaft Munich, Unit of Private Research Funding

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Publications by research staff

Published/accepted publications

Aburto, J.M., H. Beltrán-Sánchez, V.M. García-Guerrero, **V. Canudas-Romo**. (in Press). "The lost decade at the turn of the century: health disparities and heterogeneity among states in Mexico." *Health Affairs*

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