# Discussant Comments
# Concurrent Session 3A: Mortality Inequality: Impact of Socioeconomic Factors

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**S. JAY OLSHANSKY:** "The underlying message is the same: health inequalities are ubiquitous and have persisted over time."[1] This is the most important observation of the manuscript. Inequalities in longevity are foundational; they have always been there and always will be. However, various government organizations, including the World Health Organization and health organizations within countries, set targets to raise all health and longevity boats and simultaneously find ways to reduce the disparities observed among population subgroups.

So, having set these goals, it's easy to determine whether you've achieved success: Simply track the health and longevity of population subgroups across time, and if you'll excuse the expression, "mind the gap." That's the easy part. The hard part is setting forth public policy to reduce the gap. To address this issue, Alai and colleagues created a demographic tool to be used by public-policy makers to figure out how best to achieve this goal. The idea seems straightforward on the surface, but for reasons that I'll explain later, it's likely to lead to somewhat misleading results—and for reasons that you're probably not anticipating. This doesn't lessen the value of the tool, which I think is useful. It's just that I think the time has arrived to broaden our understanding of health inequalities based on a traditional and long-held belief that if we do indeed both mind and close the gap, such inequalities would disappear. I contend that while it might be true that the health inequalities we see now can and should be diminished, once we succeed—if we ever succeed—a new set of health inequalities will emerge, some of which we can already see quite clearly today. These new health inequalities are largely intractable right now, which means the first statement made by these authors that "health inequalities are ubiquitous and have persisted over time" can and should be supplemented with the statement that "and they will persist forever, but for different reasons."

So what exactly did Alai and colleagues do? When human mortality changes for any reason, one can refer to the factors that contributed to such changes as shocks to mortality. Classic examples of positive shocks through recent history include the introduction and dissemination of basic public health in the late 19th and early 20th centuries, the introduction of antibiotics in mid-20th century, the broad dissemination of viral vaccines beginning in the 1960s, new treatments and detection devices for cardiovascular diseases developed during the last quarter century, advances in nutrition science that changed our dietary habits—at least the ones that changed them in a good way, better education and declines in smoking in successive birth cohorts throughout most of the 20th century, and the forthcoming positive shock expected from the world of aging science when a therapeutic intervention to slow aging comes online. On the flip side, a few examples of negative shocks to mortality (among many) include the influenza pandemics of 1918, 1956 and 1968; the HIV epidemic beginning in 1984; the dramatic drop in life expectancy among the less educated in some developed nations during the last quarter century; the adult and childhood obesity epidemics beginning in the late 1970s, which have done nothing but accelerate in recent

[1] Daniel H. Alai, Séverine Arnold(-Gaille), Madhavi Bajekal and Andrés M. Villegas, "Causal Mortality by Socioeconomic Circumstances: A Model to Assess the Impact of Policy Options on Inequalities in Life Expectancy," paper presented at the Society of Actuaries Living to 100 Symposium, Orlando, Fla., January 4–6, 2017, p. 2. *https://www.soa.org/Library/Monographs/Life/Living-To-100/2017/2017-living-100-monograph-alai-arnold-bajekal-villegas-paper.pdf*

decades; and the accelerated rise in death rates from the indiscriminant and growing use of opioids and other prescription and nonprescription drugs.

Where is the next positive shock expected? How can we help to make it happen? And is there a tool we can use to guide us along the path toward reduced disparities? Alai and colleagues provide such a tool based on a derivative of cause-elimination life tables methods that traditionally have been used to illustrate how death rates and life expectancy would likely change if progress were made in lowering or eliminating specific causes of death. The challenge with existing models, which I've personally used, is that the underlying assumption of independence of diseases is questionable. For example, if an intervention comes along that either detects a disease earlier or yields improved survival outcomes following treatment, both of which lower case fatality rates, the age-specific risk of death for that disease drops. The operating assumption is that such an intervention influences only that disease, in isolation, with no positive or negative impact on any other disease. While in some cases this might be true—for example, coronary bypass surgery might lower the risk of death of a heart attack but is unlikely to have any direct influence on cancer or diabetes or any other major fatal condition—by contrast, losing weight or quitting smoking as a method of lowering risk can favorably influence almost all major fatal diseases simultaneously. So what exactly did Alai et al. do to solve this? Recognizing that social gradients in mortality risk and longevity already present in the population are caused, in part, by the presence of varying risk factors among these groups; one need only model these relationships, construct a mathematical procedure for linking diseases to one another, and then build an analytical tool—a multinomial logistic model—that allows the user to formulate hypothetical public-health scenarios that influence the gap in longevity. If you want to find out what works best to raise all longevity boats, tweak one disease this way (that is, reduce or eliminate it hypothetically). Want to lower disparities? Tweak another disease a different way until age-specific death rates move in the desired direction. I'm oversimplifying, of course, but this is little more than a curve-fitting exercise.

At one very important level, I like this exercise since it provides a new tool that accounts for the differential influence of disease reduction on subgroups of the population that already face differing mortality risks for these diseases. However, there are two major challenges that are not accounted for here, one of which I think the authors could have addressed; the other I would comment on quite specifically if asked to review this paper for a journal.

The authors chose to operate at the level of disease reduction, and I understand this, given that the data they used were drawn from national vital statistics in the U.K. from 1981 to 2007. What this research completely ignores—and this is not a trivial issue—is that the risk factors for disease do not operate equally on subgroups of the population *within* a given social status, and yet that is an implied assumption of the model developed here. I would encourage the authors to at least discuss the importance of risk factor modification and how the treatment of diseases has unequal impacts on the population along the very social gradient the authors are interested in studying. Introducing treatments for diabetes to the less educated has a lower success rate than when introduced to the more educated, mortality outcomes for bypass surgery are likely to be less

favorable for the very subgroups of the population for whom the gap in longevity is the largest, etc. The authors need to consider this level of analysis at least one level down from where they're at now.

And this leads me to the second and, I would suggest, more pernicious problem with this line of reasoning. One more level further down from risk factors is the biology of the organism under study. Here is where not only the authors run into difficulty, but also the World Health Organization and other public-health advocates run into trouble. And I've certainly faced this within my own school of public health, where basic or traditional epidemiology is the hammer being delivered to and used by students, and all diseases and risk factors look like nails to them. In fact, the word "aging" doesn't even appear in textbooks used to teach first-year epidemiology students about chronic diseases; I don't know if the same is true for textbooks used to teach actuaries about longevity and mortality. How can this be? No student leaves my classroom without understanding the underlying biology that determines life span in humans, and that knowledge should serve as the basic framework within which epidemiology operates. My colleagues and I have been trying to deliver the message of biological time to the world of epidemiology for more than 30 years now, and while we've had success—especially in recent years, during a time when life expectancy gains have diminished—as biodemography predicts, failure to recognize biological time leads repeatedly to mortality-modeling efforts that will, in our opinion, yield unrealistic and/or improbable results. In fact, I would suggest that in long-lived populations, we can already see the consequences of a failure to understand the biological factors that influence duration of life. The backdrop upon which all epidemiology and public health must operate is a fundamental biology that drives all life and death.

Now I'm going to do something here I wouldn't ordinarily do, but this is such a great opportunity, I just can't resist. I'm going to explain in just two minutes exactly why humans live as long as we do, what drives duration of life, and ultimately, why our current effort to combat disease will—or already has—reached a point of diminishing returns. I'm borrowing from language I used recently in a U.K. publication called *Spectator Health* to explain why centenarians can get away with smoking, drinking and eating poorly and still live so long. So here it is in a nutshell.

How long most sexually reproducing species live, including humans, is calibrated to something that has absolutely nothing at all to do with how we live our lives. Here's the chain of reasoning. The level of hostility in the environment that existed when each species arose had a direct and profound influence on when reproduction begins. A hostile environment where predation is common leads to early reproduction and an accompanying biology and physiology that support rapid physical development. These animals tend to live shorter lives. An example would be a mouse—a meal for many other living things. Thus, mice develop and reproduce quickly; they go through puberty at 30 days and live for about three years in protected environments. A relaxed environment with few predators allows other species to develop and reproduce later, with an accompanying life history strategy, biology and physiology that support

later development. An example would be a Greenland shark, an animal that has few predators. Thus, it does not go through puberty until 176 years of age and can live for 400 years.

Human reproduction and longevity are somewhere between a mouse and a Greenland shark. The point here is that duration of life is calibrated to reproduction, reproduction is calibrated to the level of hostility in the environment, human physiology and body design evolved to accommodate these unique life history traits, and therefore, the secret to species-specific longevity rests within a set of fixed genetic programs for early life developmental events over which we have no control. While natural selection could not have given rise to aging or death programs, aging happens anyway as an indirect by-product of biological clocks that regulate developmental events early in life.

Thus, there is a biological reason why mice live only 1,000 days, dogs live only 5,000 days, humans live about 28,000 days and Greenland sharks live about 146,000 days, and it has nothing at all to do with how we all live our lives, the risk factors we acquire or exhibit during our lives, disparities caused by socioeconomic status, access to health care, income, food deserts or accelerated telomere shortening among the more highly stressed deprived subgroups of the population. It is this backdrop of biological aging that marches on, independent of disease risk factors, but which influences disease expression along the way, which is being ignored here. At a practical level, what this means is that the longer we live on average, and the further out we push the envelope of human survival by whatever means, whether through behavior modification or disease reduction caused by medical technology, as a result, we expose the saved and longer-lived population to an elevated risk that aging itself becomes a more important risk factor that influences duration of life. Contrary to what you've heard that longevity for everyone, regardless of age, is driven by a simply calculated 50/50 split between environment and genetics, based on twin studies, or some other percentage split, the longer we live as a population, the greater the influence of aging as a risk factor. Time reveals the genetic variation present in every birth cohort. Time also tells us that simple notions of gene-environment interactions must be understood within the context of a fixed biology.

So what exactly is the importance that aging becomes a more important risk factor as we live longer? It means that the rise in life expectancy will decelerate unless we find a way to modulate aging itself—an argument we've been making since 1990. It means that progress made against major fatal diseases will yield diminishing returns in terms of longevity. It means that frailty and disability is expected to increase as death rates from cancer and cardiovascular diseases decline. It means we should rethink conventional views of mortality improvement scenarios that have as their foundation the assumption that health will always improve, life will forever be extended, and disparities can be reduced or eliminated by attacking one disease at a time.

Aging can most easily be understood to be the accumulated damage to the building blocks of life that accrues, inevitably, with the passage of clock time. It is the inevitable by-product of life itself. As I stated in an article in *Scientific American* years ago on human aging, "It is an inescapable biological reality that once the engine of life switches on, the body inevitably sows the seeds of its own destruction."

The weakness of this article is that the authors fail to consider the underlying biology that drives duration of life. But keep in mind that the authors are not using this methodology for forecasting purposes. If they did, they would quickly run into unrealistic scenarios. Instead, they're using it to address disparities—and quite unexpectedly discover the phenomenon of competing risks in aging bodies. They found that progress made against one disease, such as cancer or cardiovascular disease, results in an increase in the longevity gap between population subgroups. This may not sound right at first, but the reason for this is competing risks, which is at the heart of human biology operating on aging bodies. So let me be clear. The paper by Alai et al. does not account for biological aging as an underlying risk factor in a competing risk model, but since the purpose of this exercise is to develop a realistic tool to assess and reduce disparities, it works very well for this purpose, and the authors should be congratulated on having made a useful contribution to the scientific literature.

This brings me to the paper by my longtime friend Sam Gutterman.

If any of you have been following the literature on mortality projection models, you'll know that I've been heavily involved in this exercise since I wrote my dissertation on this topic more than 32 years ago. In fact, I'm delighted to note that my own simultaneous/multiple cause-delay forecasting model from my dissertation was adopted and used my Munich Re quite some time ago. I'm not sure if they're still using it, but it's gratifying to know that these models can have practical value. My own involvement in this area has, for quite some time, involved the use of basic biology in informing forecasting assumptions. This is rarely done, because, quite frankly, most scientists involved in forecasting know very little about biology, so they continue to pull out the forecasting hammer they were taught to use—which is little more than a ruler used to extend past trends into the future.

I'll show you a picture of what I mean by this in a moment, when I get to the visual part of my presentation, but basically I've suggested for many years now that a window that allows you to see into the future of mortality involves an examination of the health status of younger living cohorts, rather than developing ruler-based methods of extending mortality trends from extinguishing cohorts into the future, under the assumption that the future will be like the past. Seriously, should we really be assuming that the observed mortality experience of your grandparents and great-grandparents born during the late 19th and early 20th century is going to tell you much about the health and longevity of millennials when they grow older?

What Sam has done is he's taken two main drivers of premature mortality to illustrate this methodology—smoking and obesity—and asked a rather straightforward question: How will premature mortality (and therefore total mortality) in the future be influenced by observed secular trends in just these two variables and his predictions for their prevalence and influence on mortality, going forward in time? Sam did exactly what I agree should be done: He's examined the health status of younger living cohorts, rather than the observed mortality dynamics of extinguishing cohorts, to predict the future. The methods and data used here are a great starting point, and Sam is the first to acknowledge that this method requires a set of underlying assumptions that can easily be challenged. But that's not the point. When creating a methodology like this, you

first outline the reasoning behind it and then illustrate precisely how it works, using a practical example that can easily be replicated. So I'm not going to discuss the underlying assumptions so much as the logic behind the idea, [and] the unique advantages and challenges of having chosen smoking and obesity as examples. And then I'm going to suggest that, just like the first paper I reviewed, Sam's approach would benefit from a basic grounding in human biology, because all of these risk factors operate within the constraints imposed by a genetically fixed body design.

What are the advantages of using Sam's approach? First, he's taken us out of the centuries-old method of predicting the future by using the past. Thank goodness it's a well-respected actuary doing this, because perhaps now it'll open up some eyes to the challenges of linear mortality forecasting. I've been railing against this approach for decades now; I'm glad to see actuaries are coming on board. Second, he's chosen two variables, smoking and obesity, that he's studied extensively and which are acknowledged to be two of the main drivers of premature mortality in the 20th and 21st centuries, respectively. These are perfect examples to use. Third, Sam made this exercise incredibly simple, which is exactly how you first introduce a methodology like this.

I honestly have no significant reservations about developing and using a methodology like this, and Sam had to start somewhere. So instead of focusing on the intricate details of his specific assumptions, I'm instead going to place this methodology within a broader context. This requires a more detailed examination of the challenges that come with a methodology like this, but I'm guessing that is exactly what Sam is trying to achieve here—a thorough vetting of the methodology before it's turned on for practical purposes. So here are some of the challenges.

First, the most glaring issue with this approach is the one addressed by the previous authors: These primary risk factors for disease do not operate independent of each other. By way of example, an obese smoker, with a BMI above 35, faces a much higher risk of death than one would assume by simply adding together the health risks of smoking and obesity independently—which, by the way, is done all the time in almost all life expectancy calculators on the market today. On a related note—and this challenge has more to do with genetic heterogeneity than anything else—some people who smoke and carry excess weight are at no significantly elevated risk of death, due to genetic influences that are unequally distributed in the population. So this must be a population-based assessment tool that acknowledges, as always, that there must be distributions of death observed with any combination of risk factors considered here. Please don't think you can model your way to perfection here. I know Sam doesn't believe this, but in my time, I've run into a few too many physicists who, in the absence of any knowledge of human biology, happen to believe that all life and death can be reduced to a single equation.

Second, I simply do not trust underlying cause of death from death certificates of older people—in this case, defined as people aged 85 and older. The relevance of risk factors also becomes very complicated here. For example, many people nearing the end of their lives tend to lose considerable weight because they stop eating, so being underweight can tell a misleading story—especially when applied equally to all ages.

Third, Sam is the first to acknowledge that our understanding of the relationship between obesity and mortality is complicated by the fact that obesity will often not show up on death

certificates as an underlying risk factor for disease and death. While we've both estimated the negative impact of obesity on life expectancy for a population as less than one year, it's an easy argument to suggest that the true negative impact is actually much greater than that.

This leads to the fourth challenge. Sam acknowledges that there have been notable upward trajectories of obesity in recent decades but believes this cannot continue, and therefore dampens the future trend in obesity. At one level, I agree with this, since there must be an upper threshold beyond which no one else can become obese, because almost everyone who can become obese has already done so. I don't know if a leveling off of obesity for this reason is good news or bad news, but either way, it does not bode well for population health. I'll accept this assumption for now, but with reservations that it could grow much worse than expected, because the childhood obesity epidemic that began a quarter century ago has yet to play itself out in adult obesity and related health consequences.

The fifth challenge should be obvious. There is much more at play here than obesity and smoking, but Sam had to start somewhere. I see a potential to merge the two methodologies presented during this session and expand the list of risk factors as a way to create a new age-period-cohort methodology that more appropriately takes into account, the major challenge of competing risks. However, the same problem I had with Alai's article I would acknowledge is at play here. None of the risk factors considered nor their relationships to each other can be considered outside of the context of human biology. They all operate within that context, which means that we must all acknowledge that even if we get entire populations to eliminate major risk factors like obesity and smoking, along with a long list of other harmful risk factors, we all still age, we all still grow old, and we will all still face a 75 percent chance that death will be caused by cardiovascular disease, cancer, diabetes-related conditions and neurological failures such as Alzheimer's disease, even in a perfect risk factor world. The human body was simply not designed for long-term use, so please, let's not perpetuate the myth that we can forever continue to manufacture more survival time in the absence of altering our basic biology.