Reproduction and the carbon legacies of individuals

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ABSTRACT

Much attention has been paid to the ways that people's home energy use, travel, food choices and other routine activities affect their emissions of carbon dioxide and, ultimately, their contributions to global warming. However, the reproductive choices of an individual are rarely incorporated into calculations of his personal impact on the environment. Here we estimate the extra emissions of fossil carbon dioxide that an average individual causes when he or she chooses to have children. The summed emissions of a person's descendants, weighted by their relatedness to him, may far exceed the lifetime emissions produced by the original parent. Under current conditions in the United States, for example, each child adds about 9441 metric tons of carbon dioxide to the carbon legacy of an average female, which is 5.7 times her lifetime emissions. A person's reproductive choices must be considered along with his day-to-day activities when assessing his ultimate impact on the global environment.

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1. Introduction

Much attention has been paid to the ways that people's home energy use, travel, food choices and other routine activities affect their personal emissions of carbon dioxide and, ultimately, their potential contributions to global warming (O'Neill and Chen, 2002; Bastianoni et al., 2004; Bin and Dowlatabadi, 2005; Vandenbergh and Steinemann, 2007; Wei et al., 2007). For example, a variety of "carbon calculators" allows individuals to estimate their lifetime emissions of greenhouse gases (U.S. Environmental Protection Agency, 2007).

While population growth is obviously a key component of projections of carbon emissions at a global level (Dyson, 2005; Harte, 2007; IPCC, 2007), there has been relatively little emphasis on the environmental consequences of the reproductive choices of an individual person. Obviously, the choice to reproduce contributes to future environmental impacts. There are the immediate effects caused by each offspring over his or her lifetime (Hall et al., 1994), but, should the offspring reproduce, additional impacts could potentially accrue over many future generations.

Some authors have discussed the "externalities" of childbearing (i.e., the consequences of an individual's reproduction that are borne by society, rather than the individual himself), focusing on the costs of abatement of the impacts caused by the individual's descendants (Cline, 1992; O'Neill et al., 2001). For example, O'Neill and Wexler (2000) consider emission scenarios that lead to particular stabilization concentrations of CO_2, and they model the abatement costs incurred by the addition of a single individual (and his or her descendants) to the population.

We explore the effects of an individual's reproductive behavior by tracing a single female's genetic contribution to future generations and weighting her descendants' impacts by their relatedness to her. We apply this approach to emissions of fossil carbon dioxide with the goal of quantifying the carbon legacy of an individual and examining how it is affected by the individual's reproductive choices.

2. The carbon legacy of an individual

Our basic premise is that a person is responsible for the carbon emissions of his descendants, weighted by their relatedness to him. For a descendant that is n generations removed from the focal individual, the weight is $(1/2)^n$. So, for example, a mother and father are each responsible for one half of the emissions of their offspring, and 1/4 of the emissions of their grandchildren. Fig. 1 illustrates this simple idea.

We will refer to the weights that indicate the relatedness of a descendant to the initial parent as "genetic units". The fractional genetic unit represented by a particular descendant can be thought of as the proportion of the ancestor's genes (or alleles) that are shared with the descendant, or the "percentage of blood" that the two have in common (Lush, 1994).

At any calendar date, the persistence of a lineage can be quantified as the number of genetic units represented by members of the lineage who are alive at that time. If we integrate the number of genetic units over time, we obtain an estimate of the total

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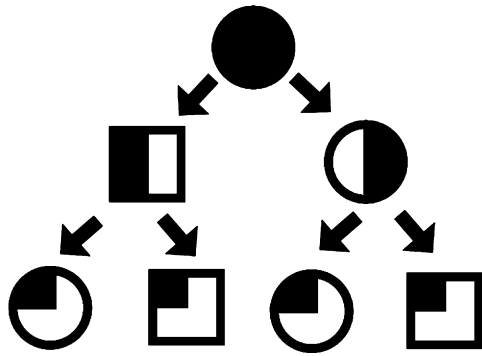E-mail address: murtaugh@science.oregonstate.edu (P.A. Murtaugh).

Fig. 1. Illustration of the propagation of genetic units in a family tree. Circles indicate females, and squares indicate males. The original female has one daughter and one son, each of whom also has one daughter and one son. The blackened areas indicate the number of genetic units (a total of 1 in each generation in this example).

number of person years that are traceable to the original parent (see Fig. 2). If we integrate the product of the number of genetic units and the per-capita rate of carbon emissions over time, we obtain an estimate of the total emissions attributable to the ancestor, or her carbon legacy.

Our goal is to quantify the consequences of the childbearing decisions of an individual. The appeal of our weighting scheme is that it provides an accounting of the extent to which a parent's genetic material propagates through subsequent generations, and it allows the emissions of any individual to be unambiguously traced back and "assigned" to ancestors from any preceding generation. For example, the responsibility for the rightmost male in the bottom line of Fig. 1 lies, in 1/4 portions, with his maternal and paternal grandparents (only one of which, the maternal grandmother, is shown in the figure).

Depending on one's view of whether, and how, future environmental impacts of an individual's descendants should be discounted, other weighting schemes are possible. O'Neill and Wexler (2000), for example, quantify the expected effect of one additional birth by following his or her descendants, but without adjusting for relatedness (see their Equation A22).
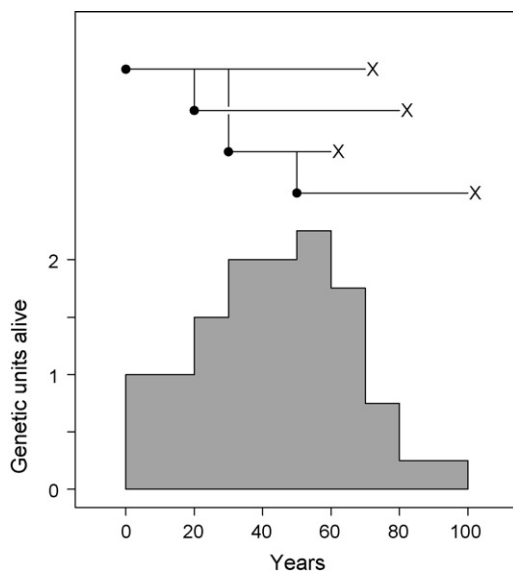

Fig. 2. Calculating person years for a genetic lineage. *Upper:* a hypothetical lineage starting with an individual born at time 0, who has two children and one grandchild (dots represent birth times, X's indicate death times). *Lower:* the number of genetic units alive vs. time. The grey area gives the total person years attributable to the ancestral individual.

3. Approaches to estimating the carbon legacy

We calculated trajectories of genetic units vs. time for genetic lineages of in each of the 11 most populous countries in the world, listed in Table 1. We used two approaches, one based on a simple analytical model and one involving numerical simulation.

3.1. Analytical model

We first develop a simple model of the propagation of family trees that provides a conceptual basis for the simulations that we used to generate the numerical results presented here. The model is developed fully in Appendix A.1; an abbreviated explanation follows.

We start with a single female born at time $t_0 = 0$ (generation 0), and assume that all reproduction occurs in pulses at times t_1, t_2, t_3, where $t_k - t_{k-1} = t_1$ is the generation time, i.e., the mean of the ages at which females give birth. If we assume that males and females are born at the same rate (see Appendix A.1.1), then the expected number of children produced per female at time t_k is $2 \cdot R(t_k)$, where $R(t_k)$ is the net reproductive rate, i.e., the average number of daughters a woman would be expected to have if she were subject to the fertility and mortality rates prevailing in the population. We assume that all members of the family tree, male and female, pair with members of the opposite sex from outside the tree, so that the reproductive rate of $2 \cdot R(t_k)$ is applied to males as well as females within the tree. As explained earlier, an individual of generation k, born at time t_k, represents $(1/2)^k$ genetic units, reflecting his relatedness to the ancestral female.

We assume further that the survival of all individuals follows a distribution characterized by the survivor function, $S(t)$, defined as the probability that an individual lives to at least age t. It can then be shown (Appendix A.1) that the expected number of genetic units alive at time t_k is

$$E[G(t_k)] = E[B(t_0)] \cdot S(t_k - t_0) + E[B(t_0)] \cdot \sum_{i=1}^{k} S(t_k - t_i) \cdot \left(\prod_{j=1}^{i} R(t_j) \right), \quad (1)$$

where $E[B(t_0)]$ is the expected number of births at time t_0, equal to one (the ancestral female).

Following the pulse of births at time t_k, mortality erodes the number of individuals, and genetic units, until the next pulse of

Table 1
Average person years associated with lineages in the world's eleven most populous countries, using medium-variant fertility projections. The initial parent contributes the number of years constituting his life expectancy. The last column is an estimate of the person years added to the ancestor's legacy for each child that he has, assuming his descendants survive and reproduce at the rates prevailing in the country. Fertility values are for 2005 (United Nations Population Division, 2007). The countries are listed in order of 2005 population; the abbreviations are as used in Fig. 7.

Country (abbreviation)	Fertility (children woman⁻¹)	Average person years	
		Ancestor's life	Added per child
China (C)	1.73	74.9	341
India (Ia)	2.81	63.8	161
United States (US)	2.05	80.2	470
Indonesia (Io)	2.18	68.6	244
Brazil (Br)	2.25	74.8	373
Pakistan (P)	3.52	63.4	268
Bangladesh (Ba)	2.83	62.8	201
Russia (R)	1.34	72.9	212
Nigeria (N)	5.32	48.8	136
Japan (J)	1.27	85.6	211
Mexico (M)	2.21	76.3	332

reproduction, at time t_{k+1}. Appendix A.1 gives expressions for a piecewise-linear model of this jagged trajectory of $E[G(t)]$ vs t.

The area under a plot of $E[G(t)]$ vs. t gives an estimate of the total person years attributable to the ancestral female. If $H(t)$ is the per-capita rate of carbon emissions at time t (mass per person per year), the area under a plot of $E[G(t)] \cdot H(t)$ vs. t provides an estimate of the total carbon emissions for which the ancestor is responsible.

3.2. Simulations

The simulations expand on the analytical model by allowing the births and deaths of individuals to be stochastic, i.e., to occur at other than set time points. This allows more realistic modeling of carbon legacies and gives an idea of how variable those legacies are among individuals.

Following lineages that include both males and females is computationally prohibitive. It turns out that the number of genetic units (of both sexes) attributable to an ancestral female is, on average, simply the number of females comprising an unbroken lineage of females descending from the ancestor (see Appendix A.2 for details). If we integrate the number of living females over time, we obtain an estimate of the total number of person years, male and female, that are traceable to the ancestral female.

Lineages were simulated with the following steps, implemented as a recursive algorithm in R (R Development Core Team, 2005):

1. Each lineage starts with a single female whose death time is chosen randomly, based on life tables for her home country (World Health Organization, 2007). A potential number of children is generated randomly from a Poisson distribution having a mean equal to the total fertility. Age-specific fertility schedules for the country (United Nations Population Division, 2007) are then used to generate the birth times and sexes of the potential children. Finally, these birth times are compared to the female's death time to determine how many (if any) births are actually attributed to her.
2. If there are female offspring, each daughter's lifetime and reproduction are simulated as done for the original female.
3. This continues until the lineage dies out, i.e., until all of the females having a direct path of female progenitors tracing back to the ancestor have perished. Some lineages persist indefinitely, in which case a pre-specified time limit terminates the simulation.
4. Each lineage is summarized as a trajectory of genetic units vs. time. As explained earlier, the number of genetic units at a particular time is estimated as the number of descendants alive at that time, assuming we are following females only. Integration of the number of genetic units over time gives the person years attributable to the ancestor. If the number of genetic units at each time is multiplied by the prevailing per-capita rate of CO_2 emissions, the integral of that quantity vs. time gives an estimate of the total CO_2 emissions attributable to the ancestral female.

Each set of simulations followed 10,000 female-only lineages subject to particular schedules of fertility and per-capita rates of carbon emissions, described in the next section.

3.3. Demographic and carbon-emission scenarios

The United Nations' "medium variant" projections of total fertility were used throughout (United Nations Population Division,

2007). These projections assume a convergence of fertility in all countries to 1.85 children per woman by 2050.

In 2005, world emissions of CO_2 from the combustion of fossil fuels were 28.1 billion metric tons, or 4.31 metric tons (t) per person per year, assuming a global population of 6.51 billion (Energy Information Administration, 2008). Three scenarios of future carbon emissions were considered for the 11 countries focused on in this paper:

1. *Optimistic:* Each country's per capita emission rate changes linearly from its 2005 value to a global target of 0.5 t CO_2 per person per year by 2100, and emissions continue at that rate indefinitely. A set of aggressive emission-reduction scenarios summarized by the IPCC (2007; Category III in Fig. 3.17) shows, on average, about an 85% reduction in global emissions between 2000 and 2100. Adjusting for a projected population size of 9.1 billion in 2100 (United Nations, 2004), this translates into a reduction in per capita emissions from 4.31 t CO_2 in 2005 to about 0.5 t CO_2 per person per year in 2100. This is an extremely ambitious target: emissions in Africa, which includes 34 of the 50 "least developed" countries in the world (United Nations Population Division, 2007), were roughly 1.2 t CO_2 per person per year in 2005.
2. *Constant:* Per capita emission rates remain indefinitely at their 2005 values. This scenario does not capture what most experts believe will be an increase in worldwide emissions in the first part of the twenty-first century (IPCC, 2007; van Vuuren et al., 2007; Energy Information Administration, 2008), and it posits long-term emission rates that are probably not sustainable, at least for the more developed countries. Nevertheless, we often use the constant-emission scenario as a reference, since it is intermediate between the other two scenarios.
3. *Pessimistic:* Each country's per capita emission rate increases linearly from its 2005 value to 1.5 times its 2005 value by 2100, and emissions continue at that rate indefinitely. The median global emission rate in a set of "business as usual" scenarios summarized by the IPCC (2007; Fig. 3.8) was 60 Gt CO_2 per year in 2100. Assuming a world population of 9.1 billion in 2100, this translates into a roughly 50% increase in the global per capita emission rate between 2000 and 2100.

For Bangladesh, with an extremely low per capita emission rate in 2005 (0.27 t person^{-1} year^{-1}), the optimistic limit was set at 0.27 and the pessimistic limit at 0.5 t person^{-1} year^{-1}.

4. Results and discussion

4.1. Genetic units and person years

Fig. 3 shows trajectories of average genetic units vs. time for lineages under scenarios of constant fertility (fixed at the 2005 value of 2.05 children per woman) and medium-variant fertility in the United States. As in the example of the U.S., any country having net reproductive rate exceeding one daughter per woman (roughly corresponding to fertility exceeding two) will have lineages with exponentially increasing person years, unless fertility decreases in the future. Even under the medium-fertility variant, with fertility decreasing to 1.85 children per woman by 2025, the average lineage still has nearly one genetic unit alive four centuries after the birth of the ancestral individual (Fig. 3).

As shown in Fig. 4, the distributions of both the duration and number of person years associated with simulated lineages can be extremely skewed. For the United States, under the scenario of medium-variant fertility, the median duration of female-only lineages is 111 years, and the mean is 168 years. The median
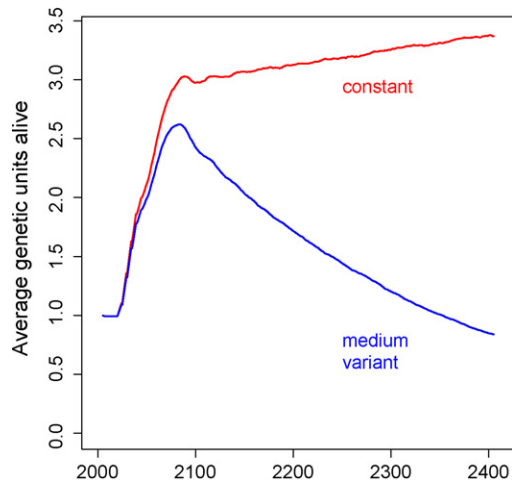
Fig. 3. For the United States, average number of genetic units vs. year, under constant and medium-variant fertility assumptions, in 10,000 simulated lineages. The starting individual's number of children is generated from the 2005 fertility rate.

number of person years per lineage (171) is less than 20% of the mean (921).

Fig. 5 shows trajectories of person years vs. time in the United States, for ancestral females that are constrained to have exactly 0, 1, 2 or 3 children, with all descendants then reproducing according to the medium-variant fertility scenario. A female bearing no children contributes, on average, a number of person years equal to the life expectancy of females in that country — this is the area under the curve corresponding to no children. Each child adds to the total person years attributable to the original female, manifested in increasing heights and skewness of the trajectories in Fig. 5.

Fig. 4. For 10,000 simulations for the United States with medium-variant fertility, distributions of the durations of lineages (upper) and the total person years associated with lineages (lower). About 0.8% of the durations exceeded 1000 years, and 7% of the areas exceeded 3000 person years.
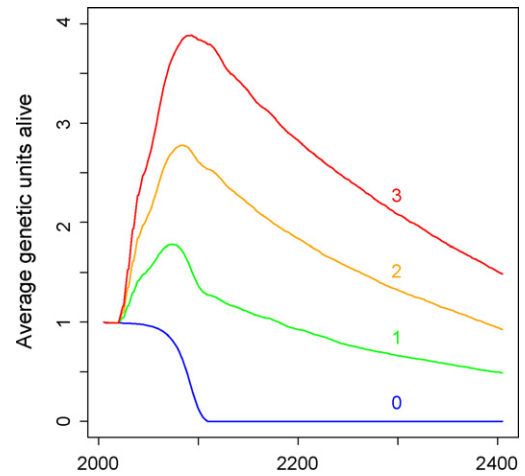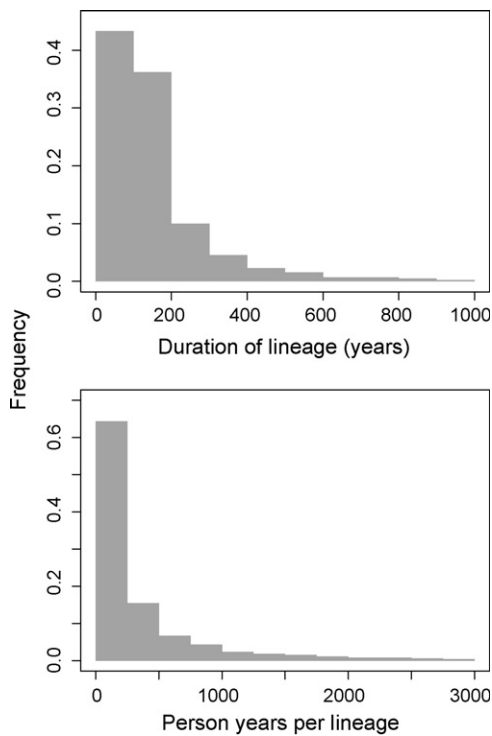

Fig. 5. Persistence of genetic lineages in the United States as a function of number of children produced by the initial parent, assuming that reproduction of descendants follows medium-variant projections of fertility. Each curve represents averaged results from 10,000 simulated lineages; the curves are labeled by the number of children. The area under each curve, extended to infinity, is the average number of person years attributable to an ancestor having the corresponding number of children.

Table 1 summarizes demographic characteristics of family trees simulated for the world's 11 most populous countries, including the United States, assuming that the initial parent has exactly one child. That child, and all of his descendants, then reproduce according to the medium-variant fertility schedule for the home country. The single child adds from 136 (Nigeria) to 470 (U.S.) person years to the ancestor's legacy. The ratios of the additional person years to the life expectancy of the ancestor (fourth divided by third columns) range from 2.5 (Japan) to 5.9 (United States).

4.2. Carbon emissions

Fig. 6 shows trajectories of average emission rates for lineages in the United States under the three different emission scenarios. The choice of scenario has an enormous effect, leading to a wide range of projected carbon contributions. This is dissatisfying, but it reflects the large variability and volatility of projections of the world's emissions, even over the next century (IPCC, 2007).
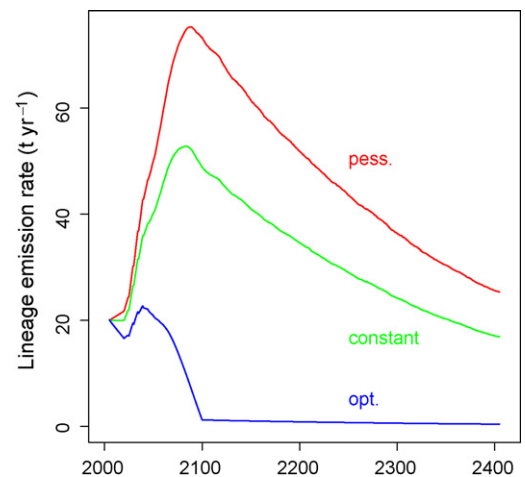
Fig. 6. For the United States with medium-variant fertility rates, average CO_2 emission rates attributable to the initial parent, under optimistic, constant and optimistic projections of per capita emissions. The area under each curve, extended to infinity, is the average mass of CO_2 for which the ancestor is responsible. The number of children borne by the initial parent follows the 2005 fertility rate.
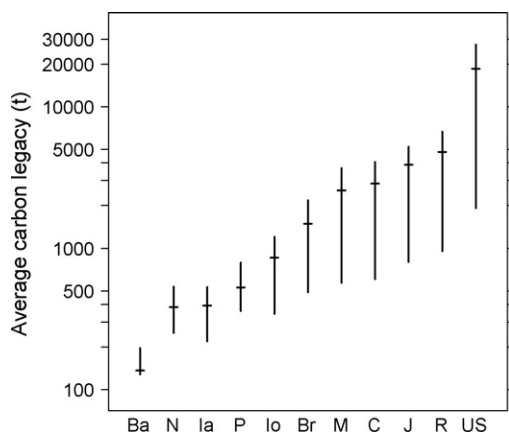
Fig. 7. Average carbon legacies (log scale) with medium-variant fertility rates for the constant-emission scenario (+), with a vertical line connecting the estimates for the optimistic and pessimistic emission scenarios. The number of children borne by the ancestral female follows the 2005 fertility rate in her home country.

Fig. 7 presents average carbon legacies for the 11 most populous countries in the world, with ranges corresponding to the different emission scenarios. Each legacy is the sum of the lifetime emissions of the ancestral female subject to the 2005 fertility rate, plus the weighted emissions of her descendants, assuming all future reproduction follows the medium-variant projection of fertility for her home country. The range of values is enormous: under the constant-emission scenario, the legacy of a United States female (18,500 t) is two orders of magnitude greater that of a female from Bangladesh (136 t).

From the point of view of this paper, which focuses on the consequences of an individual's reproductive behavior, it is useful to compare the carbon emissions added per child, rather than the emissions of females having the average number of children, among the different countries. Table 2 summarizes this metric for the 11 countries, assuming medium-variant fertility projections. Under the constant-emission scenario, the average emissions added by having a single child range from 56 t (Bangladesh) to 9441 t (United States). The ratios of the added emissions per child to the ancestor's expected emissions range from 2.4 (Japan) to 5.7 (United States).

4.3. General discussion

Table 3 compares the emissions attributable to an individual's reproduction to the emissions that are avoidable through changes

Table 2
Per capita emissions of fossil CO_2, average emissions for an individual born in 2005, and average emissions added to the individual's carbon legacy for each child produced. Estimates are from simulations assuming medium-variant fertility projections and the constant emission scenario (per capita rates fixed at their 2005 values). In parentheses are estimates based on the optimistic and pessimistic projections of per capita emissions.

Country (abbreviation)	Per capita emissions (t person^{-1} year^{-1})	Average emissions (t)	
		Ancestor's life	Added per child
China (C)	3.62	311 (183, 383)	1384 (228, 2023)
India (Ia)	1.05	70 (52, 85)	171 (87, 231)
United States (US)	20.18	1644 (883, 2030)	9441 (562, 12730)
Indonesia (Io)	1.29	110 (76, 135)	380 (143, 627)
Brazil (Br)	1.83	148 (97, 182)	721 (207, 1006)
Pakistan (P)	0.67	50 (42, 61)	205 (128, 273)
Bangladesh (Ba)	0.27	18 (18, 24)	56 (56, 94)
Russia (R)	11.70	883 (492, 1082)	2498 (295, 3497)
Nigeria (N)	0.75	41 (34, 51)	110 (73, 157)
Japan (J)	9.91	840 (453, 1047)	2026 (233, 2829)
Mexico (M)	3.67	291 (172, 360)	1241 (222, 1800)

Table 3
For the United States, lifetime emissions of CO_2 that are saved by different actions, based on the EPA's Personal Emissions Calculator (U.S. Environmental Protection Agency, 2007), and average emissions caused by having one additional child, from Table 2. Totals were obtained by multiplying the EPA's annual figures by 80, the current life expectancy of a female in the United States.

Action	CO$_2$ saved (metric tons [a])
Increase car's fuel economy from 20 to 30 mpg	148
Reduce miles driven from 231 to 155 per week	147
Replace single-glazed windows with energy-efficient windows	121
Replace ten 75-w incandescent bulbs with 25-w energy-efficient lights	36
Replace old refrigerator with energy-efficient model	19
Recycle newspaper, magazines, glass, plastic, aluminum, and steel cans	17
Reduce number of children by one	
Constant-emission scenario	9,441
Optimistic scenario	562
Pessimistic scenario	12,730

[a] One metric ton equals 2205 pounds.

in household activities and transportation during the individual's lifetime. Clearly, the potential savings from reduced reproduction are huge compared to the savings that can be achieved by changes in lifestyle. For example, a woman in the United States who adopted the six non-reproductive changes in Table 3 would save about 486 tons of CO_2 emissions during her lifetime, but, if she were to have two children, this would eventually add nearly 40 times that amount of CO_2 (18,882 t) to the earth's atmosphere.

This is not to say that lifestyle changes are unimportant; in fact, they are essential, since immediate reductions in emissions worldwide are needed to limit the damaging effects of climate change that are already being documented (Kerr, 2007; Moriarty and Honnery, 2008). The amplifying effect of an individual's reproduction documented here implies that such lifestyle changes must propagate through future generations in order to be fully effective, and that enormous future benefits can be gained by immediate changes in reproductive behavior.

It is important to remember that these analyses focus on the carbon legacies of individuals, not populations. For example, under the constant-emission scenario, an extra child born to a woman in the United States ultimately increases her carbon legacy by an amount (9441 metric tons) that is nearly seven times the analagous quantity for a woman in China (1384 tons), but, because of China's enormous population size, its total carbon emissions currently exceed those of the United States (Netherlands Environmental Assessment Agency, 2008).

Clearly, an individual's reproductive choices can have a dramatic effect on the total carbon emissions ultimately attributable to his or her genetic lineage. Understanding the ways that an individual's daily activities influence emissions and explain the huge disparities in per capita emissions among countries (Table 1) is obviously essential, but ignoring the consequences of reproduction can lead to serious underestimation of an individual's long-term impact on the global environment.

Acknowledgments

Appendix A

A.1. The analytical model

A.1.1. General assumptions

We start with a single female born at time $t_0 = 0$, and assume that all reproduction occurs in pulses at multiples of the generation time, t_1 (the mean of the ages at which females give birth), so that the members of generation k are born at time t_k and $t_k - t_{k-1} = t_1$. In the tree of relatives descending from the ancestral female, assume that each descendant pairs with a person from outside the tree. We express reproduction in terms of $R(t)$, the net reproductive rate at calendar time t, i.e., the average number of daughters produced per woman, assuming she is subject to the prevailing fertility and mortality rates. Since each male in the tree is paired with a female from outside the tree, $R(t)$ in this context can be thought of as the average number of daughters per member of the tree, male or female.

Because data on age-specific fertility obviously pertain to females, we use data on survivorship and life expectancy for females only. We assume a 1:1 sex ratio at birth, even though there is in fact a slight excess of male births worldwide (James, 1987). Error introduced by this assumption is small when compared to the uncertainty in estimates of other key demographic parameters and considered in the context of the simplified models used in our analyses.

A.1.2. Births

Assume that the only births in generation k are to parents born in generation $k - 1$. Let Y_{ki} denote the random variable for the number of children (of both sexes) born to parent i in generation k. The expected value of Y_{ki} is $2 \cdot R(t_k)$. Let $B(t_k)$ denote the number of births in generation k. We have $B(t_0) = 1$ (the ancestral female), and

$$B(t_k) = \sum_{i=1}^{B(t_{k-1})} Y_{ki} \quad \text{for } k \geq 1.$$

The conditional expected value is

$$E[B(t_k) \mid B(t_{k-1}) = b(t_{k-1})] = \sum_{i=1}^{b(t_{k-1})} E(Y_{ki}) = b(t_{k-1}) \cdot 2R(t_k).$$

This in turn has expectation

$$E[B(t_k)] = 2R(t_k) \cdot E[B(t_{k-1})] \quad \text{for } k \geq 1.$$

Expanding this recursive relationship, we obtain

$$E[B(t_k)] = E[B(t_0)] \cdot 2^k \cdot \prod_{i=1}^{k} R(t_i) \quad \text{for } k \geq 1. \tag{2}$$

A.1.3. Survival

To calculate $N(t_k)$, the total number of individuals alive at time t_k, we need to model the survival of individuals born at times $t_{k-1}, t_{k-2}, \ldots$ Let N_{ki} be the number of individuals born at t_i who survive to time t_k ($k > i$). Then

$$N(t_k) = \sum_{i=0}^{k} N_{ki}.$$

N_{ki} can be thought of as the number of "successes" (survival to time t_k) out of $B(t_i)$ "trials" (individuals born at time t_i). Given a particular value of $B(t_i)$, N_{ki} has a binomial distribution with probability $S(t_k - t_i)$, where $S(t)$ is the survivor function at t, i.e., the probability that an individual survives to at least age t:

$$[N_{ki} \mid B(t_i) = b(t_i)] \sim \text{Binomial } [b(t_i), S(t_k - t_i)] \quad \text{so that}$$
$$E[N_{ki} \mid B(t_i) = b(t_i)] = b(t_i) \cdot S(t_k - t_i) \quad \text{and}$$
$$E[N_{ki}] = E[B(t_i)] \cdot S(t_k - t_i). \tag{3}$$

Then

$$E[N(t_k)] = \sum_{i=0}^{k} E[N_{ki}] = \sum_{i=0}^{k} E[B(t_i)] \cdot S(t_k - t_i) = E[B(t_0)] \cdot S(t_k - t_0)$$
$$+ \sum_{i=1}^{k} E[B(t_0)] \cdot 2^i \left(\prod_{j=1}^{i} R(t_j) \right) S(t_k - t_i), \tag{4}$$

using Eq. (2).

A.1.4. Genetic units and carbon emissions

Since each member of generation i represents $(1/2)^i$ genetic units, the expected number of genetic units alive at time t_k is

$$E[G(t_k)] = E[B(t_0)] \cdot S(t_k - t_0) + \sum_{i=1}^{k} E[B(t_0)] \cdot S(t_k - t_i) \cdot \left(\frac{1}{2}\right)^i \cdot 2^i \cdot$$
$$\left(\prod_{j=1}^{i} R(t_j) \right) = E[B(t_0)] \cdot S(t_k - t_0) + E[B(t_0)] \cdot \sum_{i=1}^{k} S(t_k - t_i) \cdot$$
$$\left(\prod_{j=1}^{i} R(t_j) \right). \tag{5}$$

Eq. (5) gives the expected number of genetic units alive immediately after the pulse of births at time t_k. Just before t_k, we have

$$E[G(t_k^-)] = E[G(t_k)] - E[B(t_k)] \cdot \left(\frac{1}{2}\right)^k,$$

where $E[B(t_k)]$ is obtained from Eq. (2). This yields a jagged trajectory of $E[G(t)]$ vs. t, reflecting discrete pulses of reproduction followed by periods of gradual mortality. If we integrate under a piecewise linear plot of $E[G(t)]$ vs t, for $t = t_0, t_1^-, t_1, t_2^-, t_2, \ldots$, we obtain an estimate of the total person years attributable to the ancestral individual. If we integrate under a plot of $E[G(t)] \cdot H(t)$, where $H(t)$ is the per-capita rate of carbon emissions at time t (mass per person per year), we obtain an estimate of the total carbon emissions for which the ancestor is "responsible".

This analytical model gives numerical results that are very close to those obtained from the simulations. For example, for the constant-emission values presented in Fig. 7, the mean absolute deviation of the model predictions from the simulation-based results is 1.9% (range 0.3–6.4%).

A.2. Female-only lineages: a shortcut for the simulations

Suppose we follow only female descendants, denoting the number of females at time t_k as $N_f(t_k)$. The expected number of daughters per female is the net reproductive rate, $R(t_k)$. Following the same logic that led to Eq. (4), but replacing $2R(t_j)$ by $R(t_j)$, we can write:

$$E[N_f(t_k)] = E[B(t_0)] \cdot S(t_k - t_0) + E[B(t_0)] \cdot \sum_{i=1}^{k} S(t_k - t_i) \cdot \left(\prod_{j=1}^{i} R(t_j) \right), \tag{6}$$

which is identical to the expression in Eq. (5) for $E[G(t_k)]$, the expected number of genetic units alive at t_k. Consequently, in simulations we can greatly reduce the number of computations by following female-only lineages, yet still obtain an unbiased estimate of the number of genetic units of both sexes that are alive at any time.

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