ANALYZING PREHISTORIC DIETS BY LINEAR PROGRAMMING

John D. C. Little
Massachusetts Institute of Technology

Elizabeth A. Little
37 Conant Road, Lincoln, MA 01773 USA

July 13, 1996

Sloan Working Paper Number 3913

Abstract

Isotopic measurements of skeletal bone, coupled with corresponding measurements of foods that might have been eaten by prehistoric individuals, offer the promise of providing valuable information about their diets. Linear mixing equations relating bone measurements to food measurements for each of several isotopes serve to constrain the percentages of each food that could have been in the diet. Even though it is seldom possible to determine the diet uniquely, it is always possible to set bounds on the percentages of various foods that could have been part of the diet. The more isotopes that have been measured, the tighter will be the bounds. The bounds are determined by means of linear programming. We set up a basic linear model and illustrate the technique with simple examples. Then, using data and implicit mixing equations from Spielmann, Schoeninger, and Moore (1990), an extended case demonstrates how linear programming can answer archaeological questions.

PREHISTORIC DIETS, STABLE ISOTOPE RATIOS, LINEAR MIXING EQUATIONS, LINEAR PROGRAMMING

Introduction

Isotopically speaking, you are what you eat. The foods people digest determine the chemical content of their bones. Therefore isotopic studies of skeletal remains, coupled with corresponding measurements of candidate foods, offer the prospect of teaching us much about prehistoric diets. For example, Vogel and van der Merwe (1977) use carbon isotopes to provide evidence for the introduction of maize into prehistoric diets in New York State. Schoeninger, DeNiro, and Tauber (1983) and Walker and DeNiro (1986) show that carbon and nitrogen isotope ratios can identify marine and terrestrial components of prehistoric diets.

Several difficulties confront the user of such data in trying to draw archaeological conclusions. First of all, an isotope ratio found in skeletal bone is a function of the isotope ratios of all of the different foods that the individual has eaten. In simple cases, the diet may have consisted largely of one type of food, e.g., maize for certain populations, or salt water fish for others. A shift in diet from one type of food to another can be detected if the two foods have markedly different isotope ratios. If the diet is a mixture of two such foods, graphical analysis can often shed light on the archaeological issues being addressed. However, as the number of foods increases and multiple isotope ratios become available, the mixing possibilities become complex and the data difficult to interpret by simple comparisons and purely graphical methods.

To a considerable extent, the situation can be sorted out mathematically with mixing equations. As a good first approximation, the relationship between isotope ratios in food protein and those in bone collagen may be presumed linear for high protein diets, an assumption made by Chisholm, Nelson, and Schwarcz (1982), and supported by the recent experiments of Ambrose and Norr (1993). Then the greater the percentage of a diet devoted to a particular food, the greater are the contributions of its isotope ratios to the isotope ratios in skeletal bone. The contributions of a particular isotope ratio are directly proportional to its presence in the individual foods and are additive across foods. Such mixing equations have been used to estimate the percentages of two foods in a diet by Chisholm, Nelson, and Schwarcz (1982), Schwarcz et al. (1985), Keegan and DeNiro (1988), and Yesner (1988). Spielmann, Schoeninger, and Moore (1990) have considered mixing equations with four foods. See also Schwarcz (1991). More generally, by constructing relationships for multiple isotopes and multiple foods, one can define a set of simultaneous mixing equations that involve the percentages of various foods in the diet. Manipulation of these equations holds the promise of providing valuable information about the contribution of different foods to the diet.

A second problem is fractionation. In the metabolism of foods into body tissues, isotopes usually transfer differentially, or *fractionate* (van der Merwe and Vogel, 1978; DeNiro 1987). Therefore, the isotope ratios for bone need to be adjusted to obtain the isotope ratios that existed in the actual diet. Still another issue is that, if two or more foods resemble each other isotopically and nutritionally, we shall not be able to distinguish them. Thus, it is necessary to collect foods that resemble each other into groups. Finally, even after defining food groups, we shall usually have more candidate groups than isotopic measurements. This creates ambiguity in the diet implied by the data; i.e., a range of possible diets is consistent with the isotopic measurements.

The main goal of this paper is to show how to narrow the range of ambiguity in prehistoric diets by setting upper and lower bounds on the percentage of each candidate food group in the diet. We shall do this by applying the mathematical technique of linear programming. The method has been used by Little and Schoeninger (1995) to answer questions about the diet on Nantucket Island, Massachusetts, USA, between A.D.1000 and A.D.1600.

The paper begins with an example of a linear diet model with two equations and two food variables and then expands to consider three foods, which we analyze both graphically and by linear programming. Next is a general linear model and a discussion of several linear equations relevant to archaeological research. Finally, an extended example draws on data from Spielmann, Schoeninger, and Moore (1990) and illustrates how linear programming can address specific archaeological questions.

An Example of a Linear Diet Model

We start by focusing on an individual with a high protein diet. Let

j = 1 and 2 denote two types of high protein foods, for example, deer and geese.

D_j = the amount of food j in an individual's diet, expressed as a fraction of total kilocalories/day consumed.

The percentages of kilocalories contributed by each food, added up across all foods, must sum to 100, or, in terms of fractions, to one;

$$D_1 + D_2 = 1. \qquad (1)$$

Isotopes in foods and skeletal bone are measured by δ-values expressed in thousandths (o/oo). For example, the $\delta^{13}C$ value of a substance is its $^{13}C/^{12}C$ ratio divided by the same ratio in a standard material, minus one. As mentioned earlier, in going from food to bone collagen, δ-values fractionate. That is, the $\delta^{13}C$ value for bone collagen, adjusted by an experimentally estimated amount of -5 o/oo (van der Merwe and Vogel 1978), gives the $\delta^{13}C$ value for the diet. Similarly, for nitrogen, the $\delta^{15}N$ value for bone collagen, adjusted by an amount, -3 o/oo (see Keegan and DeNiro, 1988), gives an estimated $\delta^{15}N$ value for the diet.

In our two food example, let

$\delta^{13}C_j$ = $\delta^{13}C$ value in food j,

$\delta^{13}C_{diet}$ = $\delta^{13}C$ value in the diet.

We assume that, for any isotope, a food containing the isotope makes a contribution to the δ-value of the diet proportional to the food's δ-value and to the fraction of the diet coming from that food. Thus, for the isotope ^{13}C and two foods, we construct the mixing equation:

$$(\delta^{13}C_1)\ D_1 + (\delta^{13}C_2)\ D_2 = \delta^{13}C_{diet}. \qquad (2)$$

Collecting together (1) and (2), we obtain the following linear model, which we shall call M1:

$$D_1 + D_2 = 1,$$

$$(\delta^{13}C_1)\ D_1 + (\delta^{13}C_2)\ D_2 = \delta^{13}C_{diet}. \qquad (M1)$$

Model M1 is a system of two simultaneous linear equations in two dietary variables. The δs are known constants obtained from laboratory measurements. The D_js are unknown variables that describe the diet.

Continuing our example, suppose that an individual had a diet made up of foods from two groups, each constructed from animals having similar δ^{13}C values: (1) a deer group, which contains animals such as white tailed deer that consume low δ^{13}C plants, and (2) a geese group, consisting of animals such as brant geese that consume high δ^{13}C plants (e.g. eel grass). These foods have δ-values that are quite homogeneous within the groups but quite different across them. Assume that laboratory measurements of meat samples from the two groups give δ^{13}C values of, respectively, -24 and -14 o/oo. Suppose finally that bone collagen adjusts to a diet value, $\delta^{13}C_{diet}$, of -16 o/oo.

Substituting these data into model M1 and calling the result M2 gives:

$$D_1 + D_2 = 1,$$

$$-24\ D_1 - 14\ D_2 = -16. \qquad (M2)$$

If the number of equations equals the number of foods, as is the case here, M2 can be solved exactly by algebraic substitution, giving $D_1 = 1/5$ and $D_2 = 4/5$. The same result can be worked out by proportions, as illustrated in Figure 1. Therefore, the analysis of this case is straightforward: The individual's diet consisted 20% of food from the deer group and 80% from the geese group.

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Figure 1 about here

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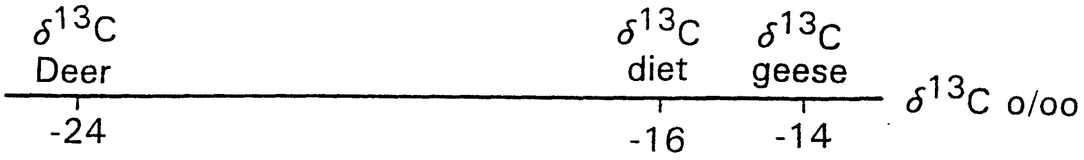

Figure 1. In the two food example of deer and geese, 80% geese and 20% deer will produce the diet value. The calculations are: (24-16)/(24-14)=0.8 and (16-14)/(24-14)=0.2.

Most of the time, however, we shall have more candidate foods than equations. This changes the situation. Suppose that a third plausible food is salt water fish, with $\delta^{13}C$ value -18 o/oo. It is easy to add a third dietary variable, D_3, the fraction of salt water fish in the diet, and extend model M2 to M3:

$$\begin{aligned} D_1 + D_2 + D_3 &= 1, \\ -24\,D_1 - 14\,D_2 - 18\,D_3 &= -16, \end{aligned} \tag{M3}$$

What can we now say about the diet? First of all, there are many combinations of values for D_1, D_2, and D_3 that will satisfy both equations. Nevertheless, the equations do restrict the variables and there are many combinations of D_js that will *not* work. In fact, we seek further ways to restrict the variables. For example, we note that the fraction of a food in the diet cannot be negative. This may seem obvious and trivial but actually turns out to be helpful and necessary, especially since we wish to perform the calculations by computer and so must specify that only non-negative values are permissible. We use the standard term, *constraint*, to refer generically to either equalities or inequalities that restrict the variables. Adding the non-negativity requirements to M3 gives a new model, M4, which has the constraints:

$$\begin{aligned} D_1 + D_2 + D_3 &= 1, \\ -24\,D_1 - 14\,D_2 - 18\,D_3 &= -16, \\ D_1 \geq 0, \quad D_2 \geq 0, \quad D_3 &\geq 0. \end{aligned} \tag{M4}$$

In this three food example, the number of foods exceeds the number of equations. Since the data and constraints do not completely specify the diet of the individual, we turn to new methods.

Analyzing the Model M4 by Linear Programming

A system of simultaneous equations and inequalities like M4 can have zero, one, or many solutions. By a *solution* to M4 is meant a set of values of the D_j, which satisfy the inequalities and which, when substituted into any of the equations, make the two sides equal. Most commonly in archaeological studies we would expect to have relatively few equations and many candidate food groups. Under these circumstances, there will be ranges of food percentages that could have made up the diet and produced the observed isotopic measurements. Nevertheless, there will usually be valuable information in the equations about how much (or how little) of a particular food group could possibly be in the diet. This is the principal use that we make of the model.

To determine such upper and lower bounds for each food in a diet, we use linear programming. For a general discussion of linear programming, see, for example, Hillier and Lieberman (1990), and, for other archaeological applications, Reidhead (1979). Linear programming is a mathematical technique that takes a linear model and finds values for its variables so as to maximize (or minimize) an *objective function*. An objective function is a weighted combination of the variables of the problem. In our case, we wish to find the largest or smallest amount of a particular food group, say the jth, that could be in the diet and still be consistent with the data and model M4. To do this, we simply take D_j as the objective function. Formally, we have the following linear program:

LP4: Find values for D_1, D_2, and D_3 that

maximize (or minimize) D_j,

subject to:

$$D_1 + D_2 + D_3 = 1,$$

$$-24 D_1 - 14 D_2 - 18 D_3 = -16,$$

$$D_1 \geq 0, \quad D_2 \geq 0, \quad D_3 \geq 0.$$

Standard computational procedures solve LP4. For example, Microsoft's spreadsheet program, Excel, has a software tool, Solver, that performs such maximizations and minimizations.

The process of solving a linear program like LP4 for each of the variables usually works smoothly, leading to upper and lower bounds for the amount of each food in the diet. However, two other outcomes are possible. First, the upper and lower bounds may be equal for each variable. This will be the case when there is only one solution to the linear system (as was true for two equations and two foods). The solution is said to be *unique*. Second, the computational procedure may not be able to find *any* collection of values for the variables that will satisfy the equations and inequalities of the model. This is the case in which the system has no solutions. The meaning of this (assuming the mixing model and the measurements are correct) is that no combinations of the candidate foods could have resulted in the observed $\delta^{13}C_{diet}$, i.e., some other foods must also have been in the diet.

For the particular case of M4, the maximum and minimum percentages of the three food groups in the diet are found by linear program LP4 to be as follows:

Food Group	Max %	Min %
deer (D_1)	20	0
geese (D_2)	80	50
salt water fish (D_3)	50	0

Thus the individual's diet could have been quite heavy in either geese or salt water fish. Furthermore, the diet could not have been more than about 20% deer and must have included at least 50% from the geese group.

Note that each entry in the above table represents a separate linear programming analysis that asks what is the largest (or smallest) percentage of a particular food that could be in a diet. Therefore, there is no inherent reason that the percentages must add up to 100. For example, the maximum percentage of geese in the diet is 80% and the maximum salt water fish is 50%, but obviously both these extremes could not have happened together. If another isotope δ-value, such as $\delta^{15}N$ is measured and added as a third equation, or as other constraining relationships are introduced, the limits on the foods will tend to grow tighter.

The numerical results just produced rely on calculations done off stage and so may seem somewhat mysterious. For this small example, we can find the answers and illustrate the ideas graphically. Use the first equation of M4 (rewritten as $D_1=1-D_2-D_3$) to eliminate D_1 from the second equation by substitution. This gets rid of the first equation and makes the second become: $5D_2+3D_3=4$. However, we must ensure that the model considers only values of D_2 and D_3 that keep $D_1 \geq 0$. This can be done by requiring $D_1=1-D_2-D_3 \geq 0$. Thus we create M4a, a two variable model equivalent to M4:

$$\begin{aligned} 5\,D_2 + 3\,D_3 &= 4, \\ D_2 + D_3 &\leq 1, \\ D_2 \geq 0, \quad D_3 &\geq 0. \end{aligned} \tag{M4a}$$

Figure 2 diagrams model M4a using axes D_2 and D_3. Each point on the plane represents a set of values for D_2 and D_3 and so defines a potential diet. For a diet to be feasible (i.e., possible), $D_2 \geq 0$, which means that satisfactory values lie above the D_2 axis. $D_3 \geq 0$ only allows values to the right of the D_3 axis. The inequality, $D_2+D_3 \leq 1$, means that feasible values must lie under the $D_2+D_3=1$ line. Finally to satisfy the equation, $5D_2+3D_3=4$, values must lie on the line represented by this equation. Therefore the only feasible diets satisfying M4 are those cross-hatched in Fig.2. The maximum and minimum values for D_2 are seen to be 0.8 and 0.5 and for D_3, 0.5 and 0. This confirms the answers for D_2 and D_3 as found earlier by linear programming. One can also confirm the answers for D_1 by a similar graphical process in which D_2 or D_3, instead of D_1, is eliminated from model M4.

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Figure 2 about here

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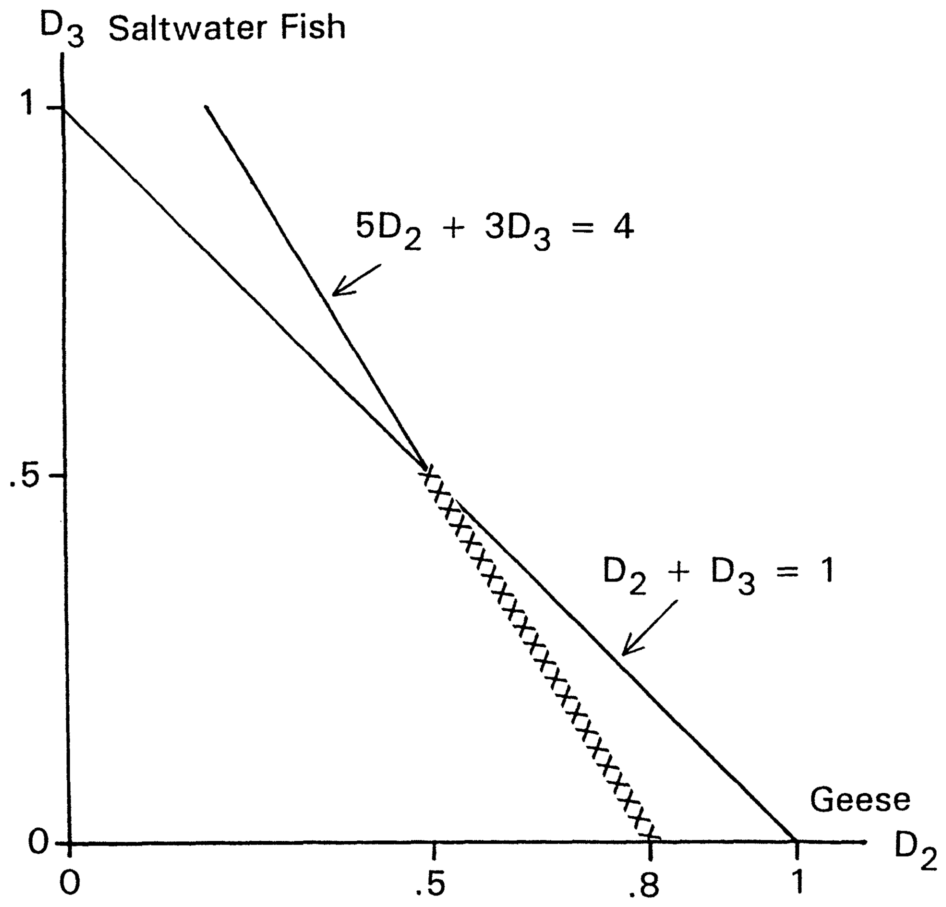

Figure 2. Constraining relations on variables D_2 (fraction of diet in geese) and D_3 (fraction in salt water fish). Their values must be positive or zero, lie under the line, $D_2+D_3=1$, and be on the line $5D_2+3D_3=4$. Therefore, only values on the cross-hatched segment are permissible.

A General Linear Model

Different researchers will make different assumptions in analyzing diets. Linear programming techniques will apply if the assumptions lead to linear models. The purpose of this section is to indicate what linear models encompass. We do this by formally writing down a quite general case. Consider, therefore, model M5 with F variables and I constraints. Let

D_j = the jth variable of the model, $j=1,..,F$. Ordinarily, each j refers to a food, but other variables are possible, in which case F will be larger than the number of foods.

b_i = right hand side constant in the ith constraint, $i=1,...,I$. For the most part, each i will refer an isotope, but other constraints (such as the sum of the food fractions equals one) will be present, making I larger than the number of isotopes.

a_{ij} = coefficient of D_j in the ith constraint.

Model M5 is

$$
\begin{array}{l}
a_{11} D_1 + a_{12} D_2 + \ldots\ldots + a_{1F} D_F = b_1 \\
\quad\quad\quad\quad \cdot \\
\quad\quad\quad\quad \cdot \\
a_{h1} D_1 + a_{h2} D_2 + \ldots\ldots + a_{hF} D_F = b_h \\
a_{h+1,1} D_1 + a_{h+1,2} D_2 + \ldots\ldots + a_{h+1,F} D_F \leq b_{h+1} \\
\quad\quad\quad\quad \cdot \\
\quad\quad\quad\quad \cdot \\
a_{I1} D_1 + a_{I2} D_2 + \ldots\ldots + a_{IF} D_F \leq b_I
\end{array}
\quad\quad (M5)
$$

$D_j \geq 0 \quad j=1, \ldots, g \qquad D_j$ unrestricted in sign for $j=g+1, \ldots., F$.

As may be seen, constraints 1 through h are equations and h+1 through I are inequalities. Variables 1 through g are restricted to be non-negative and g+1 through F are unrestricted. Although more general linear models can be defined, they can all be converted to the form of M5 by transformation of variables and manipulation of constraints. Any archaeological model that can be put into the form M5 by suitable definition of the variables, D_j, and specification of constants, a_{ij} and b_j, can be analyzed by linear programming.

Model M5 becomes a linear program if we add the goal of maximizing or minimizing an objective function. Let

c_j = the coefficient of D_j in an objective function.

Then we can define a linear program:

LP5. Find: values for $D_1, \ldots\ldots, D_F$

to maximize (or minimize) $c_1 D_1 + \ldots\ldots + c_F D_F$,

subject to: the constraints of model M5.

What makes M5 and LP5 of interest in studying prehistoric diets will be the details of how the variables D_j and the constants a_{ij}, b_i, and c_j are defined so as to create constraints and optimizations that are archaeologically meaningful. In the case of the optimizations, most of our usage here is to maximize or minimize a single variable. In LP5 terms this means one of the c_j is unity and the rest are zero. However, in the extended application to Pecos Pueblo data later, we shall have occasion to use a slightly more complicated objective function.

Linear Equations from the Literature

There are many possible ways to define constraints. We give here three types found in the archaeological literature.

(1) Diet fractions sum to one.

Let D_j = the fraction of kilocalories/day in an individual's diet supplied by food j,

$j = 1, \ldots, F$ = the foods in the diet.

Then $\Sigma_j D_j = 1$ (3)

is a required equation in the model. This generalizes (1) of our initial example to an arbitrary number of foods. Although we have defined D_j in terms of energy (kilocalories/day), this is not required and any consistent units will work from a mathematical point of view, for example, g/day.

The next two cases are algebraic versions of mixing equations implicit in Spielmann, Schoeninger and Moore (1990: 758, Fig. 4.)

(2) Energy weighting of $\delta^{13}C$ values.

$\delta^{13}C_j$ = $\delta^{13}C$ value for food j (o/oo),

$\delta^{13}C_{diet}$ = $\delta^{13}C$ value for the diet (o/oo).

Energy weighting of the food δ-values to give $\delta^{13}C_{diet}$ yields:

$\Sigma_j (\delta^{13}C_j) D_j = \delta^{13}C_{diet}.$ (4)

This is a generalized version of the mixing equation (2).

(3) Energy and protein weighting of $\delta^{15}N$ values.

Schoeninger (1989) argues that only foods containing protein can contribute to the nitrogen δ-value of skeletal bone, but such foods may also contain non-protein energy sources and some foods in the diet may contain practically no protein. Following this line of reasoning, we should determine how much of D_j is protein before using it to weight the $\delta^{15}N_j$ of the individual foods. Let

p_j = the amount of protein in food j (g/kilocalorie),

$p_j D_j$ = contribution of food j to protein in the diet (g/kilocalorie),

$P \ = \ \Sigma_j \, p_j \, D_j \ =$ total protein in the diet (g/kilocalorie), (5)

$p_j D_j / P \ =$ fraction of protein in the diet coming from food j,

$\delta^{15}N_j \ = \ \delta^{15}N$ value for food j (o/oo), and

$\delta^{15}N_{diet} \ = \$ the $\delta^{15}N$ value for the diet (o/oo).

Weighting the $\delta^{15}N_j$ for each food by its fractional contribution to the protein in the diet yields the equation

$$\Sigma_j \, (p_j D_j / P) \, (\delta^{15}N_j) \ = \ \delta^{15}N_{diet}.$$

This equation is not linear in the D_j's because they are contained in P. However, we can multiply through by P, substitute (5), and collect terms to obtain the linear equation:

$$\Sigma_j \, (\delta^{15}N_j - \delta^{15}N_{diet}) \, p_j \, D_j \ = 0. \qquad (6)$$

Still other variations are possible. For example, Little and Schoeninger (1995) use protein weighting not only for the $\delta^{15}N$ mixing equation but also for the $\delta^{13}C$ equation, which is then the analog of (6) rather than (4). Generally speaking, the more equations and inequalities, the more the diet will be restricted by the data, and the tighter will be the limits we can put on the diet variables.

An Extended Example of Linear Programming

Spielmann, Schoeninger and Moore (1990) analyze human diet at Pecos Pueblo, New Mexico, with a model that can be described by linear equations, although the authors do not express them algebraically. Their data and models provide an archaeologically interesting application for linear programming. Relevant excerpts of their data appear in Table 1. We can build a model, M6, to reproduce their Period II analysis, using as variables, M_{II}, P_{II}, D_{II} and B_{II}, the fractions of calories in maize, non-maize plants, mule deer and bison respectively. The first equation is (3), the sum of the food fractions equals one. The authors use protein weighting for the $\delta^{15}N$ equation but not for $\delta^{13}C$. Substituting data from Table 1 into (4) for carbon and (6) for nitrogen yields the second and third equations of M6. Finally, adding the non-negativity conditions, we obtain:

$$M_{II} + P_{II} + D_{II} + B_{II} = 1,$$

$$(-11.2)\, M_{II} + (-25.0)\, P_{II} + (-20.7)\, D_{II} + (-11.5)\, B_{II} = -12.5, \qquad \text{(M6)}$$

$$(7.0\text{-}5.9)(.026)\, M_{II} + (5.6\text{-}5.9)(.066)\, P_{II} + (3.9\text{-}5.9)(.167)\, D_{II} + (6.8\text{-}5.9)(.181)\, B_{II} = 0,$$

[or, simplifying, $0.0286\, M_{II} - 0.0198\, P_{II} - 0.334\, D_{II} + 0.1629\, B_{II} = 0$],

$$M_{II}, P_{II}, D_{II}, B_{II} \geq 0.$$

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Table 1 about here

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Various new questions can be addressed to model M6 using linear programming. As suggested throughout the paper, we can set bounds on the percentages of foods in the diet: What is the largest (and smallest) percentage of each food that could have been in the Period II diet (and be compatible with the measured data)? The answers are:

Food Item	Max %	Min %
Maize (M_{II})	88.3	72.4
Non-maize plants (P_{II})	4.4	0
Mule deer (D_{II})	13.2	7.3
Bison (B_{II})	14.4	0

A similar analysis applies to Period VI. The authors' data yields model M7:

$$M_{VI} + P_{VI} + D_{VI} + B_{VI} = 1,$$

$$(-11.2)\, M_{VI} + (-25.0)\, P_{VI} + (-20.7)\, D_{VI} + (-11.5)\, B_{VI} = -13.5, \qquad \text{(M7)}$$

$$(7.0\text{-}6.3)(.026)\, M_{VI} + (5.6\text{-}6.3)(.066)\, P_{VI} + (3.9\text{-}6.3)(.167)\, D_{VI} + (6.8\text{-}6.3)(.181)\, B_{VI} = 0,$$

[or $0.0182\, M_{VI} - 0.0462\, P_{VI} - 0.4008\, D_{VI} + 0.0905\, B_{VI} = 0$],

$$M_{VI}, P_{VI}, D_{VI}, B_{VI} \geq 0.$$

Table 1.

Table 1. Food and skeletal bone measurements for Pecos Pueblo, New Mexico, from Spielmann, Schoeninger and Moore (1990: 758,9, Table 2, Table 4).

Food Item	δ^{13}C (o/oo)	δ^{15}N (o/oo)	Protein (g/kilocalorie)
1. Maize (M)	-11.2	7.0	.026
2. Non-maize plants (P)	-25.0	5.6	.066
3. Mule deer (D)	-20.7	3.9	.167
4. Bison (B)	-11.5	6.8	.181
Skeletal Bone			
Collagen values			
Period II	-7.5	8.9	
Period VI	-8.5	9.3	
Diet-collagen adjustment	-5.0	-3.0	
Diet values			
Period II	-12.5	5.9	
Period VI	-13.5	6.3	

Linear programming provides bounds on food consumption in period VI:

Food Item	Max %	Min %
Maize (M_{VI})	82.7	0
Non-maize plants (P_{VI})	15.3	2.8
Mule deer (D_{VI})	17.6	2.0
Bison (B_{VI})	79.6	0

Spielmann, Schoeninger and Moore (1990) investigate a variety of archaeological issues. To illustrate how linear modeling could be used for their purposes, we address one of their questions:

Did bison largely replace mule deer in the Pecos diet between periods II and VI?

We restate this as:

How large could the change in bison consumption have been between periods II and VI and still be consistent with the data?

For this analysis combine models M6 and M7 into a single system and add another linear relation implicit in the authors' discussion. They argue, from the constancy of strontium measurements on skeletal bone across the two periods, that total meat consumption was unchanged. Expressed in our variables, this says:

$$D_{II} + B_{II} = D_{VI} + B_{VI} . \qquad (7)$$

Combining the models and adding (7) yields a new set of constraints that will be called model M8. We can then solve a linear program that maximizes the difference in bison consumption between the two periods, (B_{VI} - B_{II}), subject to M8. The computational procedure determines this to be 0.07. Therefore the answer to the question is:

The largest change in bison consumption consistent with the data is 7 % of the diet.

This result quantifies the authors' argument that the bison content in the diet of the Pecos inhabitants did not increase substantially between periods II and VI. Note that, although the analysis of Period II indicates that not much bison was in the diet, the analysis of Period VI in isolation left open the possibility of rather high bison consumption at this later time -- up to as much as 80%. However, the introduction of the further constraint that the total meat consumed was equal in the two periods, resulted in a much tighter bound on the increase in consumption in bison between periods.

As part of their analysis, the authors systematically devise many hypothetical diets (i.e., plausible sets of values of M_{II}, P_{II}, D_{II}, B_{II} that add to 100%), substitute them into the left hand sides of the second and third equations of model M2, and determine how closely the results match the right hand sides. They construct a composite measure of the differences as a score to help identify which diets might most likely be characteristic of the Pecos population for that time period. Small values of the score are better. Linear equation techniques could simplify the authors' task. In fact, it can be shown that there are many diets that would give a zero score.

Sensitivity Analysis

The development so far has assumed that the data being used in the linear programs are exactly correct. This, of course, is never true. At present the precision of the input parameters is probably limited to an accuracy of about 8-10% (Ambrose 1993:112). Errors and uncertainties in the original inputs will propagate into the upper and lower bounds on diet percentages. This does not necessarily happen in a simple way, since different manipulations of the original data will enter into the calculation of different bounds.

A standard approach to understanding the effects of measurement error on model outputs is to perform a sensitivity analysis. After analyzing a model with one's best data estimates, one can vary them in a systematic way and rerun the model. For example, the original estimate of a particular δ-value can be replaced by a slightly different one, considered to be within the range of measurement error. Then the analysis can be rerun. The changes in the resulting bounds indicate their sensitivity to errors in that particular δ-value. Wagner (1995) describes how to conduct this process on all the input data at once in a formal, global sensitivity analysis.

Conclusions

We have demonstrated how isotopic measurements of skeletal bone can be combined with corresponding measurements on candidate foods into linear mixing models and then manipulated to provide insights about archaeological issues relating to prehistoric diets. Each measured isotope defines an equation. Usually there are more candidate foods than equations. Then the diet will not ordinarily be unique, but, by using linear programming, we can set bounds on the largest and smallest amounts of each food that could have been in the diet. Sometimes these bounds may be quite far apart, in which case we have not learned much. In other cases they may be quite tight and instructive. In general the more isotopes measured, the more equations, and the tighter will be the bounds.

In this paper we have derived linear models by making specific assumptions about how food isotope ratios affect bone isotope ratios or have adopted archaeological or biochemical models implicit in the work of others. However, the linear programming technique of bounding the contributions of foods to diet will work with any linear model, no matter how derived. The quality of the answers, of course, will be entirely dependent on the quality of the data input and of the model.

Although we have assumed that linear additive models relate the isotopic ratios of skeletal bone to those of foods eaten, this is not strictly required to determine bounds on the components of diet. Quite likely, some of the processes involved are nonlinear. However, if archaeological scientists, as challenged by Sillen, Sealy, and van der Merwe (1989), can determine the relationships, the bounds can, in principle, be determined using the techniques of nonlinear programming, even though the computations are likely to become more extensive and complex.

Acknowledgements: We thank two reviewers, Katherine A. Spielmann and Henry P. Schwarcz, for helpful comments and suggestions.

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