Chapter 8: Life histories

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**Doing (ecological) science:** Explaining and predicting patterns using key biological processes!
Sandhill crane

Sandhill Crane Productivity, 1998-2012

YEAR

NUMBER


Nests Young fledged

0 5 10 15 20 25 30 35 40 45

Sandhill crane
**Gymnogyps californianus**

**Fig. 7.** Estimated total wild population of the California Condor, 1965–1980. Data are from October surveys as listed by Wilbur (1980) and Snyder and Johnson (1985).
Fig. 5. Estimated number of adult females in the Yellowstone National Park grizzly bear population, 1959–1987. Data, listed by Eberhardt et al. (1986) and supplemented by recent figures, consist of a 3-yr moving sum of the yearly number of adult females seen with cubs.
Grus americana

Fig. 4. Total size of the Aransas/Wood Buffalo Whooping Crane population, from 1938–1988. Data are from Boyce (1987), supplemented by more recent counts.
Lynx rufus

A) Bobcats, Idaho

Abundance

Time (yr)


400 600 800 1000 1200 1400

Reports to illustrate the OUSS model. All the data sets in Fig. 1 are among those included in the R programs presented in the Supplement.

The parameter $l$ tends to be estimated with precision, according to the REML bootstrap confidence intervals (Fig. 1). The parameters $h$, $b^2$, and $s^2$ are not estimated well for these data, as suggested by the wide confidence intervals (Fig. 1). The GSS model, and by implication the OUSS model, sometimes has ridge-like likelihoods, or likelihoods with multiple local maxima corresponding to sub-models with all observation error or all process noise (Dennis et al. 2006, 2011, Knape 2008), especially for short time series. Replicating the sampling process one or more times at selected sampling times can substantially improve parameter estimation (Dennis et al. 2010), as can substantial amounts of transience in the data (non-stationarity) resulting from initiating the time series far from equilibrium (Dennis and Taper 1994).

**DISCUSSION**

If unequal sampling intervals are due simply to data missing from otherwise equally spaced observations (such as the data in Fig. 1), then the ordinary GSS model can in fact be used with modification. The GSS model, like the OUSS model, has observations with a multivariate normal log-likelihood (Eq. 19). To calculate ML estimates for the GSS model, the missing observations in question are deleted from the vector $y$, the entries corresponding to the missing observations are deleted from $m$, and the rows and columns corresponding to the missing observations are deleted from $V$. The resulting expression is the proper log-likelihood function for the multivariate normal distribution of the remaining observations, under a standard property of the multivariate normal distribution (Seber 1984). While deleting observations from the GSS is easy in principle, programming software to automate the deletions in...

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BRIAN DENNIS AND JOSE´ MIGUEL PONCIANO

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Arctocephallus gazella

Fig. 4 Antarctic fur-seal pup production at Cape Shirreff and San Telmo Islets, South Shetlands (1966–2002) with 3% error bars. The fitted line corresponds to the logistic model parameterized by $K = 9294; t_{50} = 1991; r = 0.2625$. Also shown in boxes is the percent rate of increase for different periods and the standard error of the mean (SEM) for the series ranging from 1992 to 2002.
Bull trout in Montana

The graph shows the abundance of bull trout over time, with years ranging from 1980 to 2010. The y-axis represents abundance, ranging from 0 to 100, and the x-axis represents years. The data points indicate fluctuations in abundance over the years, with certain periods highlighted to emphasize changes. The graph also includes a scale for the persistence probability on the right side, ranging from 0.00 to 1.00, with specific values indicated for comparison.
Point estimates of change in community composition

Predicting a Human Gut Microbiota’s Response to Diet in Gnotobiotic Mice

Jeremiah J. Faith, Nathan P. McNulty, Federico E. Rey, Jeffrey I. Gordon*

The interrelationships between our diets and the structure and operations of our gut microbial communities are poorly understood. A model community of 10 sequenced human gut bacteria was introduced into gnotobiotic mice, and changes in species abundance and microbial gene expression were measured in response to randomized perturbations of four defined ingredients in the host diet. From the responses, we developed a statistical model that predicted over 60% of the variation in species abundance evoked by diet perturbations, and we were able to identify which factors in the diet best explained changes seen for each community member. The approach is generally applicable, as shown by a follow-up study involving diets containing various mixtures of pureed human baby foods.

Subject w14

Age: 37  Race: White  No. Sex Prtrs: 10  No. Drinks Last 60d: 4(2)  Yeast Inf Last 60d: No

Phylotype
- L. jensenii
- Streptococcus
- Corynebacterium
- Prevotella
- Anaerococcus
- Peptoniphilus
- Finegoldia
- Dialister
- Arthrobacter
- Bacteroides
Phylotype relative abundance (%)

Phylootypes:
- L. crispatus
- Streptococcus
- L. reuteri
- Bifidobacterium
- Anaerococcus
- Prevotella
- Finegoldia
- Peptostreptococcus
- Escherichia
- Alloscardovia

Time (weeks)

Menses
Tampon
Douching
Nugent [low, intermediate, high]
Vaginal Intercourse
Anal Sex
Oral Sex
Digital Penetration
Sex Toy
Lubricant
Subject w23
Age: 38  Race: Black  No. Sex Prtrs: 6  No. Drinks Last 60d: 6(1)  Yeast Inf Last 60d: No

Phylotype
- Atopobium
- Proteobacteria 2
- L iners
- Ruminococcaceae 4
- Arcanobacterium
- Megasphaera
- Proteobacteria 1
- Prevotella
- Sneathia
- Proteobacteria 13
- Parvimonas
- Ruminococcaceae 6

Nugent Score
- 4
- 5
- 6
- 7

pH
- 1
- 3
- 5

Stress
- 0
- 1
- 2
- 3

WBC
- weeks
- 0 1 2 3 4 5 6 7 8 9 10

Menses
- Blood Flow
- low
- medium
- high

Vaginal Odor
Vaginal Irritation
Vaginal Discharge

Sex Toy
Lubricant
Figure 3

Gajer et al, 2012: (PRINCIPAL COMPONENT ANALYSIS: Reduce dimensionality of system and view it!)
types and other lactic acid–producing bacteria that are abundant in these communities. The prominence of these populations and their important role in modulating vaginal pH suggests they might be drivers in these communities and thought of in terms of Walker’s driver–passenger model (34, 35). This model posits that ecological function resides in “driver” species or in functional groups of such species that have key ecological functions that significantly structure ecosystems, whereas “passenger” species are those that have minor ecological impact. Studies done to tease out the influence of these various factors on vaginal community ecology will be important to understanding community stability, resistance, and resilience so that strategies can be developed to maintain human vaginal health and prevent disease.

Vaginal Community Space. The relationships among communities were visualized by principal component analysis and displayed in 3D space. The three principle components explained 82% of the variance. Each point in Fig. 4 represents the vaginal community of an individual. Communities dominated by species of *Lactobacillus* and representing groups I, II, III, and V are shown at each of the four outer vertices of the tetrahedron, with communities of group IV at the inner vertex. Communities found on the edges joining two vertices are mixtures of the two *Lactobacillus* species that dominate the communities found at the corresponding vertices, with an equal proportion of each species at the midpoint of the edge. We refer to each location in this 3D space as a community state, and one can consider the entire space to represent the plausible alternative community states, or vaginal bacterial community space. The cross-sectional design of this study with only one sample from each subject precludes knowing whether the locations of these communities in vaginal community space vary over time. Nonetheless, at this stage we can propose four distinct conceptual models for the variation of community composition over time. The first is the "dynamic equilibrium hypothesis," in which the composition of a community is comparatively invariant over time and exists in a single dynamic equilibrium. A second "community space hypothesis" is the opposite of the first, and each community can and does occupy any position in community space over time and throughout a woman’s lifetime. These changes are postulated to occur in response to hormonal cycles, an individual’s habits and practices, changes in diet, or some other ecological force. A third model is an "alternative equilibrium states hypothesis," wherein a woman’s community can change over time, but the number of alternative states are limited in number and governed by unknown factors. A fourth possibility is a "community resilience hypothesis," in which a community normally resides in a single region of space. Under this scenario the composition and structure of a vaginal community can change to a transitional state in response to disturbance, but the resistance and resilience of a community determine the extent and duration of a change, whereas homeostatic mechanisms drive communities back to their "ground state." We expect that no single hypothesis will explain the dynamics of all communities. Each of these hypotheses can only be

![Fig. 4.](https://www.pnas.org/cgi/doi/10.1073/pnas.1002611107) Relationships among vaginal bacterial communities visualized by principal component analysis in which the relative abundances are expressed as proportions of the total community and displayed in 3D space. Communities dominated by species of *Lactobacillus* and representing community groups I, II, III, and V are shown at each of the four outer vertices of the tetrahedron, with communities of group IV at the inner vertex and shown in the Inset. (A) Each point corresponds to a single subject and was colored according to the proportions of phylotypes in each community. (B) pH of each vaginal community shown in A. (C) Nugent score category of each vaginal community shown in A.

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- Managing the world fisheries?!
Understanding change

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Generality... 1) gives us applicability to a wide array of problems, 2) forces us to focus on identifying key processes that can be targeted for management, prediction and understanding.
Let’s see an example
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Well, many examples in fact...
Life histories of organisms are bound to drive changes in population sizes

The assumption of continuous births that the book uses in chapters 12 and 13 later on does not work well for many organisms. In fact, models in which reproduction occurs in discrete-time are much easier to read and interpret. Here's some life histories of organisms with discrete-time reproduction

- **Plants:** Herbs often flower in their first year and then die after setting seed. These are monocarpic plants.
  - Many monocarpic plants are annuals, few are long lived. Many bamboos are long-lived, flower once and then die. Others have flowering times of 1, 3, 11, 15, 30, 48 and 60 years. One Japanese species *Phyllostachys bambusoides* waits 120 years to flower!!
  - Some bamboo species also synchronize reproduction within cohorts!. The Spring 1983 simultaneous mass flowering and death of *Fargasia spathacea* and *sinarundinaria fangiana* resulted in the starvation and eat of many pandas.
  - *Agave deserti*, also monocarpic, lives 20 to 25 years before flowering. Also reproduces via clones!
Insects

Semelparity is for animals what monocarpy is for plants (where does this strange name come from?). Semelparous insects can be

- Univoltine: one generation per year (Mayflies)
- Bivoltine: two generations per year
- Multivoltine: multiple generations per year

Some semelparous insects are long lived (13 and 17 year cycles!). Can you think of a semelparous vertebrate? There are no semelparous birds! All birds are iteroparous. Strong climatic conditions can drive synchrony. For example, the largest breeding area for the Greater Snow Geese *Chen caerulescens* is on Bylot Island in Canada. In 1957, 15000 birds nested in the area and ALL egg laying started on 8 June, stopped on 20th June and hatching occurred between 8-13 July.

There are 9 small marsupials in the genera *Antechinus* and *Phascogale* that are semelparous. Males become sexually active after 11 months and die exactly 3-4 weeks later. All of them. Births are highly synchronized. These species live in very predictable environments with precise insect blooms (global warming???)
Organizing all this info using key dichotomies in reproductive strategy and developmental rate

- **Reproductive strategy** can be classified as semelparous (reproducing only once) or iteroparous (reproducing multiple times)

- **Development** can be classified as precocious (rapid development to maturity) or delayed

Crossing these two biological dichotomies gives us a very general set of combinations of life-histories
# Life cycles table

<table>
<thead>
<tr>
<th>Developmental strategy</th>
<th>Reproductive strategy</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Semelparous</td>
</tr>
<tr>
<td></td>
<td>Iteroparous</td>
</tr>
<tr>
<td><strong>Precocious</strong></td>
<td>Annual plants and insects with rapid development and 1 reproduction</td>
</tr>
<tr>
<td></td>
<td>Small mammals and birds that begin reproduction young but live many years</td>
</tr>
<tr>
<td><strong>Delayed</strong></td>
<td>Periodical cicadas, bamboos that reproduce only once but take many years to do so</td>
</tr>
<tr>
<td></td>
<td>Organisms with long pre-reproductive periods and then survive and reproduce for many years</td>
</tr>
</tbody>
</table>
Life cycle graph: youngs and adults

\[ \text{reprod: # of offspring} \]

\[ n_1 \quad \text{surv. & no matur.} \quad n_2 \quad \text{surv.} \]

\[ n_1 \quad \text{surv. & matur.} \quad n_2 \]
\[ \sigma_1(1 - \gamma) \]

\[ \sigma_1, \sigma_2 : \text{denote the fraction of juveniles and of adults alive at time } t \text{ that survive to time } t + 1 \]

\[ \gamma : \text{the fraction of surviving juveniles that mature to become adults} \]

\[ \phi : \text{the number of juveniles at time } t + 1 \text{ that are produced by one adult at time } t \]
Modeling the basic discrete life-cycle

The basic life cycle consists of two stages: reproducing adults and non-reproducing juveniles. Let

\( \sigma_1, \sigma_2 \) : denote respectively the fraction of juveniles and of adults alive at time \( t \) that survive to time \( t + 1 \)

\( \gamma \) : the fraction of surviving juveniles that mature to become adults

\( \phi \) : the number of juveniles at time \( t + 1 \) that are produced by one adult at time \( t \)

Now, let’s write a mathematical model that tracks the changes in the number of adults and juveniles (Board notes now...)