Machine Learning Methods for Timing of Biological Events

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Phenology and Climate

• One potential impact of climate change is to change the timing of life cycle events (“Phenology”)
  – Bird Migration
  – Moth Flight Times
  – Pollinator Flight Times
  – Timing of leaf-out and flowering
• What determines the timing of these events?
  – Day length? (will not change with climate)
  – Temperature, precipitation, wind (will change with climate)
• Phenological asynchrony could lead to major changes in food web structure
  – Local extinctions
  – Rapid evolutionary pressures
Challenges to Data-Driven Modeling of Phenology

- **What we have**: periodic observations of organism “activity”
  - Moth trap counts
  - Bird surveys

- **What we want**: timing of life history events
  - When did adult moths emerge from cocoons?
  - When did migrating birds arrive?

- How to bridge the gap?
What was the flight period of *Nepytia umbrosaria* in 2004?
Example: eBird Data

- Bird watchers record their observations in a database through eBird.org.
  - “Citizen Science”

- Features
  - LOTS of data!
    - ~3 million observations reported in May
  - ~3,000 bird species
  - Year-round, Continent-scale
Challenges

- We do not *directly* observe the events we are interested in:
  - Moth emergence
  - Bird arrival

- Surveys are infrequent
  - May miss “peak” activity

- Naive approaches don’t use all of the data
  - Date of first moth, first bird
  - Date of maximum abundance
A General Approach: Collective Graphical Models

- **Step 1: Define a model of the behavior of individual organism**
  - $E_i$: emergence date for organism $i$
    - $E_i \sim \text{Norm}(E_i | \mu, \sigma)$
  - $S_i$: lifespan
    - $S_i \sim \text{Exp}(S_i | \lambda)$
  - $F_i$: flight period (start, end)
    - start = $E_i$
    - end = $E_i + S_i$
  - $T_t$: trapping date
  - $Y_{it}$: 1 if moth was trapped on date $t$, 0 otherwise

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Step 2: Assume a population of iid individuals

- We assume all moths are drawn from the same distribution
Step 3: Introduce aggregate observation variables

- $Y_1 = \sum_i Y_{i1}$
- $Y_2 = \sum_i Y_{2i}$
- $Y_3 = \sum_i Y_{3i}$
Step 4: Marginalize away the individuals

- Theorem (Dawid & Lauritzen, 1993): Resulting graph has same dependency structure as the individual model
- No combinatorial explosion of dependencies
Step 5: Fit via maximum likelihood (etc.)

- Example of fitted model
Modeling Climate Dependence

- Introduce covariates on emergence time
- Linear regression to determine mean and variance
CGM for Bird Migration

- Define grid over US
- Aggregate eBird observations into # birds per cell

<table>
<thead>
<tr>
<th>Cell</th>
<th>Time</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>87</td>
<td>61</td>
<td>22</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>13</td>
<td>39</td>
<td>78</td>
<td></td>
</tr>
</tbody>
</table>
Step 1: Individual Model

- Each bird is a sample from a Markov Chain
  - $X_{it}$: Cell of bird $i$ at time $t$
Step 2: Population of Individuals

\[ X_{i1} \rightarrow X_{i2} \rightarrow \cdots \rightarrow X_{iT} \]

\[ i = 1, ..., N \]
Step 3: Derive Aggregate Counts

\[ X_{i1} \xrightarrow{} X_{i2} \xrightarrow{} \cdots \xrightarrow{} X_{iT} \]

\[ n_1 \xrightarrow{} n_2 \xrightarrow{} \cdots \xrightarrow{} n_T \]

\( i = 1, \ldots, N \)

true # birds in each cell at time \( t \)
Step 3b: Introduce Stochastic Observation Model

- Each bird is detected with probability $d_t$ by eBirders
Step 4: Marginalize away the individuals

\[ n_1 \rightarrow n_{12} \rightarrow n_2 \rightarrow n_{23} \rightarrow \cdots \rightarrow n_T \]

\[ y_1 \rightarrow y_2 \rightarrow \cdots \rightarrow y_T \]
Step 5: Add climate covariates

\[ \begin{align*}
&x_1 \rightarrow n_1 \rightarrow y_1 \\
&x_{12} \rightarrow n_{12} \rightarrow y_2 \\
&x_2 \rightarrow n_2 \rightarrow y_2 \\
&x_{23} \rightarrow n_{23} \\
&
\end{align*} \]
Step 6: Fit via maximum likelihood

- Very challenging inference problem
- State = all ways of partitioning $N$ birds across $K$ sites
- Solution: Gibbs sampling algorithm that takes time independent of $N$
Gibbs Sampler Experiment

- Running time on simple GCM task

  - Running time independent of population size
  
  - Previous best: exponential

  - Best exact method (variable elimination; cubic in M)
  
  - Our method (to 2% relative error)

Running time *independent of population size*

- Previous best: exponential

[Sheldon & Dietterich, NIPS 2011]

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New Project: BirdCast

- Goal: Continent-wide bird migration forecasting
- Additional data sources:
  - Doppler weather radar
  - Night flight calls
  - Wind observations (assimilated to wind forecast model)
BirdCast Collective Graphical Model:

- $n_t^s(c) = \#$ of birds of species $s$ at cell $c$ and time $t$.
- $x_t^s(i, o) = \text{eBird count for visit } o \text{ at site } i \text{ species } s \text{ and time } t$
- $y_{t,t+1}^s(k) = \# \text{ of flight calls for species } s \text{ at site } k \text{ on the night } (t, t + 1)$
- $z_{t,t+1} = \# \text{ of birds (all species) observed at radar } v \text{ on night } (t, t + 1)$

- Occupancy changes each night
- Covariates (not shown): wind, precipitation, land cover, green up, elevation, urbanization
Concluding Remarks

- Collective Graphical Models provide a formalism for modeling phenology from aggregate observations
  - assume a population of iid individuals
  - introduce aggregate observation variables
  - marginalize away individuals
  - fit to data

- CGM Gibbs sampler has running time independent of population size $N$
  - we do not yet understand dependence on the number of cells $K$