Comparison of discrete measurements by directed graphical models using Gibbs Sampling

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Using Gibbs Sampling
by Directed Graphical Models
Comparison of Discrete Measurements
Which method is best to screen for cervical cancer?

- Biopsy analyzed in DNA smear analyzed by DNA
- Biopsy analyzed in microscopy smear analyzed in microscopy

For 106 women HPV in uterine cervix detected by 4 screening methods:

Screening for cervical cancer:

Motivation
Inference about $\Theta$

$\Theta$: parameters

$\lambda$: latent variables

$\gamma$: unobserved data and/or

X: observed data

where

$\Theta \cap \gamma \cap X = \Lambda$

| Vertices
| Termiology
| Directed Graphical Models

$\Lambda \cap \gamma \cap X = \Lambda$

Directed Local Markov Property:

$\lambda \cap \gamma \cap X = \Lambda$

Recursivity factorization:

$\delta \Theta \cup \gamma \cup X = \Lambda$

Directed Markov wrt to $\delta$

Joint distribution of $\Lambda$ is

$\Lambda \cup \gamma \cup X = \Lambda$

Directed Acyclic Graph

Defined by

$\Lambda \cup \gamma \cup X = \Lambda$

E: set of directed edges

$\Lambda \cup \gamma \cup X = \Lambda$

Directed Acyclic Graph

$\Lambda \cup \gamma \cup X = \Lambda$

Directed Graphical Models

Launhzen (1996)
Inference is based on summary statistics of simulated values

Marginalize by considering only parts of simulated values

\[ \pi(x|\theta, \mathbf{b}) \]

Converges to a Markov chain with stationary distribution \( p(x|\theta) \)

\[ \Theta \cap \Lambda \supseteq \Lambda \]

\[ \prod_{\Sigma \subseteq \Theta} \left( \prod_{\Theta} p(\lambda|\theta) \right) \propto (\Lambda \setminus \Lambda|\Theta) \]

Successfully simulate values from the full conditionals

Gibbs Sampling:

\[ \int p(x|\theta, \mathbf{b}) \, dx = (x|\theta) \, d(\theta) \]

Posterior

\[ \int p(\theta) \, d(\theta) \]

Prior

Bayesian Inference: all quantities random

Bayesian Inference by MCMC Methods
Influence of prior

Prior sensitivity analysis by likelihood inference

- Prior: a prerequisite

- CODA (Convergence Diagnostics and Output Analysis)

- BUGS (Bayesian Inference Using Gibbs Sampling)

Software:
\[
\left( \frac{d\hat{\phi}^i(x|\theta)}{d\theta} \right) \frac{d\phi^j(x|\theta)}{d\theta} = \left( \frac{d\hat{\phi}^i(x|\theta)}{d\theta} \right) \frac{d\phi^j(x|\theta)}{d\theta}
\]

Likelihood Inference by MCMC Methods
Log-likelihood of function

3. Maximize wrt. log-likelihood value over bin to approximate profile

2. Bin pairs wrt. function value corresponding log-likelihood approximation

1. Compute function value of each grid point and pair this with profile log-likelihood

2. Maximize over the grid to approximate profile log-likelihood

1. Compute \( \log L(\theta|\theta_0)^N \) in grid formed by quantiles of Gibbs output

Profile log-likelihood Approximation by Gibbs Sampling:

\[
\log L(\theta|\theta) \downarrow \sup_{\theta} \log P_{\theta} = (x|\theta) \downarrow \log L(\theta|\theta_0)^N
\]
Directed Graphical Model: Screening for Cervical Cancer
Screening for Cervical Cancer
Screening for Cervical Cancer

<table>
<thead>
<tr>
<th>Prior 1</th>
<th>Prior 2</th>
<th>Prior 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>B(9.4, 281) b(1.2)</td>
<td>B(9.4, 281) b(1.2)</td>
<td>B(9.4, 281) b(1.2)</td>
</tr>
<tr>
<td>B(3.2, 1.5) b(1.2)</td>
<td>B(3.2, 1.5) b(1.2)</td>
<td>B(3.2, 1.5) b(1.2)</td>
</tr>
<tr>
<td>B(1.3, 8.2) b(2.1)</td>
<td>B(1.3, 8.2) b(2.1)</td>
<td>B(1.3, 8.2) b(2.1)</td>
</tr>
<tr>
<td>B(69.6, 2.2) b(2.1)</td>
<td>B(69.6, 2.2) b(2.1)</td>
<td>B(69.6, 2.2) b(2.1)</td>
</tr>
</tbody>
</table>

Quantities of Interest:

\[ \text{Sens} = \frac{1}{1 - (1 - \text{Spec})(1 - \text{Prior})} \]

\[ \text{Spec} = \frac{1}{1 - (1 - \text{Sens})(1 - \text{Prior})} \]
Prior sensitivity analysis by approximating profile log-likelihood

DNA has a few false positives

Prior 2 (large variance) contradicts the well-known fact that DNA has few false positives

Prior 3

Prior 2

Prior 1

Prior Great Influence

Posterior

Bayesian Analysis:

Screening for Cervical Cancer
Likelihood analysis reveals problems with default prior
Conclusions very dependent on prior

DNA has a few false positives

Projected log-likelihood
Screening for Cervical Cancer
measurements where true class unknown

Analysis forms basis for a general method to compare discrete

supplement to the Bayesian analysis

Likelihood analysis reveals problems with default priors

Prior sensitivity analysis is possible by MCMC likelihood inference

Discussion:

based on prior information that DNA has no false positives

Smear analyzed by DNA is most sensitive and most specific

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Posterior mean</th>
<th>95% Cred. Interval</th>
<th>MLE 95% Conf. Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sens</td>
<td>0.32</td>
<td>0.26 – 0.40</td>
<td>0.31</td>
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<tr>
<td>SensM</td>
<td>0.85</td>
<td>0.76 – 0.93</td>
<td>0.85</td>
</tr>
<tr>
<td>SensM8</td>
<td>0.48</td>
<td>0.48 – 0.67</td>
<td>0.48</td>
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<tr>
<td>SensM86</td>
<td>0.72</td>
<td>0.55 – 0.80</td>
<td>0.72</td>
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<tr>
<td>SensM865</td>
<td>0.79</td>
<td>0.69 – 0.89</td>
<td>0.79</td>
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<tr>
<td>SensM8654</td>
<td>0.86</td>
<td>0.76 – 0.96</td>
<td>0.86</td>
</tr>
<tr>
<td>SensM86549</td>
<td>0.97</td>
<td>0.86 – 0.98</td>
<td>0.97</td>
</tr>
</tbody>
</table>

Summary: (Prior 1 and Prior 3)

Screening for Cervical Cancer
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