Mixture Models for Capture-Recapture Data

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Invited Lecture at

Mixture Models between Theory and Applications" Rome, September 13, 2002

How many cases **n** in a population?

- Registry identifies n_{obs} cases
- p₀ probability of being **not** identified by the registry
- Then:

 $n = n p_0 + (1 - p_0) n$

= unobserved + observed cases = $n p_0 + n_{obs}$



$$n_{\rm HTE} = n_{\rm obs} / (1 - p_0)$$

(Horwitz-Thompson)

An Example

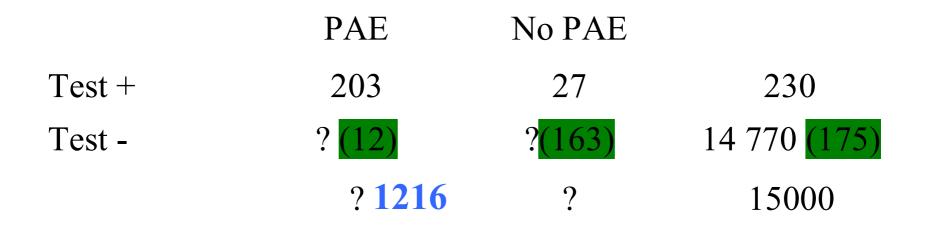
- A registry could identify 250 cases from a study population
- Assume that the inclusion probability $(1-p_0) = 0.25$ known

• Then $n_{HTE} = n_{obs} / (1-p_0)$ = 250 /0.25 =1000

How HAT-approach can be used for Screening

• "In a large population survey of 15000 persons were screened given **chest radiographs**, and the physicians noted possible pulmonary artery enlargement (PAE) in 230 of these patients. The enlargement was confirmed in a second reading in 203 of these 230 persons. A sample of 175 of the 14770 chest radiographs in which no enlargement of the pulmonary artery was noted yielded 12 radiographs that were actually postive for pulmonary enlargement." Levy & Lemeshow 91

What do we have ?



PPV = P(D+|T+) = 203/230 = 0.8826 using Bayes theorem NPV = P(D-|T-) = 163/175 = 0.9314 Sensitivity = 0.1670

 $n_{HTE} = n_{obs} / (1 - p_0) = 203 / 0.1670 = 1216$

Horwitz-Thompson-Approach seems easy, but ...

inclusion probability often unknown and, consequently,

approaches differ in the way they estimate the inclusion probability, or in other words, how they

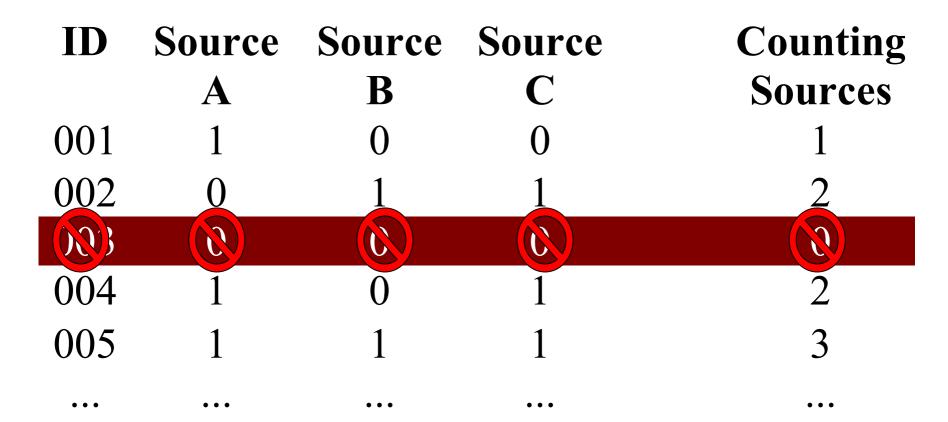
model p_0



Information typically available in a disease (cancer) registry

- A case is identified by at least one source, typically several sources such as pathology, hospitals, physicians, death certificate,
- Potentially further covariates are available such as age at diagnosis, gender, ..

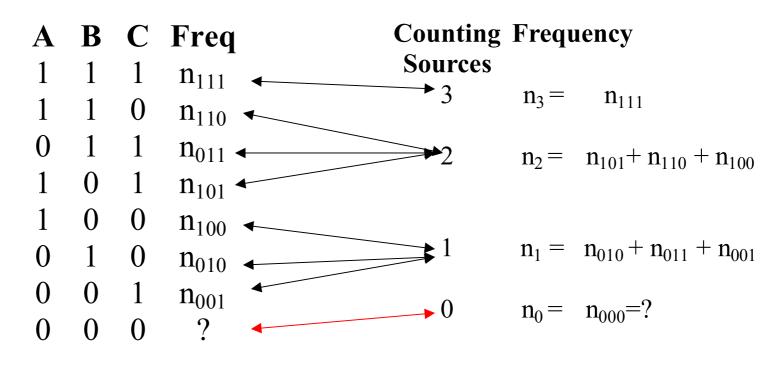
... in more detail



Two major streams of development ...

illustrated with 3 sources

- contingeny table
- modelling a multiway modelling the counting sources distribution



An Example for first approach with two sources

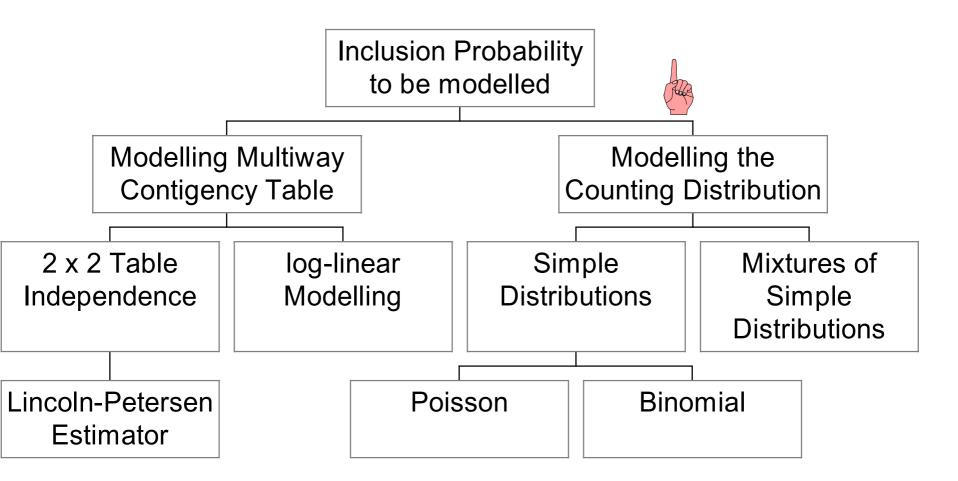
• Inclusion probabilities • Associated data

$p_{11} p_{10}$	$n_{11} n_{10}$
$p_{01} p_{00}$	$n_{01} n_{00}$

a) estimate p_{11} as n_{11}/n

b) on the other hand, using *independence* $p_{11} = p_1$. $p_{.1}$ one can estimate p_{11} as n_1 . / $n \times n_{.1}/n$ equating a) and b), leads to $n_{LP} = n_1$. $n_{.1}/n_{11}$ the Lincoln-Petersen estimate of number of cases

Elaborate Developments



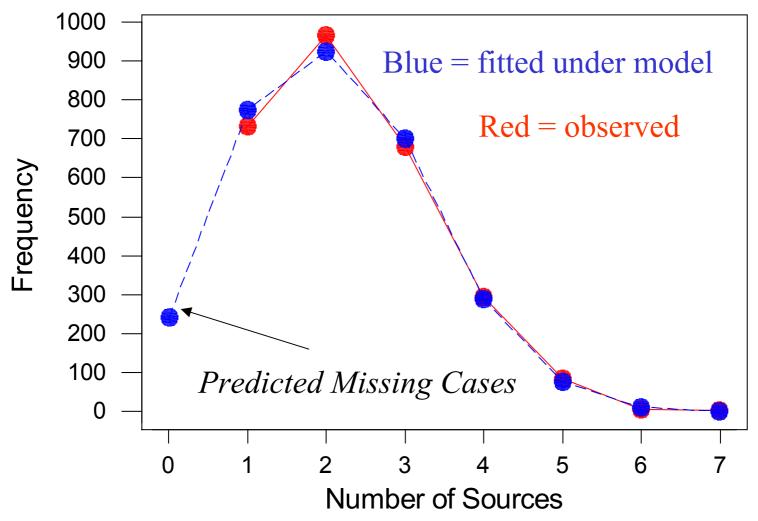
Reasons for *not* following the first approach

- (log-linear) modelling becomes quite complex; with 4 sources more than 100, with 5 sources more than 7000 possible models
- potential danger of one dominating source
- wortking with the counting sources distribution will only require the decision about one model

The Counting Distribution

ID	Source	Source	Source		Counting
	Α	B	С	•••	Sources
001	1	0	0	• • •	1
002	0	1	1	•••	2
003	0	1	0	•••	1
004	1	0	1	•••	2
005	1	1	1	•••	3
• • •	• • •	• • •	• • •		• • •

Distribution of Observed and Predicted Counts of Sources for fictional registry data



Simple Distributional Count Models

Binomial

$$\begin{split} f(y,\theta) &= \begin{pmatrix} m \\ y \end{pmatrix} \theta^{y} (1-\theta)^{m-y} , y=0,1,...,m \\ (m = \text{Number of Sources}, \theta = \text{Listing Probability}) \\ \textbf{Predicted Probability of a Zero:} \\ p_{0} &= f(y=0,\theta) = \begin{pmatrix} m \\ 0 \end{pmatrix} \theta^{0} (1-\theta)^{m-0} = (1-\theta)^{m} \end{split}$$

Number of cases

Suppose, θ where *known*, then the *estimated number of cases*

$$n_{\rm HTE} = n_{\rm obs} / (1 - p_0)$$

where $p_0 = (1-\theta)^m$.

Estimation of Listing Probability

in summary:

 $n = n_{obs} / (1 - p_0)$, where $p_0 = (1 - \theta)^m$,

also, if n is given

 $\theta = (n_0 \ 0 + n_1 \ 1 + n_2 \ 2 + \dots + n_m \ m) / (n \ m)$

Estimation of Listing Probability Consequently,

Step 0. Choose, some initial value for $\theta = \theta^{(1)}$ (for ex. $\theta = 1/2$)

Step 1. Compute $n^{(1)} = n_{obs} / (1 - p_0^{(1)})$, where $p_0^{(1)} = (1 - \theta^{(1)})^m$

Step 2. Compute $\theta^{(2)} = (n_1 \ 1 \ +... \ + \ n_m \ m) / (m \ n^{(1)})$

Step 3. Continue iteration until convergence.

Estimation of Listing Probability

Step 1. Compute $n^{(2)} = n_{obs} / (1 - p_0^{(2)})$, where $p_0^{(2)} = (1 - \theta^{(2)})^m$

Step 2. Compute

$$\theta^{(3)} = (n_1 \ 1 \ +... \ + \ n_m \ m) / (n^{(2)} \ m)$$

Version of EM algorithm (DLR 1977)

- for finding maximum likelihood estimator of θ
- imputing the number of missing data (as by-product)
- (strong) convergence is assured (in this case)

A Demonstration

Iteration j	<mark>(i)</mark>	n ^(j)
1	0.50	2790
2	0.3260	2955
3	0.3078	2996
•••	•••	•••
20	0.3021	3011
21	0.3021	3011

Simple Distributional Count Models

Poisson

$$f(y,\theta) = e^{-\theta} \theta^{y} / y !, y=0,1, ...$$
(suitable for m = Number of Sources large)

Predicted Probability of a Zero:
$$p_{0} = f(y=0,\theta) = e^{-\theta} \theta^{y} / y ! = e^{-\theta}$$

Estimation of Listing Parameter and Prediction of Number of Cases

Similar to the Binomial, only difference is the way the missing cases are predicted:

Poisson: $p_0 = f(y=0,\theta) = e^{-\theta}$ Binomial: $p_0 = f(y=0,\theta) = (1-\theta)^m$ More flexible and robust approach through mixtures

- Simple counting sources distributions such as Binomial and Poisson require assumptions such as homogeneity of listing probabilities that are seldom met in reality
- allowing the listing probability to vary in unobserved sub-populations will be more realistic

The mixture approach in a nutshell

homogeneity

one-parametric density f(y,θ) (typically f(y,θ) will be a simple density like Binomial or Poisson)

heterogeneity

$$\lambda_1 \lambda_2 \lambda_3 \lambda_4$$

density in subpop. j: $f(y, \theta_j)$

The mixture approach in a nutshell

latent variable Z describing population membership

joint density f(x,z) with $f(x,z) = f(x | z)f(z) = f(x,\theta_z)q_z$

marginal or mixture density:

$$f(x,Q) = f(x,\theta_1)q_1 + \dots + f(x,\theta_k)q_k Q = \begin{pmatrix} \theta_1 \dots \theta_k \\ q_1 \dots q_k \end{pmatrix}$$
 is mixing distribution

Estimation of parameters works in principle as before, though technically more elaborated **in summary**:

if Q =
$$\begin{pmatrix} \theta_1 \dots \theta_k \\ q_1 \dots q_k \end{pmatrix}$$
 given, then estimate

 $n = n_{obs} / (1 - p_0)$, where $p_0 = f(y=0,Q)$,

also, if n is *given*, then estimate

Q by the NPMLE

Special Mixtures

Mixtures of Binomials

$$f(y, \theta_j, q_j) = \sum_{j=1}^{k} q_j \begin{pmatrix} m \\ y \end{pmatrix} \theta_j^y (1-\theta_j)^{m-y}, y=0, 1, ..., m$$

(m = Number of Sources, θ_j = Listing Probability in sub-population j, q_j = weight of sub-population)

Predicted Probability of a Zero: $p_0 = f(y=0,\theta_j,q_j) = \sum_{j=1}^{k} q_j (1-\theta_j)^m$

Special Mixtures

Mixtures of Poissons

$$f(y, \theta_j, q_j) = \sum_{j=1}^{k} q_j \exp(-\theta_j) \theta_j^{y} / y!, y=0,1, ...$$

 $(\theta_j = \text{Listing parameter in sub-population } j, q_i = \text{weight of sub-population})$

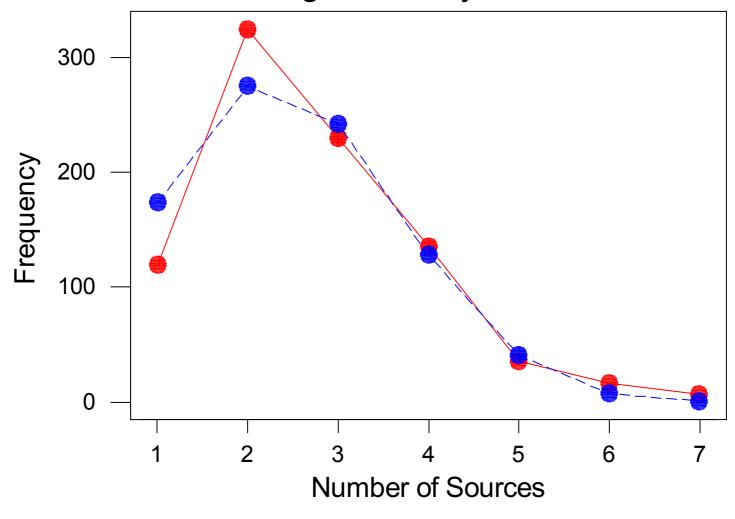
Predicted Probability of a Zero: $p_0 = f(y=0,\theta_j,q_j) = \sum_{j=1}^{k} q_j \exp(-\theta_j)$

Results of Analysis for Cancer Registry of Saarland

- Joint project with Robert Koch Institute, Berlin, Dachorganisation Krebs (Dr. Dieter Schön)
- Six main sources, and subsidiar sources which occur from 40 hospital categories and 31 departmental categories
- counting sources variable seldom > 10
- years considered: 1994 1998
- here 3 sites: lung cancer, female breast cancer and prostata cancer

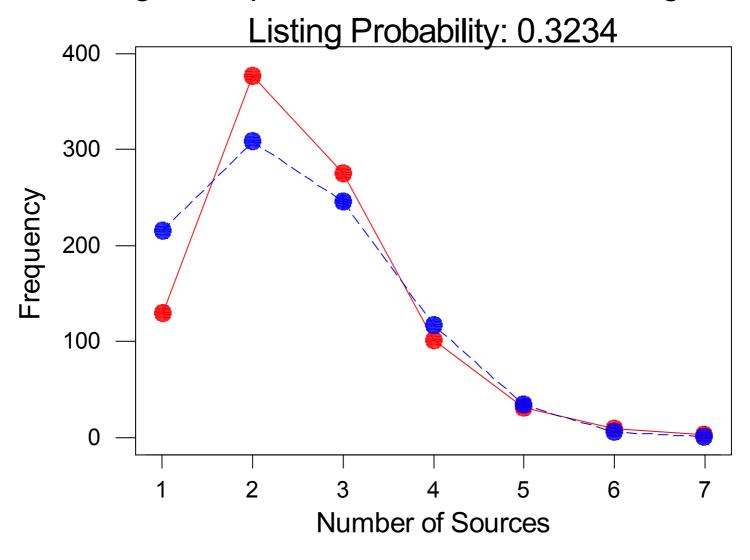
Lung Cancer (using mixtures of binomials) Distribution of Observed and Predicted Counts of Sources

Age Group < 59 Years at Diagnosis Listing Probability: 0.3684



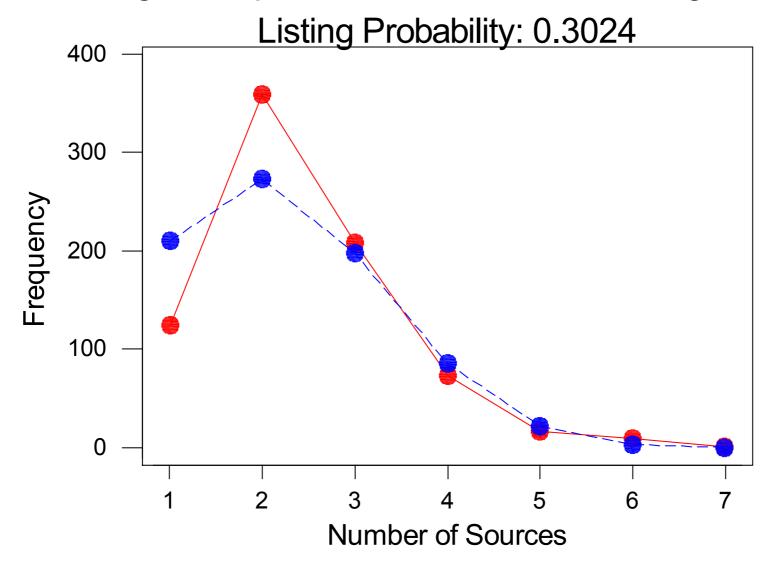
Distribution of Observed and Predicted Counts of Sources

Age Group > 59 and < 67 Years at Diagnosis



Distribution of Observed and Predicted Counts of Sources

Age Group > 67 and < 73 Years at Diagnosis



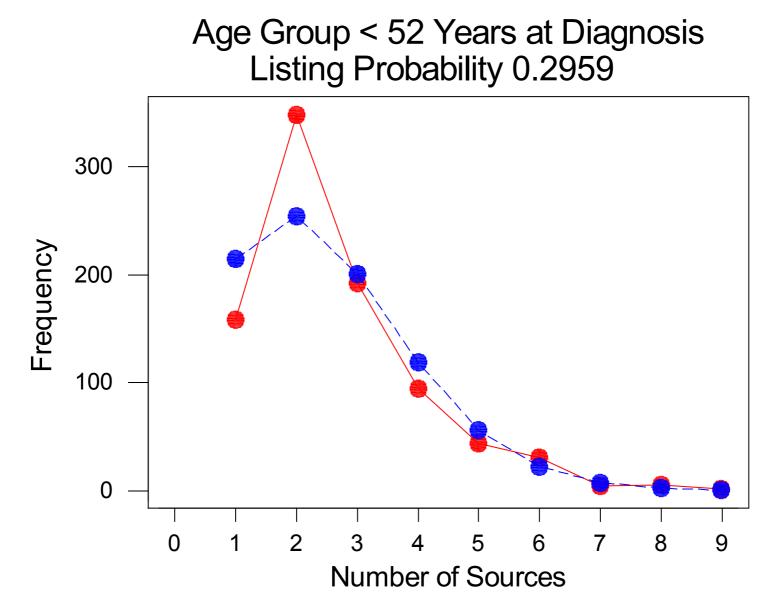
Distribution of Observed and Predicted Counts of Sources Age Group > 73 Years at Diagnosis Listing Probability: 0.2680 Frequency Number of Sources

Summary Table for Lung Cancer

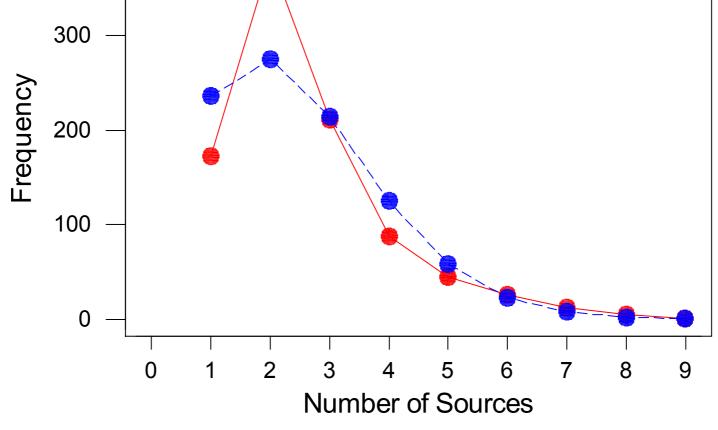
Age group	n _{obs}	n _o	Listing Probability	Complete- ness (%)
- 59	866	47	0.3684	94.8521
- 67	926	64	0.3234	93.5354
- 73	792	67	0.3057	92.2002
> 73	785	143	0.2680	84.5905
Total	3369	321	0.3125	91.3008

Breast Cancer (using mixtures of Poissons)

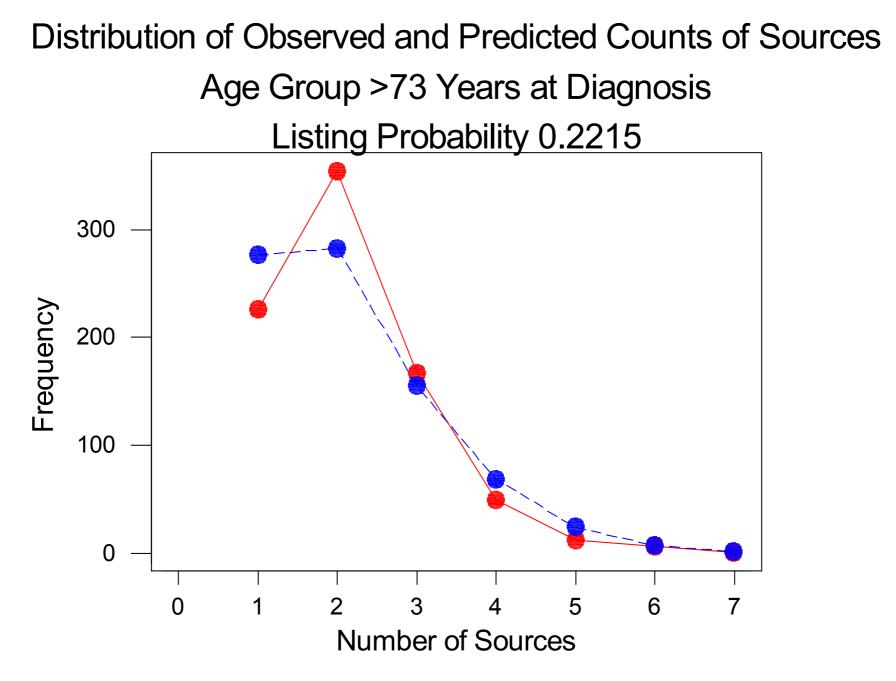
Distribution of Observed and Predicted Counts of Sources



Distribution of Observed and Predicted Counts of Sources Age Group >52 and < 63 Years at Diagnosis Listing Probability 0.2917



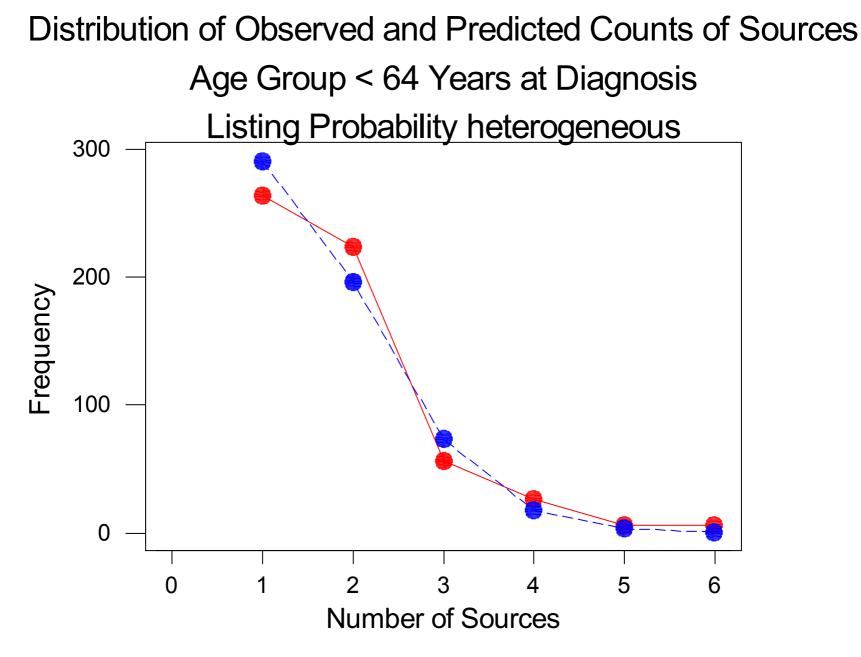
Distribution of Observed and Predicted Counts of Sources Age Group >63 and < 73 Years at Diagnosis Listing Probability 0.2594 Frequency Number of Sources

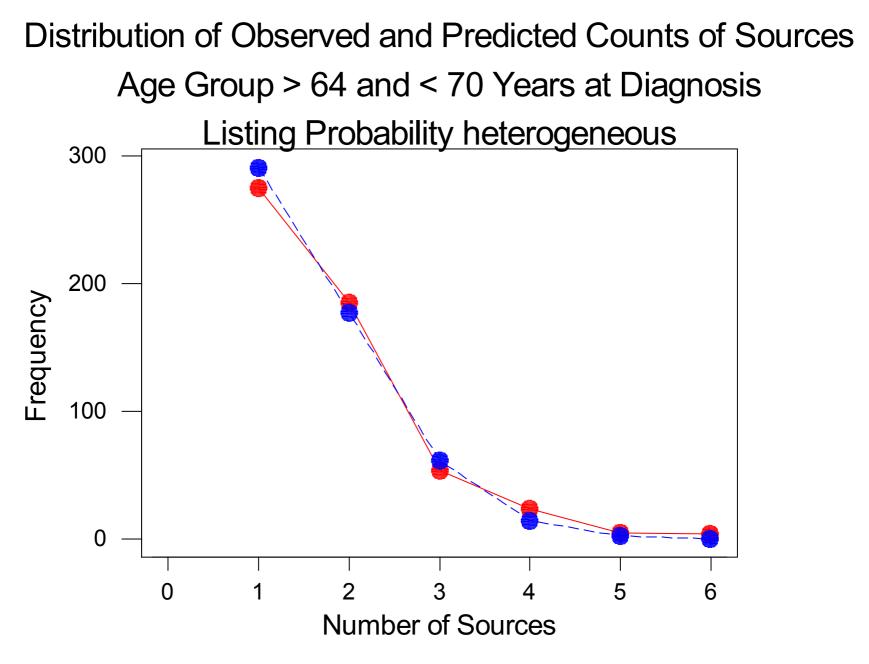


Summary Table for Breast Cancer

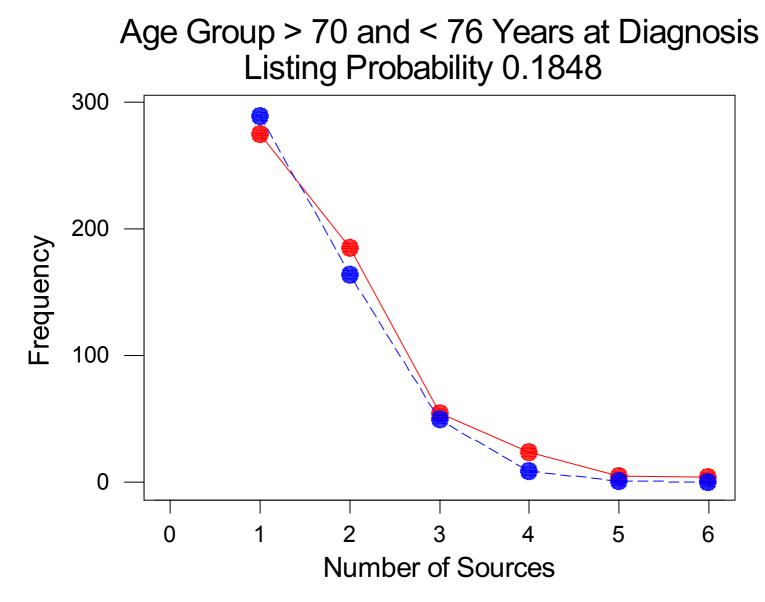
Age group	n _{obs}	n _o	Listing Probability	Complete- ness (%)
- 52	877	91	0.2959	90.5992
- 63	942	101	0.2917	90.3164
- 73	845	121	0.2594	87.4741
> 73	817	143	0.2215	85.1042
Total	3481	456	0.2687	88.4176

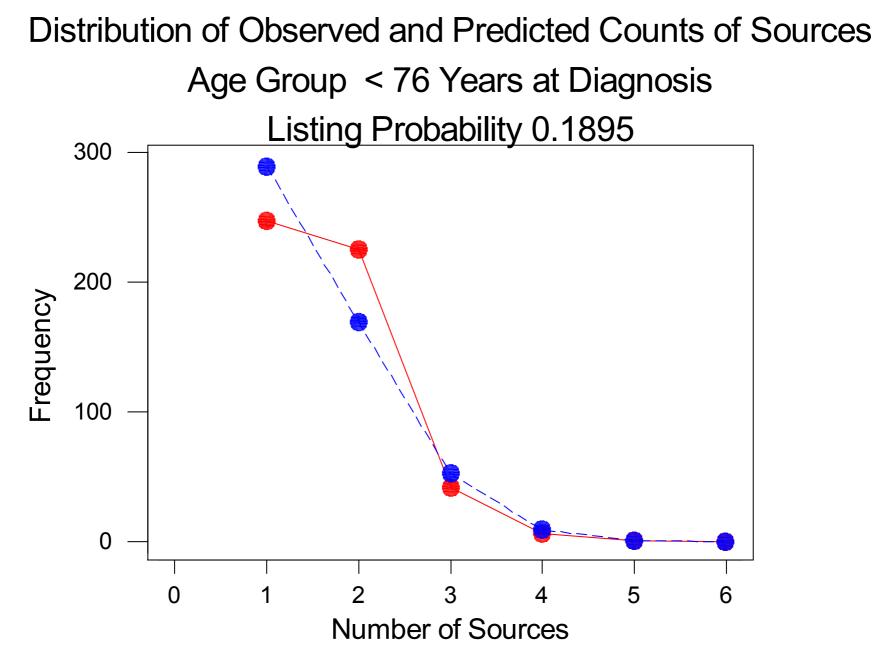
Prostate Cancer (using mixtures of Binomials)





Distribution of Observed and Predicted Counts of Sources





Summary Table for Prostate Cancer

Age group	n _{obs}	n _o	LP 1.	LP 2.	Weight 2. Comp.	Complete -ness (%)
- 64	582	181	0.2111	0.5534	0.0184	76.2779
- 70	547	203	0.1910	0.4525	0.0368	72.9333
- 76	512	213	0.1848	-	1.0000	70.6207
> 76	521	206	0.1895	-	1.0000	71.6644
Total	2162	803	0.2010	-	1.0000	72.9174

Thank You!

