

Personal Background and Areas of Interest

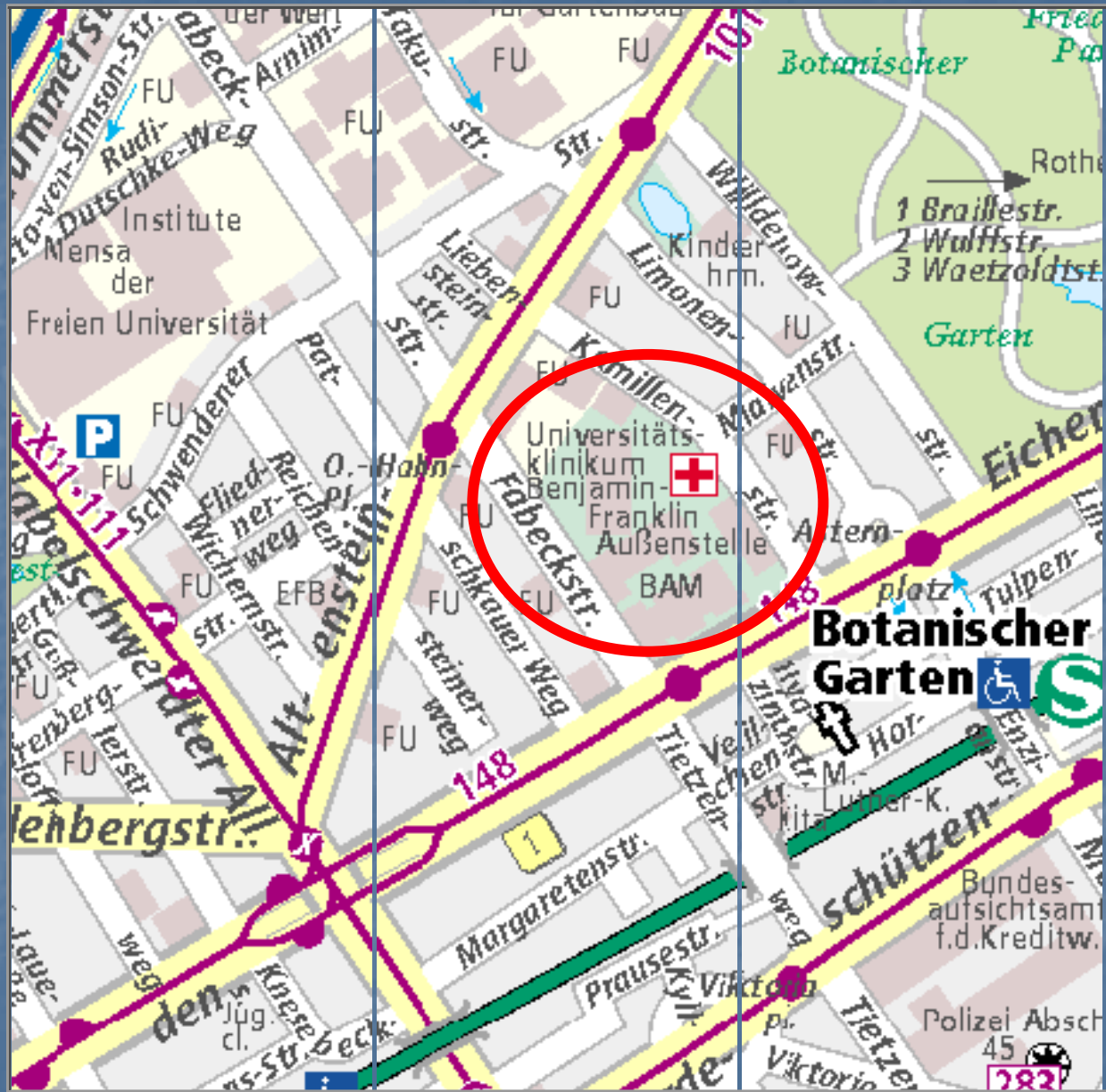
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Charité Medical School Berlin





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Overview

- History
- General Topics
- Current Areas of Interest
- Research Areas in Preperation

Overview

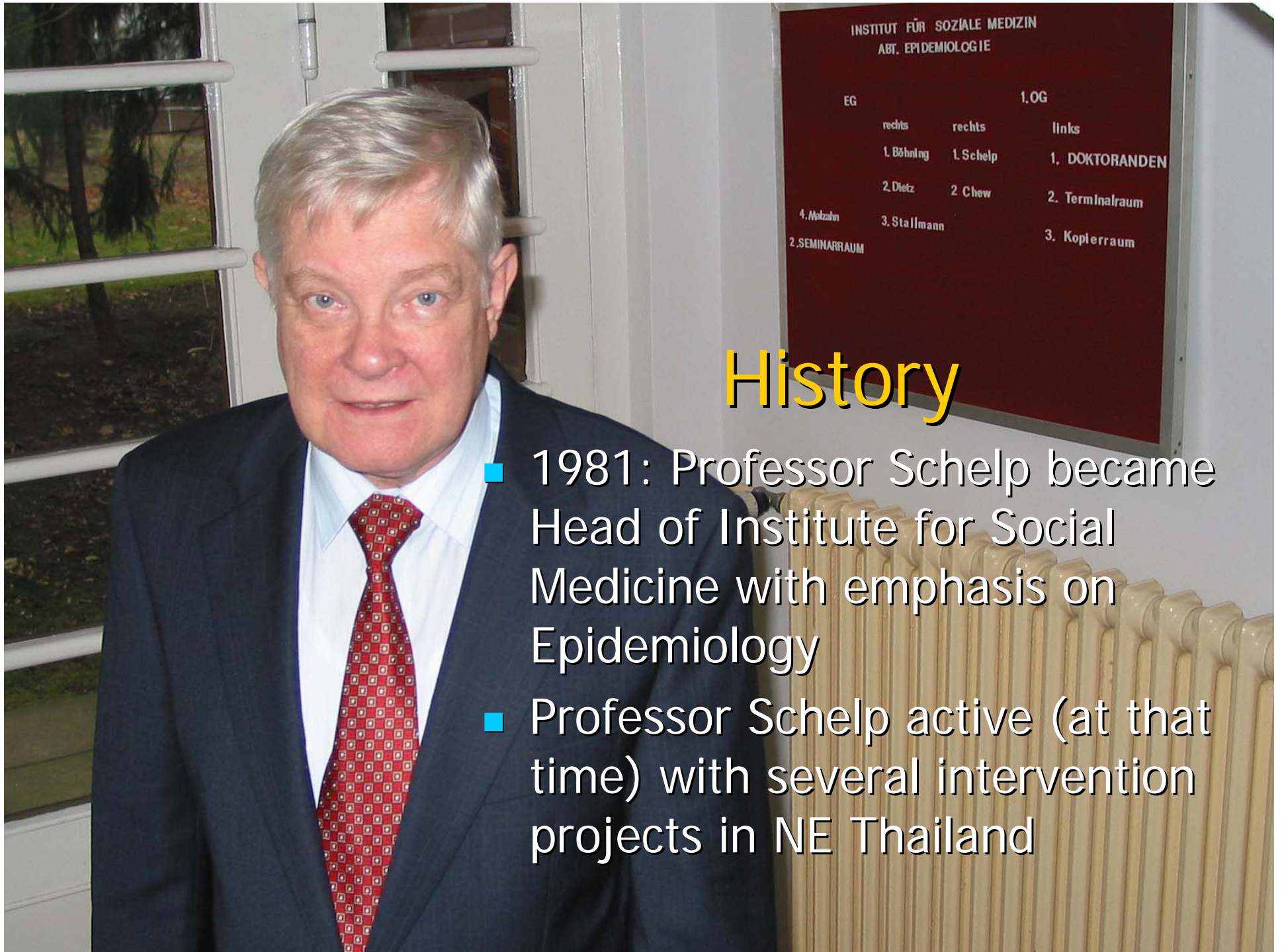
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Personal Background

- Studies
 - Mathematics (main) and social sciences (Bielefeld and Berlin)
- Degrees
 - M.Sc. (optimal design) Dr. (algorithms)
 - Habil. (medicine: epidemiology/biometry)
- Cooperation
 - Numerous Institutions in Europe, USA, Australia, Thailand, and Philippines
- Visiting
 - 85-86 Statistics, PennState
 - 96 Psychology, Vienna
 - 98-99 Statistics, Munich
 - 04 International EpiLab, Copenhagen
 - Several Visits to Philippines and Thailand

History

- 1982: after completion of my PhD take up junior position at the Institute of Social Medicine
- 1992: v. I. in Medical Statistics and Epidemiology
- 2000: Award of the Title of *Professor*
- Several co-workers 1990-2004: Dietz, Kuhnert, Malzahn, Schlattmann, Stallmann, Schleinitz, ...



History

- 1981: Professor Schelp became Head of Institute for Social Medicine with emphasis on Epidemiology
- Professor Schelp active (at that time) with several intervention projects in NE Thailand

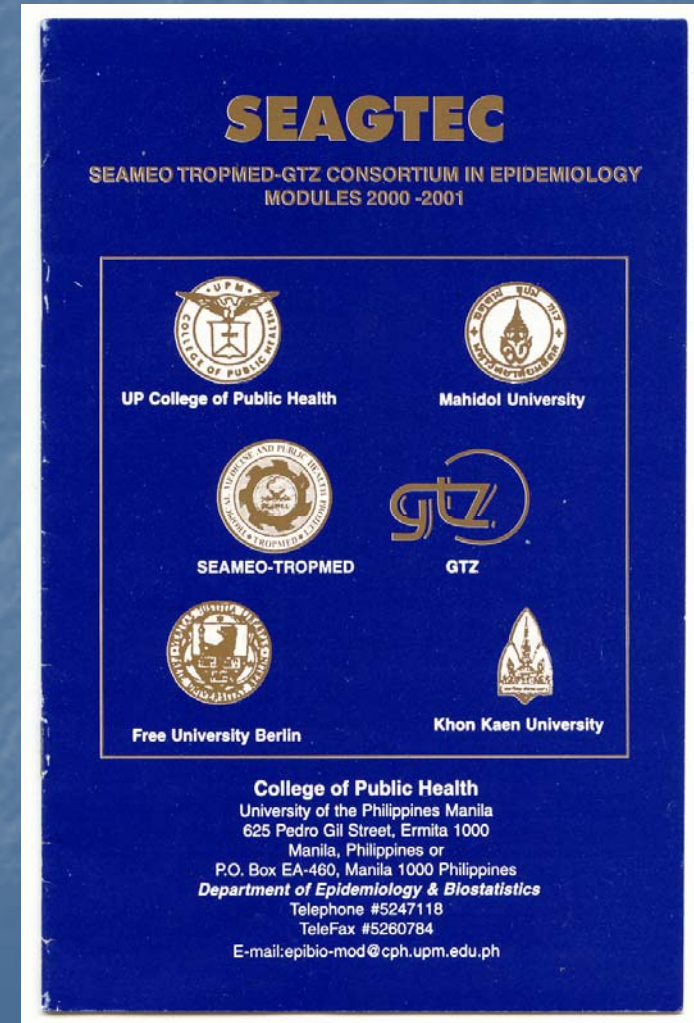
History

Besides cooperating in several projects in SE Asia

one major activity 1990-2000:

M.Sc. in Epidemiology

at UP Manila under participation of the universities of Mahidol (Bangkok, Th), Khon Kaen(Th), FU Berlin, UP Manila (Ph)



Cooperation Projects with SE ASIA

- Partner: Faculty for Public Health, Mahidol University, Bkk, Thailand
- Prof. Chukiatt Viwatwongkasem (Counterpart)
- Funding: DFG, BMZ und National Research Council of Thailand (NRCT)



Capture-Recapture Procedures in Public Health

Welcome all participants to a special lecture
"Capture-Recapture Procedures in Public Health"
Speaker: Prof. Dr. Dankmar Böhning
Organized by Department of Biostatistics, Faculty of Public Health,
Izahidol University. March 15 - April 16, 2004.

Surveillance Project on Illicit Drug Use
in Thailand using Truncated Counting
Distributions

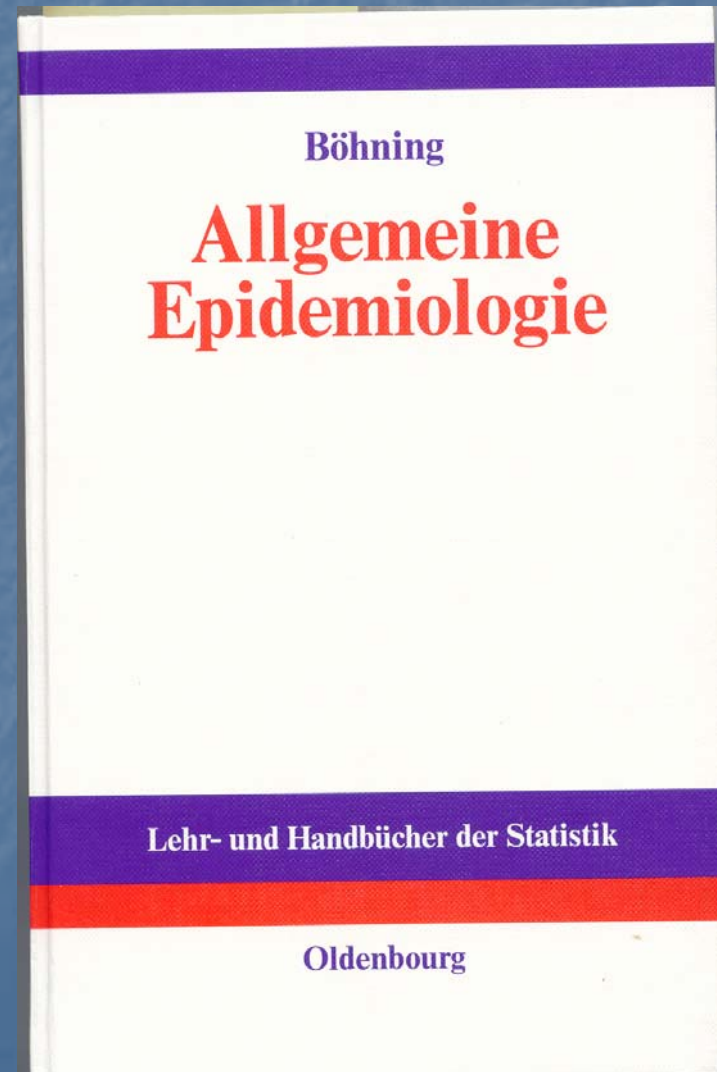


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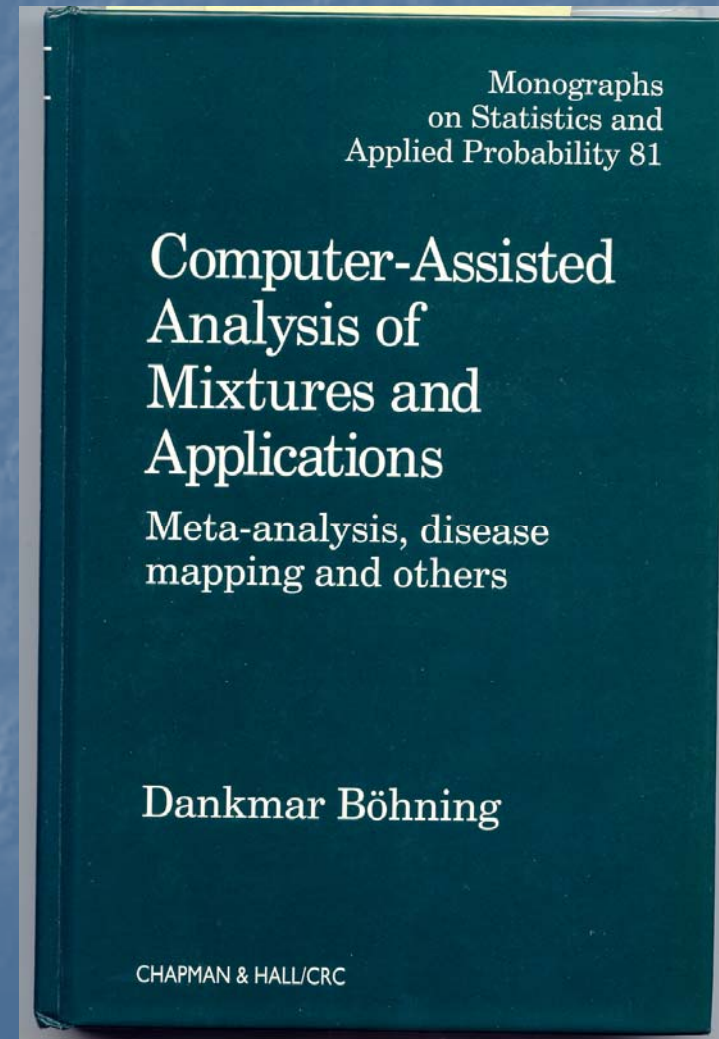
General Topics

- General Epidemiology
- Problems of Inference in Epidemiology
- Epidemiologic Modelling



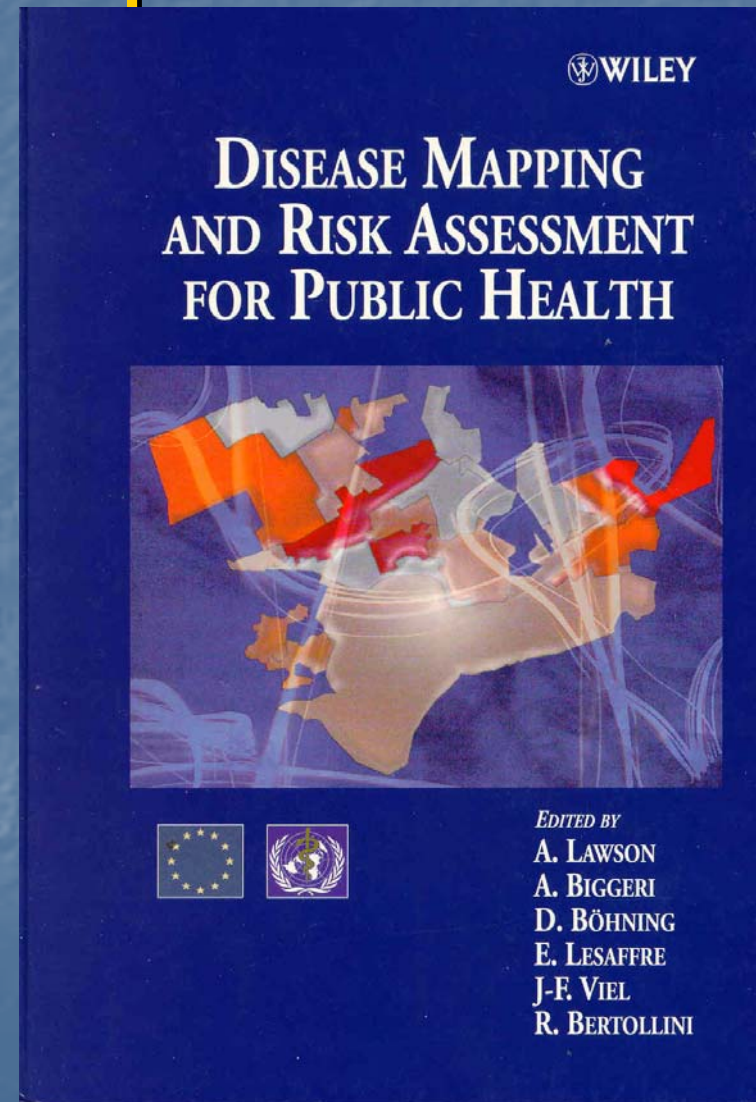
General Topics

- Mixture models
- Applications in Biometry and Epidemiology



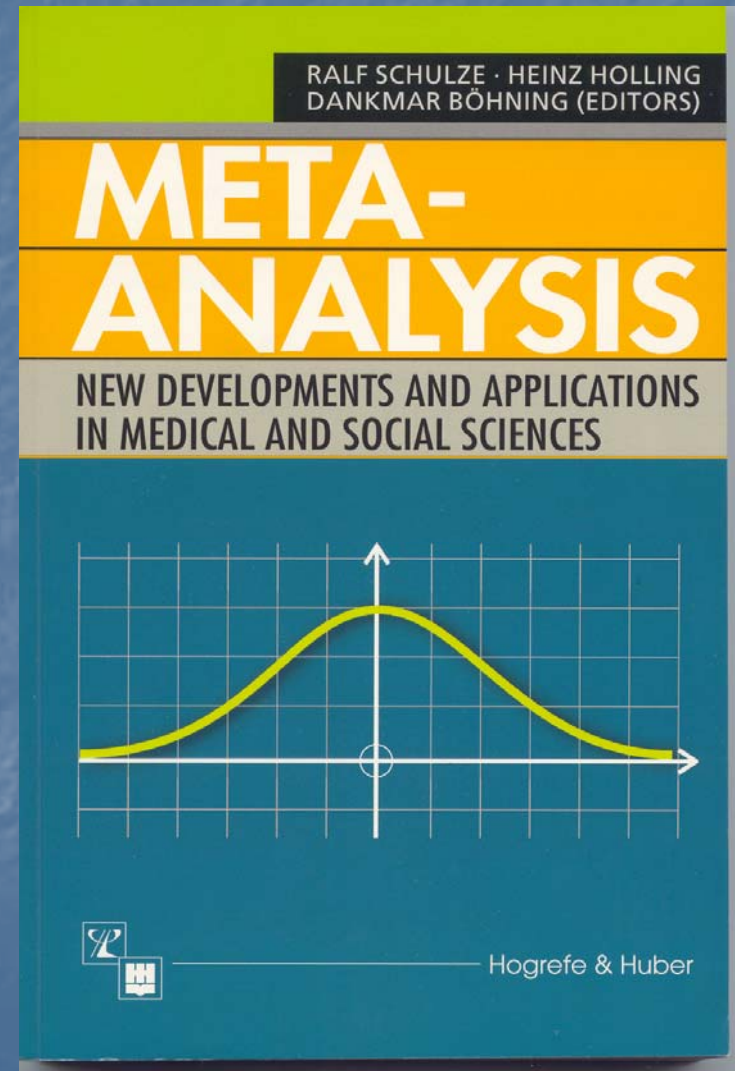
General Topics

- Disease Mapping and Geographical Epidemiology
- Smoothed Estimates of Geographical Risk



General Topics

- Systematic Reviews and Meta-Analysis
- Heterogeneity, Covariate and Publications Bias Modelling
- Unifying Concept



Personal Background: Editorial Board

- Biometrics (1992)
- Statistical Modelling (1999)
- Biometrical Journal (2004)

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Modelling Effect- and Nuisance Parameter in Multi-Center Studies

- Typical setting: treatment- and control Arm
- For treatment arm:
 - x^T number of events
 - P^T person-time
 - λ^T event rate
- For control arm:
 - x^C, P^C, λ^C

Modelling Effect in Multi-Center Studies: A Typical Example

| Center | Treatment | | Control | |
|--------|-------------------|------------------------|-------------------|-----------------------|
| | events x_i^T | person-time P_i^T | events x_i^C | under risk P_i^C |
| 1 | 29 | 116 | 21 | 113 |
| 2 | 6 | 73 | 3 | 121 |
| 3 | 30 | 50 | 23 | 50 |
| 4 | 23 | 180 | 15 | 172 |
| ... | ... | ... | ... | ... |
| 59 | 15 | 60 | 4 | 60 |

Modelling Effect- and Nuisance Parameter in Multi-Center Studies

- parameter of interest:

$$\text{risk ratio: } \theta = \lambda^T / \lambda^C$$

- nuisance parameter:

λ^C event rate in control arm

poisson log-likelihood (for one center):

$$-\lambda^T P^T + x^T \log(\lambda^T P^T) - \lambda^C P^C + x^C \log(\lambda^C P^C)$$

Modelling Effect- and Nuisance Parameter in Multi-Center Studies

$$-\lambda^T P^T + x^T \log(\lambda^T P^T) \quad -\lambda^C P^C + x^C \log(\lambda^C P^C)$$

becomes using $\theta = \lambda^T / \lambda^C$ or $\lambda^T = \theta \lambda^C$

$$-\theta \lambda^C P^T + x^T \log(\theta \lambda^C P^T) \quad -\lambda^C P^C + x^C \log(\lambda^C P^C)$$

Keeping the parameter of interest fixed and maximizing for the nuisance parameter ...

$$\hat{\lambda}^c = \frac{x^c + x^T}{P^c + \theta P^T}$$

replacing λ^c by its estimate $\hat{\lambda}^c$

$$-\theta \hat{\lambda}^c P^T + x^T \log(\theta \hat{\lambda}^c P^T) - \hat{\lambda}^c P^c + x^c \log(\hat{\lambda}^c P^c)$$

leads to the beautiful simple
Profile Log-likelihood ...

$$x^T \log(\theta) - (x^T + x^C) \log(P^C + \theta P^T)$$

... building the profile over all centers:

$$\sum_{i=1}^k x_i^T \log(\theta_i) - (x_i^T + x_i^C) \log(P_i^C + \theta_i P_i^T)$$

Advantages

- nuisance parameter eliminated
- Profile likelihood is simple (in this case):

$$\sum_{i=1}^k x_i^T \log(\theta_i) - (x_i^T + x_i^C) \log(P_i^C + \theta_i P_i^T)$$

- beneficial not only for effect structures but also for covariance structures (simplification of Fisher information)

Problems looked at: homogenous case

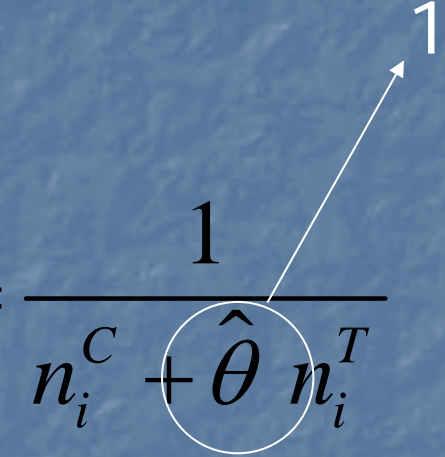
$\theta_i = \theta$ for all centers $i = 1, \dots, k$:

$$\sum_{i=1}^k x_i^T \log(\theta) - (x_i^T + x_i^C) \log(P_i^C + \theta P_i^T)$$

Score equation for profile MLE gives:

$$\hat{\theta} = \frac{\sum_{i=1}^k x_i^T n_i^C w_i(\hat{\theta})}{\sum_{i=1}^k x_i^C n_i^T w_i(\hat{\theta})}, \quad w_i(\hat{\theta}) = \frac{1}{n_i^C + \hat{\theta} n_i^T}$$

Problems looked at: homogenous case

$$\hat{\theta} = \frac{\sum_{i=1}^k x_i^T n_i^C w_i(\hat{\theta})}{\sum_{i=1}^k x_i^C n_i^T w_i(\hat{\theta})}, \quad w_i(\hat{\theta}) = \frac{1}{n_i^C + \hat{\theta} n_i^T}$$


- Close connection to Mantel-Haenszel:
 - arms balanced then: PMLE = MH
 - Non-sparsity: PMLE and MH close
 - Sparsity: PMLE more efficient

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Modelling Effect-Heterogeneity in Multi-Center Studies: Unobserved Heterogeneity

- Allowing for unobserved heterogeneity leads to mixtures of profile log-likelihoods

$$\sum_{i=1}^k \log \int_{\theta} [\theta^{x_i^T} / (P_i^C + \theta P_i^T)^{x_i^T + x_i^C}] Q(d\theta)$$

- where mixing distribution can be parametric
- or **non-parametric**
 - strong results on NPMLE possible using convex theory
 - estimation with EM or global ascent algorithms

Modelling Effect-Heterogeneity in Multi-Center Studies:

Unobserved Heterogeneity

- Comparison with other approaches such as
 - approximating normal (problem: use empirical estimate of trial variance)

$$\sum_{i=1}^k \log \int_{\lambda^C} \phi\left((z_i - \log \theta) / \sigma_i \right) Q(d \log \theta)$$

where z_i obs. log-rate ratio and $\sigma_i^2 = 1/x_i^T + 1/x_i^C$

- multi-level approach (a la Murray Aitkin)

$$\sum_{i=1}^k \log \int_{\lambda^C} [\exp(-\theta \lambda^C P_i^T) (\theta \lambda^C P_i^T)^{x_i^T} \exp(-\lambda^C P_i^C) (\lambda^C P_i^C)^{x_i^C}] Q(d \lambda^C)$$

Modelling Effect-Heterogeneity in Multi-Center Studies: Observed Heterogeneity-Covariate Information

- Often additional trial information is available s.a. study date, treatment modifications, patient characteristics
- Suppose information is captured in a covariate vector

z_i for center i : (GLM-type formulation)

$$\theta_i = \exp(\beta_0 + \beta' z_i)$$

Modelling Effect-Heterogeneity in Multi-Center Studies: Observed Heterogeneity-Covariate Information

Log-likelihood becomes

$$\sum_{i=1}^k x_i^T \log \theta_i - (x_i^T + x_i^C) \log(P_i^C + \theta_i P_i^T) \quad \text{using } \theta_i = \exp(\beta_0 + \beta' z_i)$$

$$= \sum_{i=1}^k x_i^T (\beta_0 + \beta' z_i) - (x_i^T + x_i^C) \log[P_i^C + \exp(\beta_0 + \beta' z_i) P_i^T]$$

- Strong results possible:
 - Hessian has simple structure
 - Hessian has lower bound (lower bound algorithm possible)
 - Guaranteed convergence to MLE

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Capture-Recapture Procedures based upon Counting Distributions

- Basic objective of CR: estimate population size
- In particular of interest in areas where direct counting is difficult such as
 - a wildlife population (historic genesis)
 - how many people drive a car without license?
 - how many practicing physicians are alcohol dep.?
 - how many cases of a disease remain undetected?
- Adjustment for undercount




How many cases N in a population?

- Some mechanism identifies n cases
- p_0 probability of being **not** identified by the mechanism
- **Then:**

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


= unobserved + observed cases


$$= N p_0 + n$$

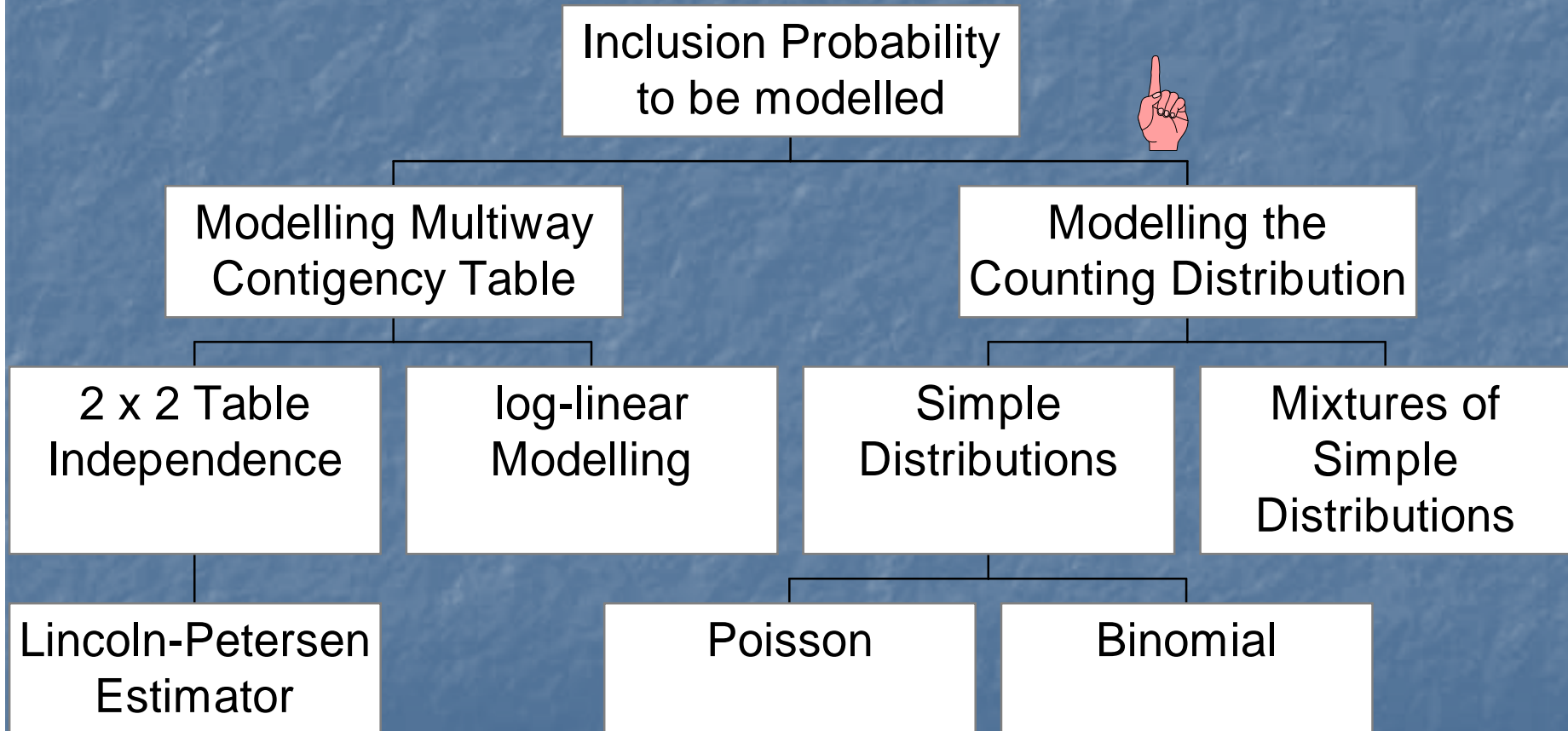
$$\hat{N} = n / (1 - p_0)$$

(Horwitz-Thompson)

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 ρ_0 

Developments

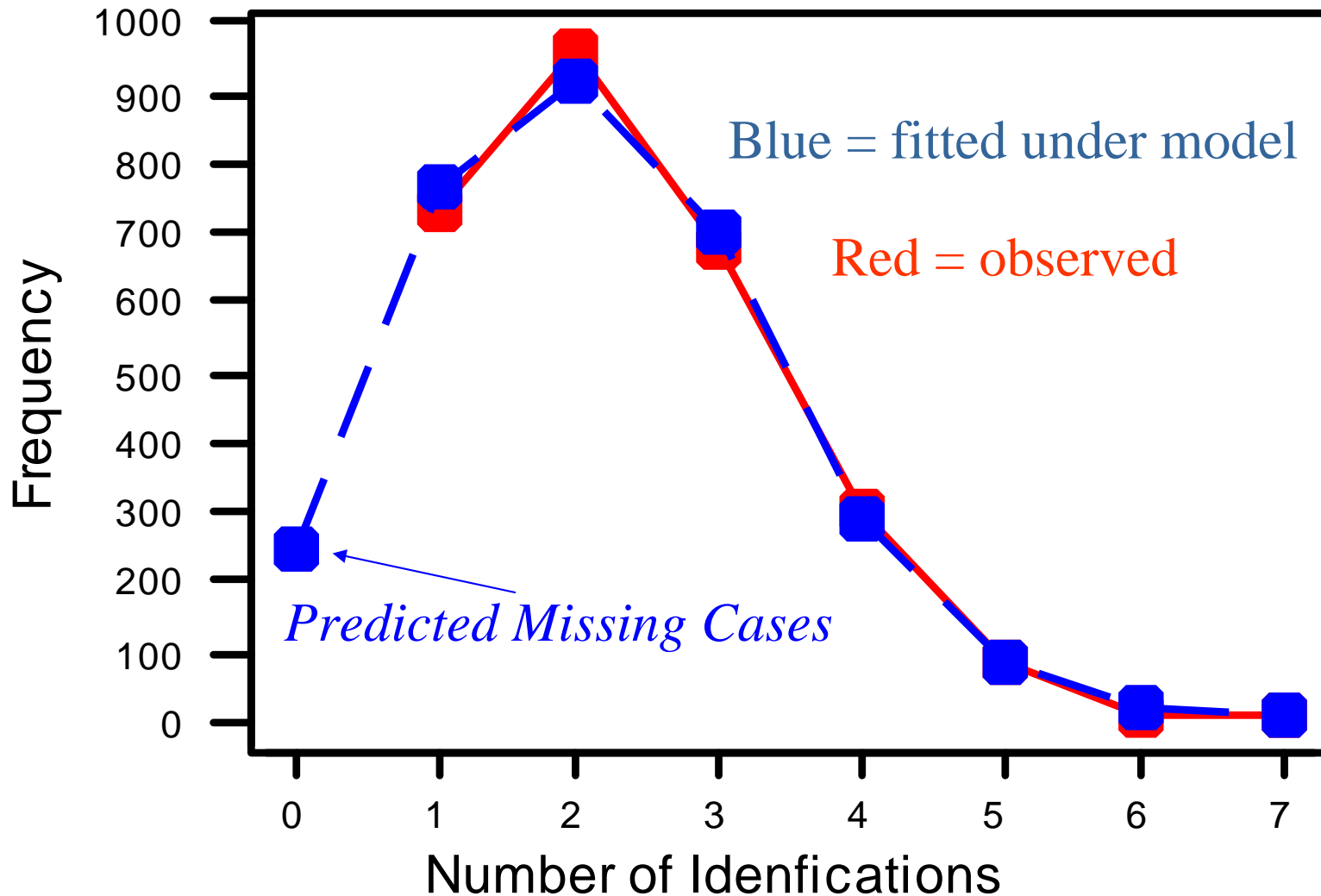


The Counting Distribution

... occurs when the mechanism can catch multiple identifications (s.a. police identifies and expells an illegal immigrant several times)

| Count of identifications i | Frequency of counts with i identifications | observed |
|----------------------------------------------------|------------------------------------------------------------------------|-----------------|
| 0 | n_0 | no |
| 1 | n_1 | yes |
| 2 | n_2 | yes |
| 3 | n_3 | yes |
| 4 | n_4 | yes |
| ... | ... | ... |

Distribution of Observed and Predicted Counts of Sources *for fictional data of multiple identifications*






The Counting Distribution: A historic Example

- McKendrick's cholera data
- Village in India had households with cholera cases $n_1=32$, $n_2=16$, $n_3=6$, $n_4=1$
- McKendrick ignored the houses with no cases
- Constructed an estimate (moment) based upon a Poisson assumption for the counts

Cholera Epidemic in an Indian Village (1915-1920)



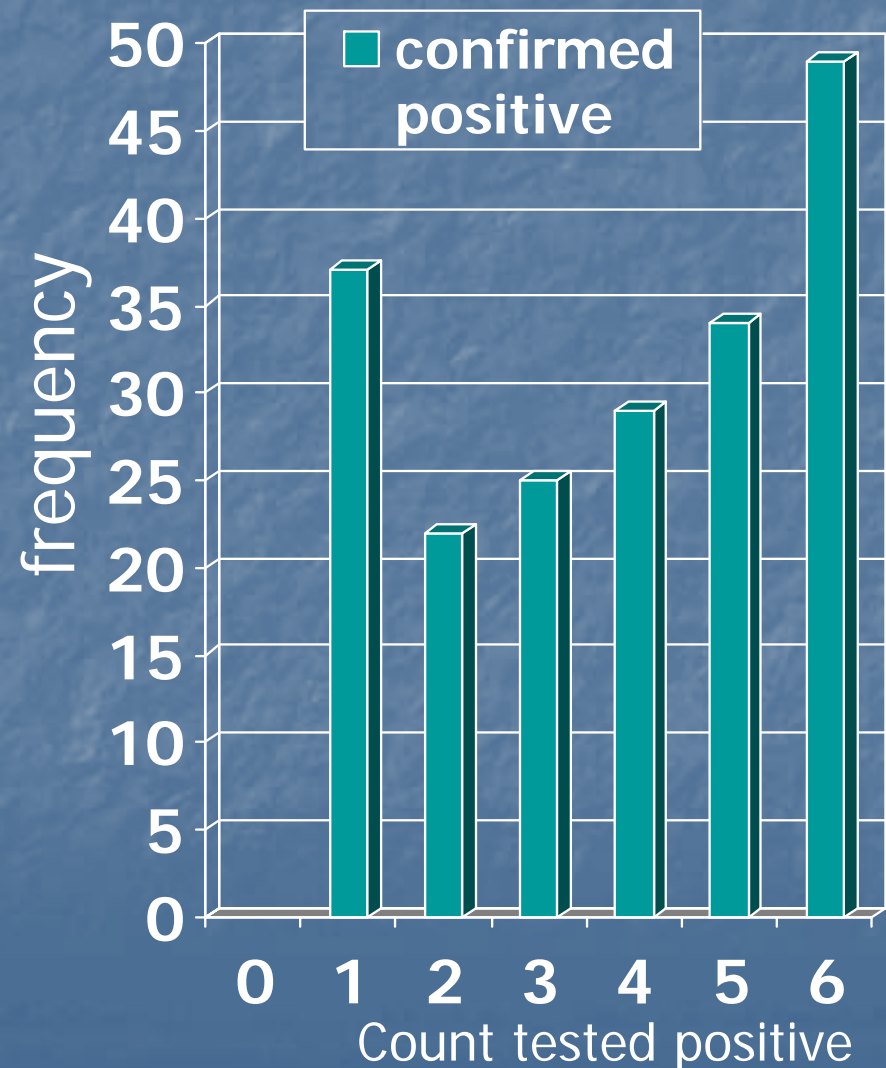
-  House not affected, no cases
-  House affected, no cases
-  House affected, m cases

The counting distribution: a recent example from screening

- Lloyd & Frommer (2004, Applied Statistics) screening for bowel cancer
- 38,000 men screened in Sidney at 6 consecutive days by means of self-tesing for blood in stools
- 3,000 tested positively at least once and cancer status evaluated
- 196 were confirmed positive to have bowel cancer
- How many of 35,000 **unconfirmed** negative have bowel cancer?

The counting distribution: a recent example from screening

- frequency n_0 of those tested negative at all 6 times with bowel cancer is unknown
- an estimate of n_0 might be constructed from the distribution n_1, n_2, n_3, \dots of counts



Simple Distributional Count Models

Poisson (for unobservable counts)

$$f(y, \theta) = e^{-\theta} \theta^y / y! , y = 0, 1, 2 \dots$$

truncated Poisson (for observable counts)

$$f(y, \theta) = \frac{1}{1 - e^{-\theta}} e^{-\theta} \theta^y / y! , y = 1, 2 \dots$$

Predicted Probability of a Zero:

$$p_0 = f(y, \theta) = e^{-\theta}$$

Simple Distributional Count Models

after θ is identified ...

.... probability of a zero count:

$$p_0 = f(y = 0, \theta) = e^{-\theta}$$

$$\Rightarrow \hat{N} = \frac{n}{1 - p_0} = \frac{n}{1 - e^{-\theta}}$$

ML-Estimation in Zero-Truncated Poisson Models

Step 1: suppose \hat{n}_0 would be available

$$\hat{\theta} = \frac{1}{n + \hat{n}_0} \sum_{i=1}^m i n_i$$

Step 2: suppose $\hat{\theta}$ would be available

$$\hat{N} = \frac{n}{1 - p_0} = \frac{n}{1 - e^{-\hat{\theta}}} \Rightarrow \hat{n}_0 = \hat{N} - n = n \frac{e^{-\hat{\theta}}}{1 - e^{-\hat{\theta}}}$$

EM-Algorithm

Step 1 (M-Step): suppose \hat{n}_0 would be available

$$\hat{\theta} = \frac{1}{n + \hat{n}_0} \sum_{i=1}^m i n_i$$

Step 2 (E-Step): suppose $\hat{\theta}$ would be available

$$\hat{n}_0 = E(n_0 | \hat{\theta}; n_1, n_2, \dots) = n \frac{p_0}{1 - p_0} = n \frac{e^{-\hat{\theta}}}{1 - e^{-\hat{\theta}}}$$

ML-Estimation in Zero-Truncated Count Models

general count distribution

$$f(y, \theta), y = 0, 1, 2, \dots$$

assoc. **zero-truncated** distribution

$$\frac{1}{1 - f(0, \theta)} f(y, \theta), y = 1, 2, \dots$$

EM-Algorithm

Step 1 (M-Step): suppose \hat{n}_0 is given:

$$\hat{\theta} = MLE, \text{ based upon } \hat{n}_0, n_1, n_2, \dots$$

Step 2 (E-Step): suppose $\hat{\theta}$ is given:

$$\hat{n}_0 = E(n_0 \mid \hat{\theta}; n_1, n_2, \dots) = n \frac{p_0}{1 - p_0} = n \frac{f(0, \hat{\theta})}{1 - f(0, \hat{\theta})}$$

More flexible and robust approach through mixtures

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

The mixture approach in a nutshell

mixture density:

$$f(y, \theta) = f(y, \lambda_1)q_1 + \dots + f(y, \lambda_k)q_k$$

$f(y, \lambda)$ is component density

(Example: $f(y, \lambda) = e^{-\lambda} \lambda^y / y!$)

$\theta = \begin{pmatrix} \lambda_1 & \dots & \lambda_k \\ q_1 & \dots & q_k \end{pmatrix}$ is mixing distribution

Nested EM-Algorithm

Step 1 (M-Step): suppose \hat{n}_0 is given:

$$\hat{\theta} = MLE \text{ of mixing distribution } \theta = \begin{pmatrix} \lambda_1 & \dots & \lambda_k \\ q_1 & \dots & q_k \end{pmatrix}$$

provided by EM algorithm for mixtures

Step 2 (E-Step): suppose $\hat{\theta}$ is given:

$$\begin{aligned} \hat{n}_0 &= E(n_0 \mid \hat{\theta}; n_1, n_2, \dots) = n \frac{p_0}{1 - p_0} \\ &= n \frac{f(0, \hat{\theta})}{1 - f(0, \hat{\theta})} = n \frac{\hat{q}_1 e^{-\hat{\lambda}_1} + \dots + \hat{q}_k e^{-\hat{\lambda}_k}}{1 - (\hat{q}_1 e^{-\hat{\lambda}_1} + \dots + \hat{q}_k e^{-\hat{\lambda}_k})} \end{aligned}$$

Application: surveillance study on drug use in Thailand

- Ministry of Public Health (Th) collects routinely data on drug use via the ONCB on drug users visiting treatment institutions

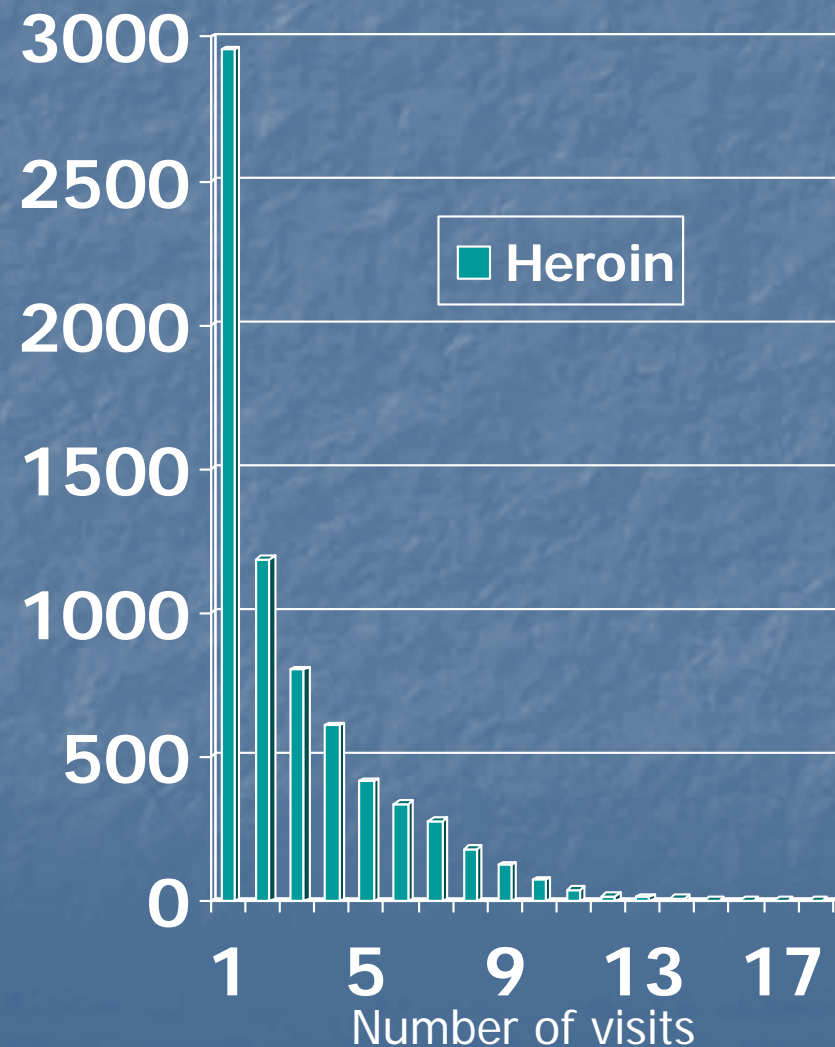
- In a pilot study (Böhning, Busaba, Chukiat et al. 2004 *EUJE*) CR-Poisson mixture model applied to data from 2002 (last quarter)

- Major emphasis on heroin and metamphetamin users



Application: surveillance study on drug use in Thailand

- Count distribution (counting number of visits) for heroin users
- $n = 7,048$ observed heroin users (2001, 4)



Counting contacts to treatment institutions not uncommon

- Previous modelling done primarily by practitioners with publications in
 - Addiction, Addiction Research & Theory, Journal of Drug Issues, Journal of Quantitative Criminology
- Modelling uses primarily simple Poisson
 - simple to understand, to apply and use, and to communicate
 - however: often not appropriate
- better: semi-parametric models for counts such as Poisson mixtures

Some results

- $n=7,048$ (observed)
- $N=17,278$
- $N-n=10,230$ (hidden)
- Ratio:
observed/hidden=0.69

Estimating the Number of Heroin Users:

| k | $\hat{\lambda}_j$ | \hat{q}_j | log-likelih. | AIC | BIC | \hat{N} |
|-----|-------------------------------|------------------------------|--------------|---------------|---------------|-----------|
| 1 | 2,75 | 1,00 | -15462 | -30927 | -30934 | 7543 |
| 2 | 0,88 5,40 | 0,75 0,25 | -13214 | -26434 | -26455 | 10226 |
| 3 | 0,41 2,97 6,80 | 0,69 0,22 0,09 | -13134 | -26279 | -26313 | 13350 |
| 4 | 0,21 2,13 5,84 12,20 | 0,70 0,19 0,10 0,01 | -13120 | -26255 | -26303 | 17278 |

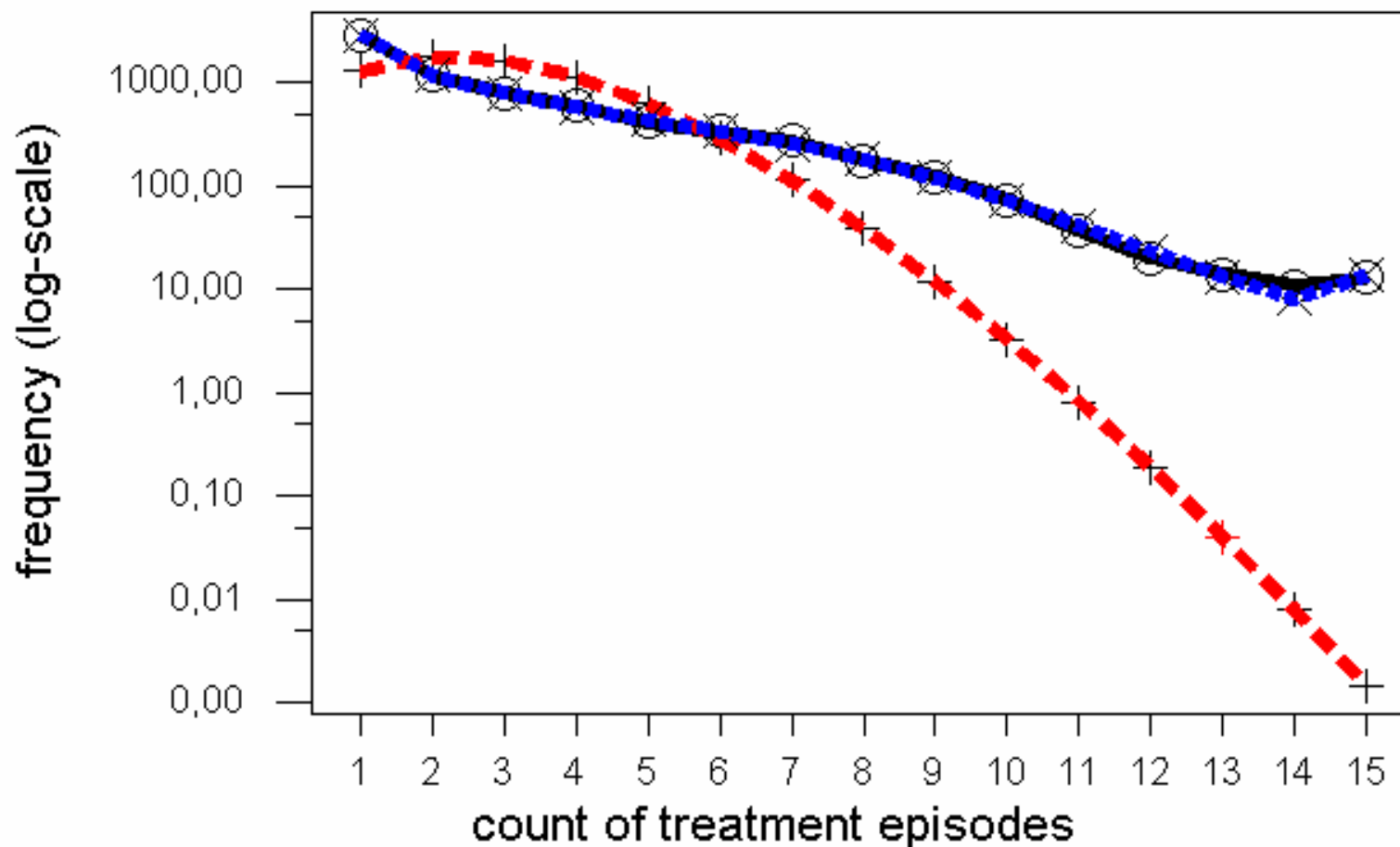
$$AIC = 2 \times \log\text{-likelihood} - (2k - 1)2$$

$$BIC = 2 \times \log\text{-likelihood} - (2k - 1) \log(n)$$

Pilot study for Bangkok, 2001 (4)

count distributions of treatment episodes for heroin users

(empirical = black; simple Poisson = red; Poisson mixture = blue)



take
another
look

Estimating the Number of Heroin Users:

| k | $\hat{\lambda}_j$ | \hat{q}_j | log-likelih. | AIC | BIC | \hat{N} |
|-----|-------------------------------|------------------------------|--------------|---------------|---------------|-----------|
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$$AIC = 2 \times \log\text{-likelihood} - (2k - 1)2$$

$$BIC = 2 \times \log\text{-likelihood} - (2k - 1) \log(n)$$

V. A Monotonicity Property for the Population Size Estimator

proof uses:

- a) Jensen's inequality
- b) mean of the MLE of the mixing distribution = sample mean

Result: Böhning and Schön (*JRSS C* 2004)

\hat{N}_k MLE of population size w.r.t. a truncated Poisson mixture with k components, $k = 1, 2, \dots$ Then:

$$\hat{N}_k \geq \hat{N}_1$$

likely, the **more general statement** is also true:

$$\hat{N}_{k+1} \geq \hat{N}_k$$

A scenic landscape photograph showing a wide river delta with a large body of water in the center, surrounded by dense green forest. In the background, there are several mountain ranges under a clear blue sky. The foreground is filled with lush green trees, and a large tree branch is visible on the left side of the frame.

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Concluding Remarks

Open Problems and Research Questions

- Standard errors and confidence intervals
- Suitable modification of resampling techniques
- Validation studies
- Comparison to other approaches (Pollock-Norris or Zelterman)
- ... Mixtures of binomials

very recent work in perspective

- truncated mixture of Poisson distributions
- or ...
- mixture of truncated Poisson distributions

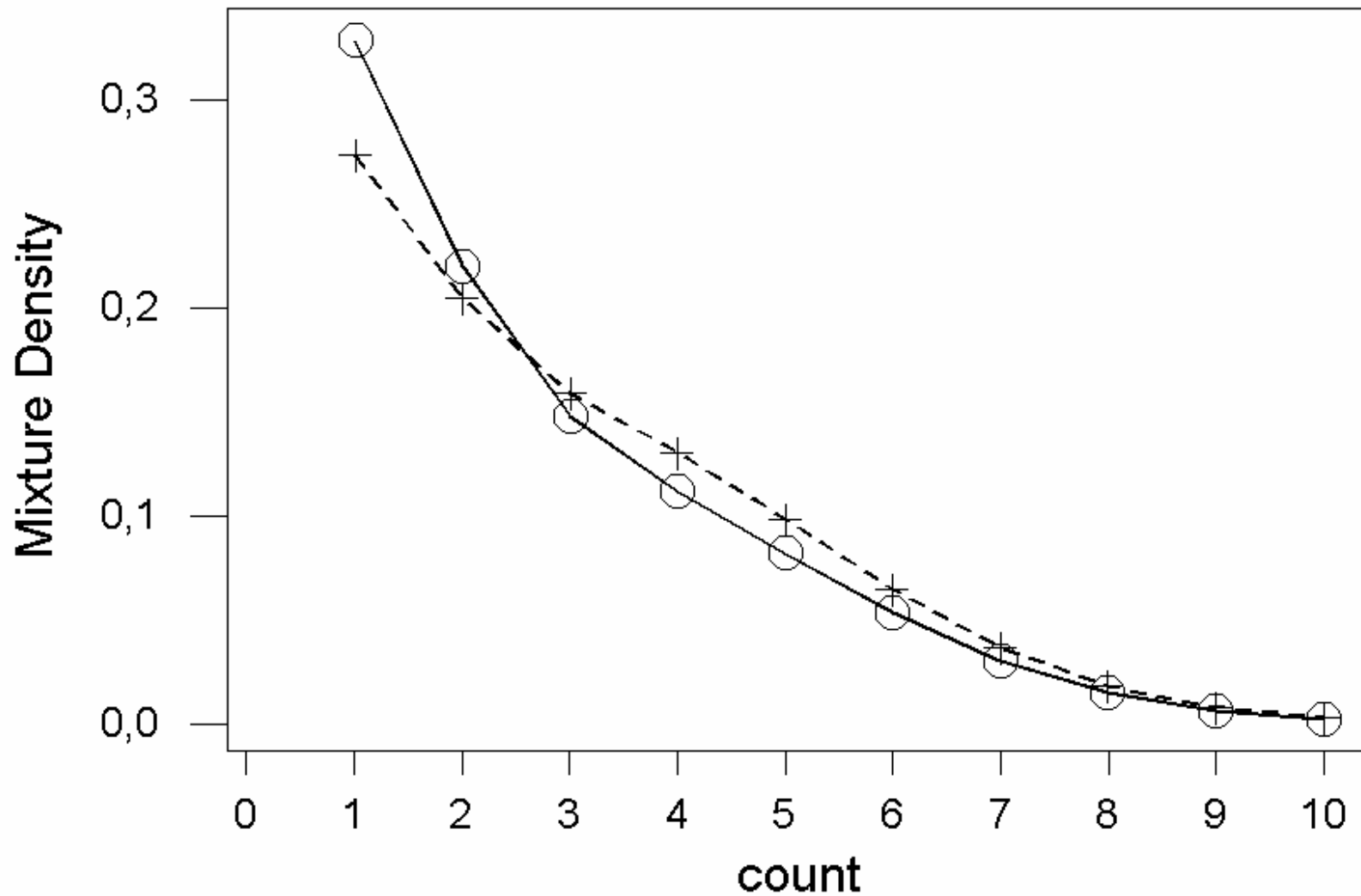
truncated Poisson mixture (dual model)

$$\frac{\sum_{j=1}^k q_j \text{Po}(y, \lambda_j)}{1 - \sum_{j=1}^k q_j \text{Po}(0, \lambda_j)}$$

mixture of truncated Poissons (primal model)

$$\sum_{j=1}^k q_j' \frac{Po(y, \lambda_j')}{1 - Po(0, \lambda_j')}$$

Illustration: dual model (ring) and primal model (+)
use equal weights and component means 1 and 4



truncated Poisson mixture (dual model)

$$\frac{\sum_{j=1}^k q_j \text{Po}(y, \lambda_j)}{1 - \sum_{j=1}^k q_j \text{Po}(0, \lambda_j)}$$

- close to the original problem, easy to understand and to communicate
- But technical difficult, because of **non-linearity**

mixture of truncated Poissons (primal model)

$$\sum_{j=1}^k q_j' \frac{Po(y, \lambda_j')}{1 - Po(0, \lambda_j')}$$

- less close to the original problem
- but convex problem with strong results available on NPMLE and global ML estimation

How are dual and primal model related?

- Böhning and Kuhnert (2005, JASA)
- Both share the same likelihood surfaces
- MLEs can be explicitly transformed into each other
- $\hat{N} = \hat{N}'$

Other areas ongoing interest

- Birth-cohort disease-free with applications to BSE
- Count data modelling with excess zeros
- Mixture models
- Global and reliable algorithms
- ...