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Bartlett and Wald Sequential Hypothesis Testing with Correlated Data

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Introduction



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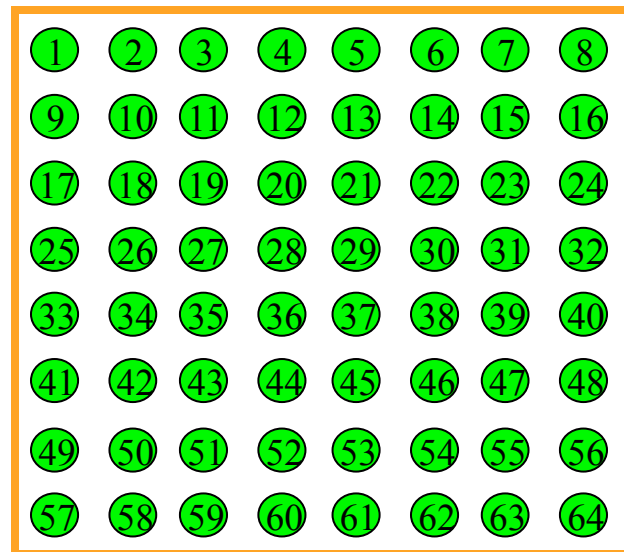


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- It is important to map the pest density in targeting inputs of pesticide
- An understanding of the spatial distribution of the pest is required for accurate pest population density estimation

Example: The citricola scale is known as a soft scale and is considered to be a pest problem for citrus trees in California





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Hypothesis

- If we denote the mean of number of bugs on the twig by μ , the Entomologist want to test the hypothesis:

$$H_0 : \mu = \mu_0 \quad \text{vs.} \quad H_1 : \mu = \mu_1$$

- In classical statistical analyses, the data is collected using a fixed sample size and is then analyzed using the complete dataset.
- What is a cost effective approach to pest assessment?

Sequential Sampling Designs

- Recent studies on sequential sampling application (Shah, Jeske and Luck 2009)
- Can often reach a decision more quickly than using fixed sample size methods
- Considerable savings in terms of human labor and financial budgets



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Wald Sequential Probability Ratio Test (SPRT)

If X_1, \dots, X_n are the counts of the bugs on the twigs over a grove with n trees, X_1, \dots, X_n are from a pdf $f(x_i; \mu)$. At each stage, an observation is taken from the tree and the likelihood ratio

$$\lambda_n = \prod_{i=1}^n \frac{f(x_i; \mu_1)}{f(x_i; \mu_0)}$$

is constructed. Based on the values of the likelihood ratio, one of the following decisions is made (Wald 1947) :

- a) Accept H_0 if $\lambda_n \leq B$
- b) Accept H_1 if $\lambda_n \geq A$
- c) Continue sampling otherwise

Wald's approximation is to choose

$$A = \frac{1 - \beta}{\alpha} \quad B = \frac{\beta}{1 - \alpha}$$

in order to achieve

$$\Pr(\text{Reject } H_0 \mid H_0) = \alpha$$

$$\Pr(\text{Reject } H_1 \mid H_1) = \beta$$



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The Optimality Property of SPRT

Among all tests (sequential or not) for testing $H_0 : \mu = \mu_0$ versus $H_1 : \mu = \mu_1$

$$\Pr(\text{Rejecting } H_0 \mid \mu_0) \leq \alpha$$

$$\Pr(\text{Accepting } H_0 \mid \mu_1) \leq \beta$$

and for which

$$E(N \mid \mu_0) < \infty$$

$$E(N \mid \mu_1) < \infty$$

the SPRT with error probabilities a and b minimizes both $E(N \mid \mu_0)$ and $E(N \mid \mu_1)$

Wald's SPRT is the most popular and used sequential hypothesis test

However, it does not take into account the problem of nuisance parameters



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Bartlett's Sequential Test

Bartlett's Test (Bartlett 1946) is an approximate SPRT of the following problem:

X_1, \dots, X_n are from a pdf $f(x_i; \mu, \gamma)$, where γ is a nuisance parameter, wish to test hypothesis $H_0 : \mu = \mu_0$ vs. $H_1 : \mu = \mu_1$

take one sample at a time and perform the analysis at each step:

The likelihood ratio $\lambda_n = \left\{ \frac{L(\mu_1, \hat{\gamma}_1)}{L(\mu_0, \hat{\gamma}_0)} \right\}$ is calculated

where

$\hat{\gamma}_1$ is the conditional MLE given $\mu = \mu_1$

$\hat{\gamma}_0$ is the conditional MLE given $\mu = \mu_0$



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Bartlett's Sequential Test (Continued)

Based on λ_n value, one of the following decisions is made:

- a) Accept H_0 if $\lambda_n \leq \frac{\beta}{1-\alpha}$
- b) Accept H_1 if $\lambda_n \geq \frac{1-\beta}{\alpha}$
- c) Continue sampling otherwise

where α and β are the proposed type I and type II errors for the test

Sequential Aligned Systematic Sampling Scheme (SEAS)



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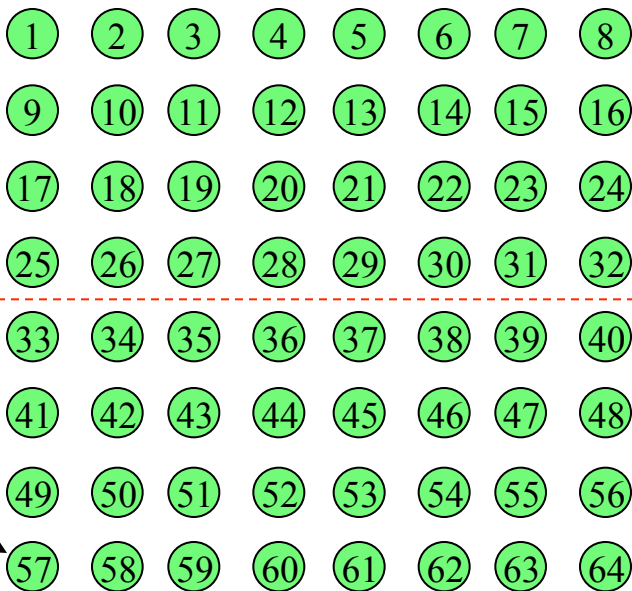
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Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.

Sequential Aligned Systematic Sampling Scheme (SEAS)



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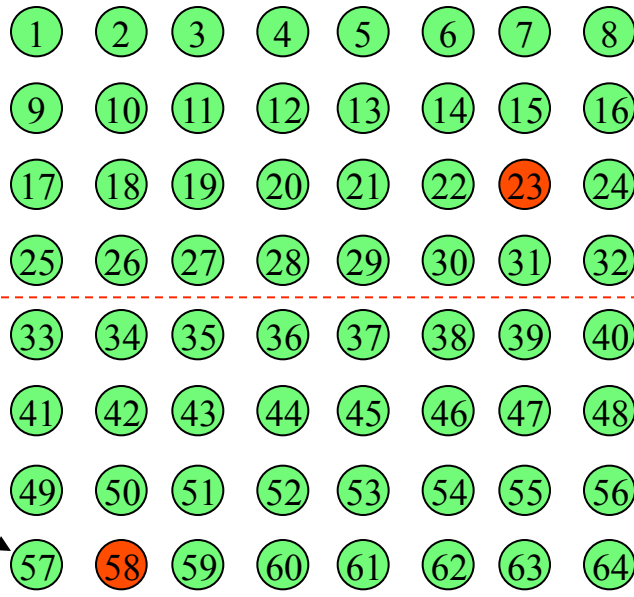
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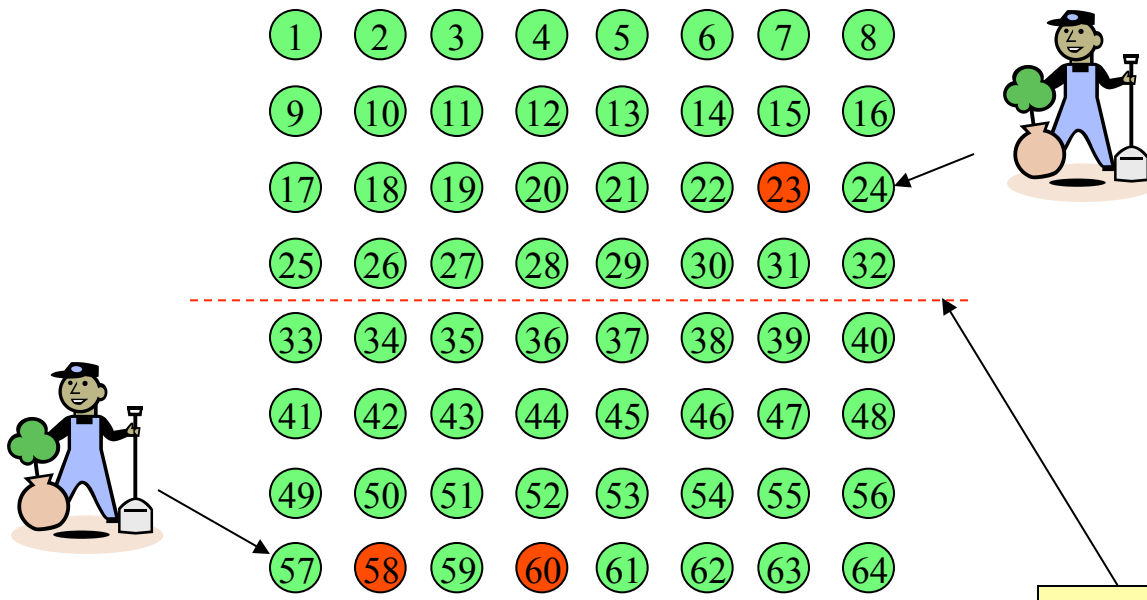


Each person randomly pick a row and sample every other n tress. Every time a new observation is sampled, sequential test is performed.

Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.



Sequential Aligned Systematic Sampling Scheme (SEAS)



Each person randomly pick a row and sample every other n tress. Every time a new observation is sampled, sequential test is performed.

Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.

Sequential Aligned Systematic Sampling Scheme (SEAS)



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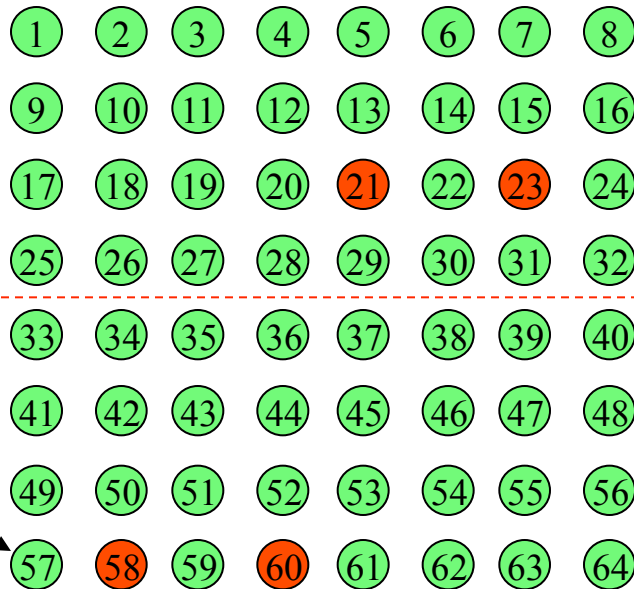
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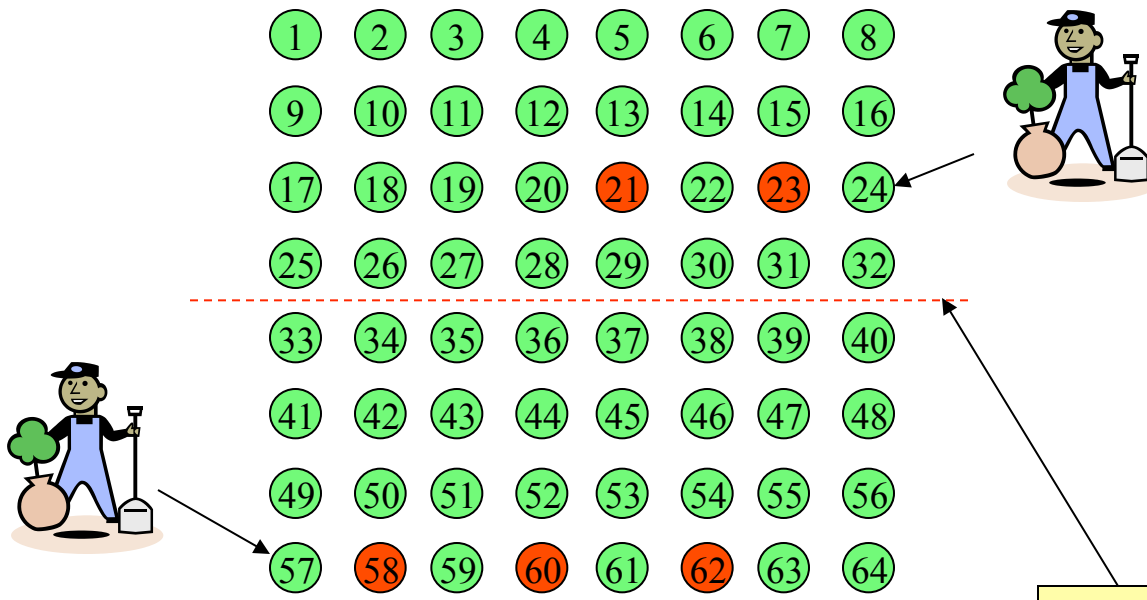


Each person randomly pick a row and sample every other n tress. Every time a new observation is sampled, sequential test is performed.

Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.



Sequential Aligned Systematic Sampling Scheme (SEAS)



Each person randomly pick a row and sample every other n tress. Every time a new observation is sampled, sequential test is performed.

Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.



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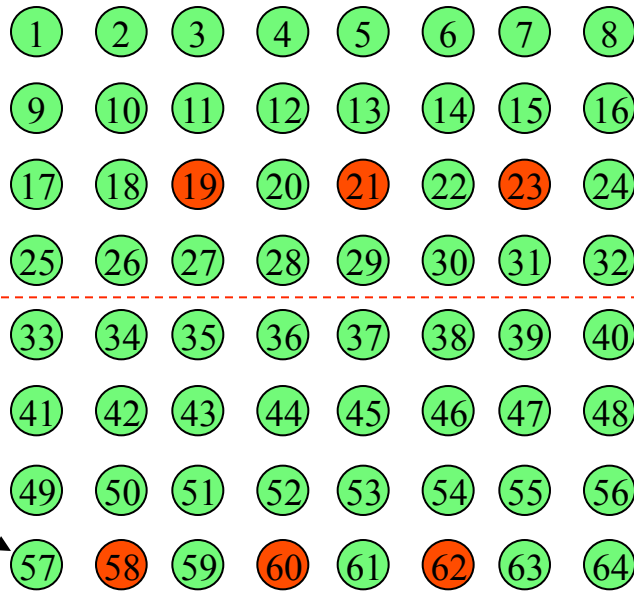


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Sequential Aligned Systematic Sampling Scheme (SEAS)



Sample until we reach the sequential sampling stop lines, or all the other trees have been sampled

Divide the whole grove into two clusters, and two persons sample in each cluster from the opposite directions.

Each person randomly pick a row and sample every other n tress. Every time a new observation is sampled, sequential test is performed.



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Spatial Linear Model

Spatial Linear Model (LM)

$$Z(s_i) = \mu + e(s_i), \quad e(\underline{s}) \sim G(0, \Sigma(\sigma^2, \theta))$$

- $Z(s_i)$ is the logarithm transform of the bug count data
- Linear relationship between $Z(s_i)$ and the mean
- The component of the error term is spatially correlated
- $\{e(\underline{s})\}$ is a Gaussian random field with mean 0 and exponential covariance function modeled as $\sigma^2 \rho_S(s_i - s_j; \theta)$

where $\rho_S(s_i - s_j; \theta) = e^{-\|s_i - s_j\|/\theta}$

s is the location at which Z is observed, a (2×1) vector of coordinates,

$s_i = (x_{i1}, x_{i2})$, $s_j = (x_{j1}, x_{j2})$, and $\|s_i - s_j\| = \sqrt{(x_{i1} - x_{j1})^2 + (x_{i2} - x_{j2})^2}$



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Simulation Study

- During forest insect surveys, the entomologists want to decide whether to spray against a certain defoliator or not.
- 10 or less insects per branch, no big damage will be caused; 20 or more, need to spray
- Assume the original data follows lognormal distribution, then the log transformed data will be normal distributed. Hypothesis to be tested:

$$\mu_0 = 2.2 \text{ against } \mu_1 = 2.9$$

- Simulate normal data on a 30 by 30 grove, with exponential spatial covariance with $\sigma^2 = 0.22$ and $\theta = 5$
- Bartlett sequential tests are performed based on SEAS sampling with maximum 210 trees
- The result is based on 1000 simulations for each value of u

Simulation Result



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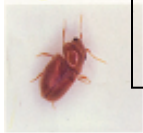
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μ	Conditional OC	Conditional ASN	Nonstop
1.85	1.00	31.84	115
2.03	1.00	18.22	38
2.20	0.98	18.88	48
2.38	0.88	21.39	158
2.55	0.49	25.12	277
2.73	0.12	21.51	153
2.90	0.03	17.77	34
3.08	0.00	21.74	34
3.25	0.00	32.96	123

Nominal Operating Characteristics value to be 0.9 and 0.1

Average Sample Number increases as the mean is further away from the true

Large number of nonstop cases

There seems to be room for improvement of the model



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Transformed Bartlett Test and Wald Test

Transformation:

$Z_{n \times n}$ denote spatial log count data, where $Z_{n \times n} \sim MVN(\mu_{1_{n \times 1}}, \Sigma(\sigma^2, \theta))$

$$\Sigma(\sigma^2, \theta) = \sigma^2 \rho(\theta) = \sigma^2 \Gamma'(\theta) \Gamma(\theta)$$

Where $\Gamma(\theta)$ is the Cholesky factorization of $\rho(\theta)$

$$\Gamma'(\theta)^{-1} Z \sim MVN(\Gamma'(\theta)^{-1} \mu_{1_{n \times 1}}, \sigma^2 I_{n \times n})$$

Transformed Bartlett Sequential Test is based on:

$$\Gamma'(\hat{\theta})^{-1} Z \sim MVN(\Gamma'(\hat{\theta})^{-1} \mu_{1_{n \times 1}}, \sigma^2 I_{n \times n})$$

Transformed Wald Sequential Test is based on:

$$\frac{1}{\sigma} \Gamma'(\hat{\theta})^{-1} Z \sim MVN\left(\frac{1}{\sigma} \Gamma'(\hat{\theta})^{-1} \mu_{1_{n \times 1}}, I_{n \times n}\right)$$

Where $\hat{\theta}$ and $\hat{\sigma}^2$ denote the unconditional MLE of θ and σ^2



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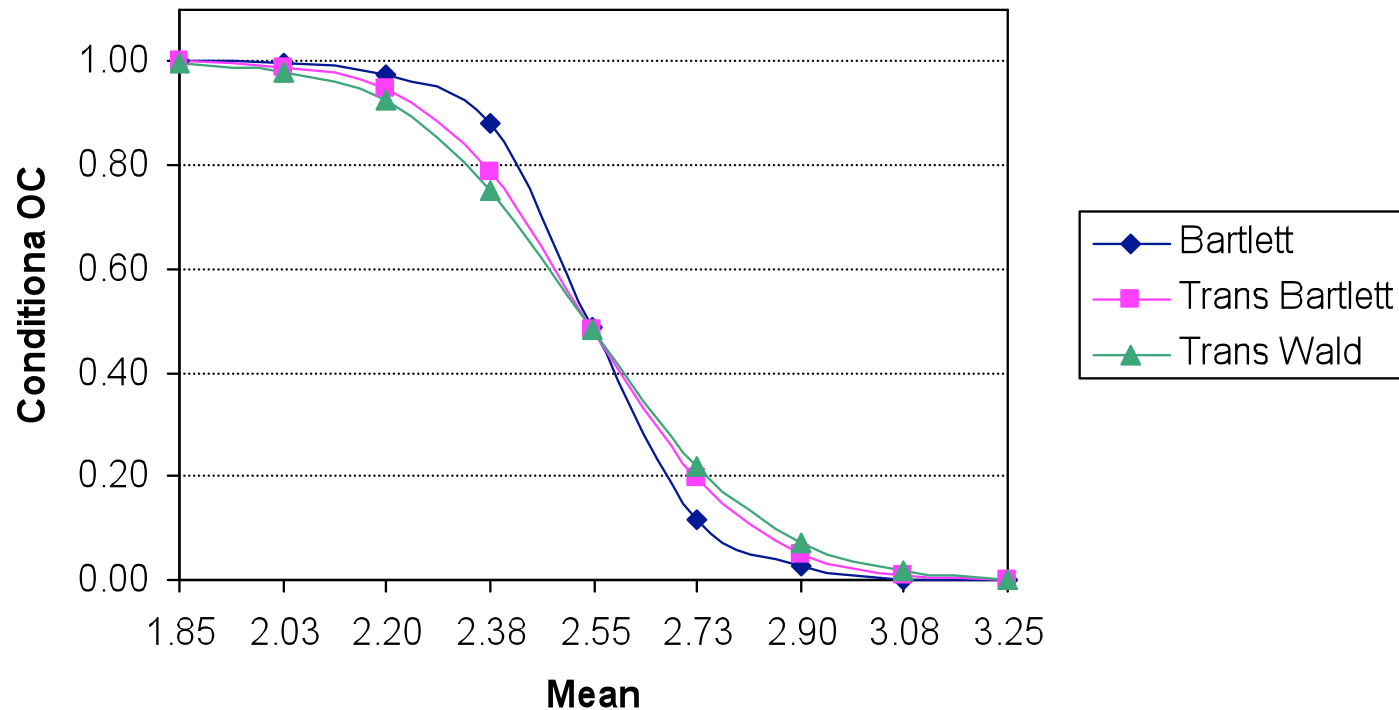
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Simulation Results of Operating Characteristics



All of the three tests have conservative OC values

Transformed Wald test has the OC values closest to the nominal values



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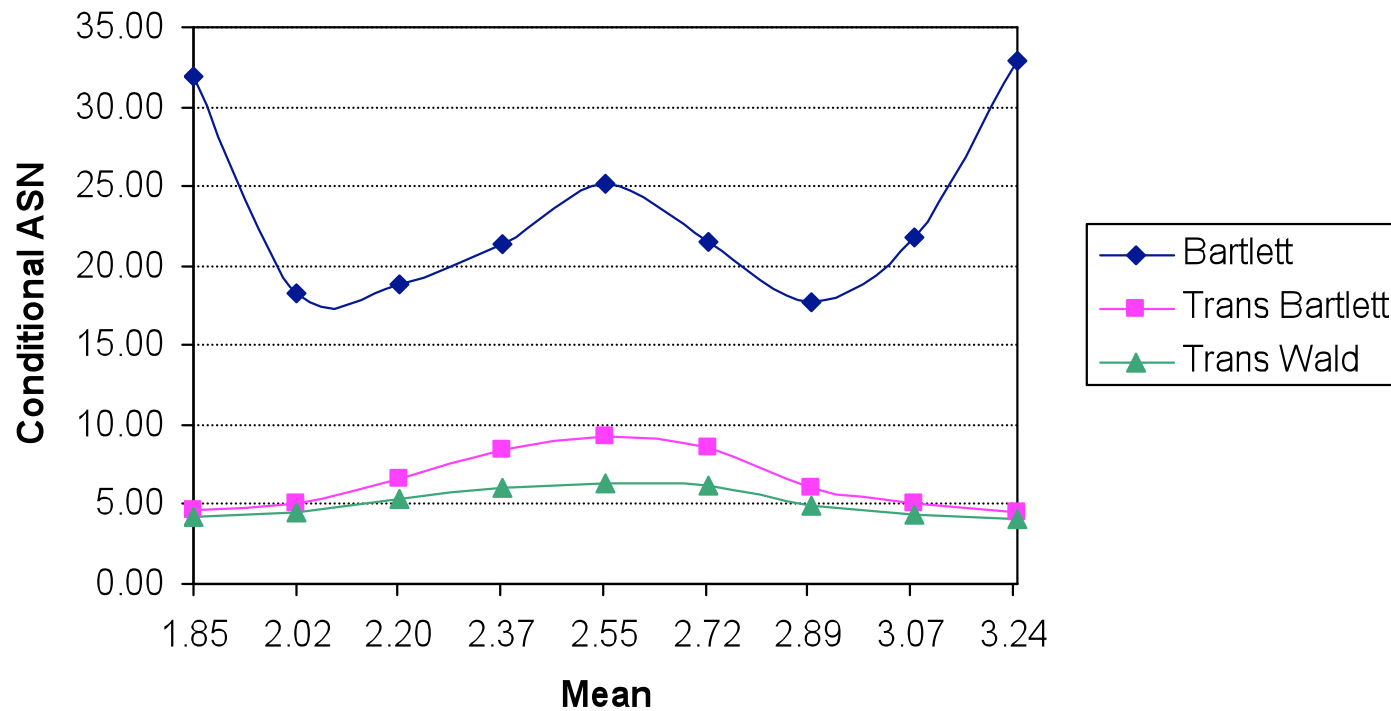
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Simulation Results of Average Sample Number



Bartlett test has the largest average sample size

Transformed Wald test has the smallest sample size



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Spatial Generalized Linear Mixed Model (GLMM)

The count data are conditionally dependent on an underlying, smooth, spatial process $\{G(\underline{s}) : \underline{s} \in D\}$

$$\mu(\underline{s}) = E[Z(\underline{s}) | G(\underline{s})]$$

$$g(\mu(\underline{s})) = X(\underline{s})\beta + G(\underline{s})$$

$G(\underline{s})$ is the random effects at a set of locations \underline{s} in the Gaussian random field with some spatial covariance function $\sigma^2 \rho(s_i - s_j, \theta)$.

At any location s , $G(s)$ represents a random addition to the intercept that varies with spatial location (Christensen and Waagepetersen 2001)



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Spatial Poisson Log linear Mixed Model

Let $Z(s)$ denote the number of bugs we observed at a single location s ,

$$Z(s) \mid G(s) \sim \text{Poisson}(\lambda(s))$$

Consider about a set of locations \underline{s} , we have:

$$\log(\lambda(\underline{s})_{n \times 1}) = \mu \mathbf{1}_{n \times 1} + G(\underline{s})_{n \times 1},$$

where $G(\underline{s}) \sim MVN(0, \Sigma(\sigma^2, \theta))$, the covariance function Σ is modelled as exponential covariance structure:

$$\sigma^2 \rho(s_i - s_j; \theta) = \sigma^2 \exp^{-\|s_i - s_j\|/\theta} \quad \text{where } s_i = (x_{i1}, x_{i2}), s_j = (x_{j1}, x_{j2}),$$

$$\|s_i - s_j\| = \sqrt{(x_{i1} - x_{j1})^2 + (x_{i2} - x_{j2})^2}$$

Hypothesis



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For bug count data, it is easy to show that e^μ is the median of the mean of the number of bugs observed. Therefore, it will be very meaningful to test hypothesis about e^μ .

Decision of pesticide application can be based on:

$$\left\{ \begin{array}{l} H_0 : e^\mu = m' \\ H_1 : e^\mu = m'' \end{array} \right\} \text{ (testing the median of the mean of the number of bugs)}$$

We want to test the same hypothesis in previous forest insect surveys example.

Decision is based on the number of insects per branch:

$$\left\{ \begin{array}{l} H_0 : e^\mu = 10 \\ H_1 : e^\mu = 20 \end{array} \right\} \text{ (not spray 10 or less, spray 20 or more)}$$



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Pseudo Likelihood Approach

In order to adapt Bartlett Test to GLMM model, we need to write out the likelihood function of the spatial negative binomial loglinear mixed model:

$$L(Z(\underline{s}), \mu, \sigma^2, \theta) = \int f(Z(\underline{s}), g(\underline{s}), \mu, \sigma^2, \theta) dg(\underline{s})$$

The integral over the random variables in $G(\underline{s})$ (an n -dimensional problem) is our computational challenge:

- Gaussian-Hermite quadrature is not likely to be feasible for our model
- MCEM algorithm with MCMC sampling is computationally very expensive
- Pseudo-likelihood has been successful for estimating parameters in GLMM (Wolfinger and O'Connell, 1993). We propose to use pseudo likelihood approach in conjunction with sequential test.

Simulation Study



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μ	Conditional OC	Conditional ASN	Nonstop
1.95	1.00	36.71	80
2.13	0.98	34.16	130
2.30	0.93	34.56	232
2.48	0.72	38.56	336
2.65	0.38	40.40	344
2.83	0.12	37.71	239
3.00	0.03	37.02	155
3.18	0.01	38.91	142
3.35	0.01	41.27	176

Nominal Operating Characteristics value to be 0.9 and 0.1

Average Sample Number increases as the mean is further away from the true

Large number of nonstop cases

- Simulate count data on a 30 by 30 grove, with exponential spatial covariance with $\sigma^2 = 0.5$ and $\theta = 5$
- Bartlett sequential tests of hypothesis $H_0 : \mu = 2.3$ vs. $H_1 : \mu = 3$ are performed based on SEAS sampling with maximum 210 trees
- The output is based on 1000 simulations for each value of μ



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Transformed Wald Test

Transformation

In the last step of pseudo likelihood estimation, the pseudo data

$$\underline{V} \sim \text{MVN}(\underline{\mu}, \Sigma^*) \text{ with } \Sigma^* = \begin{pmatrix} e^{\hat{\lambda}_1} & & 0 \\ & \ddots & \\ 0 & & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} + \Sigma(\hat{\sigma}^2, \hat{\theta})$$

$$\text{denote } \Sigma^*(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta}) = \Gamma'(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})\Gamma(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})$$

Where $\Gamma(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})$ is the Cholesky factorization of $\Sigma^*(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})$

Transformed Wald Sequential Test is based on:

$$\Gamma'(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})^{-1} \underline{V} \sim \text{MVN}(\Gamma'(\hat{\lambda}, \hat{\sigma}^2, \hat{\theta})^{-1} \underline{\mu}, I_{n \times n})$$

Where $\hat{\lambda}, \hat{\sigma}^2, \hat{\theta}$ denote the pseudo likelihood estimate of λ, σ^2 , and θ



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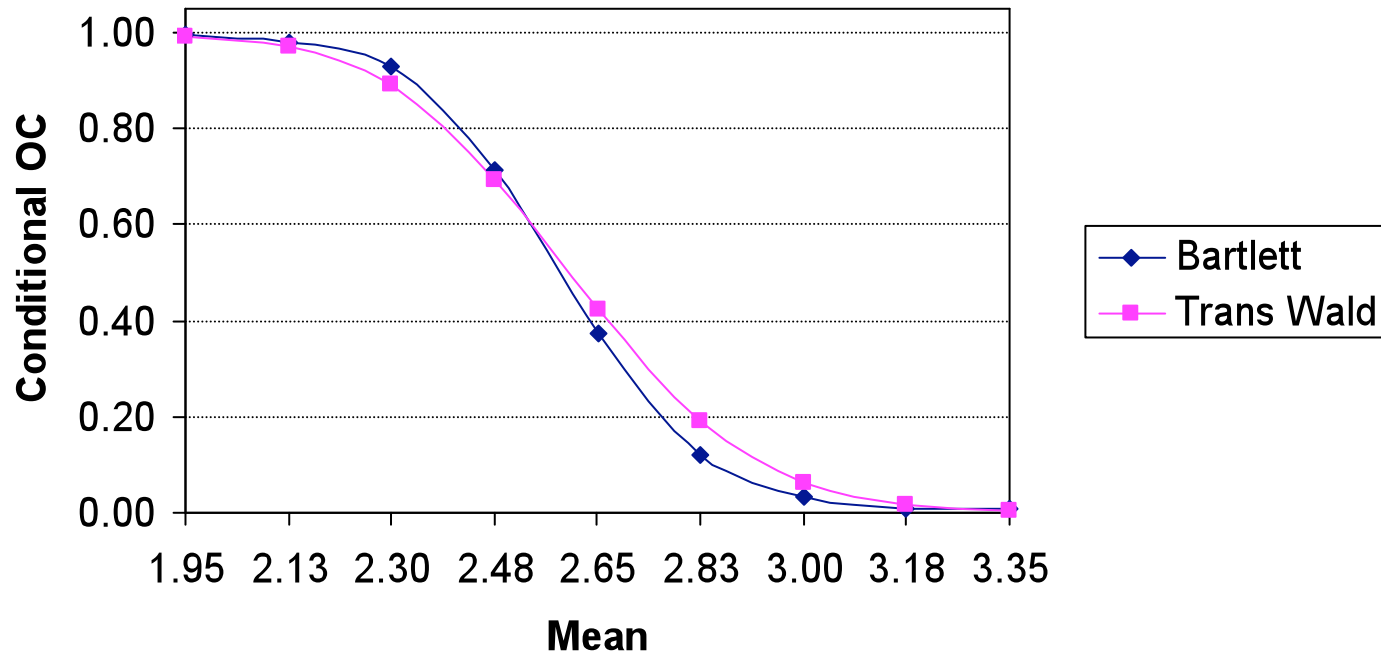
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Simulation Results of Operating Characteristics



Similar with the linear mixed model case, transformed Wald test has the OC values closest to the nominal values



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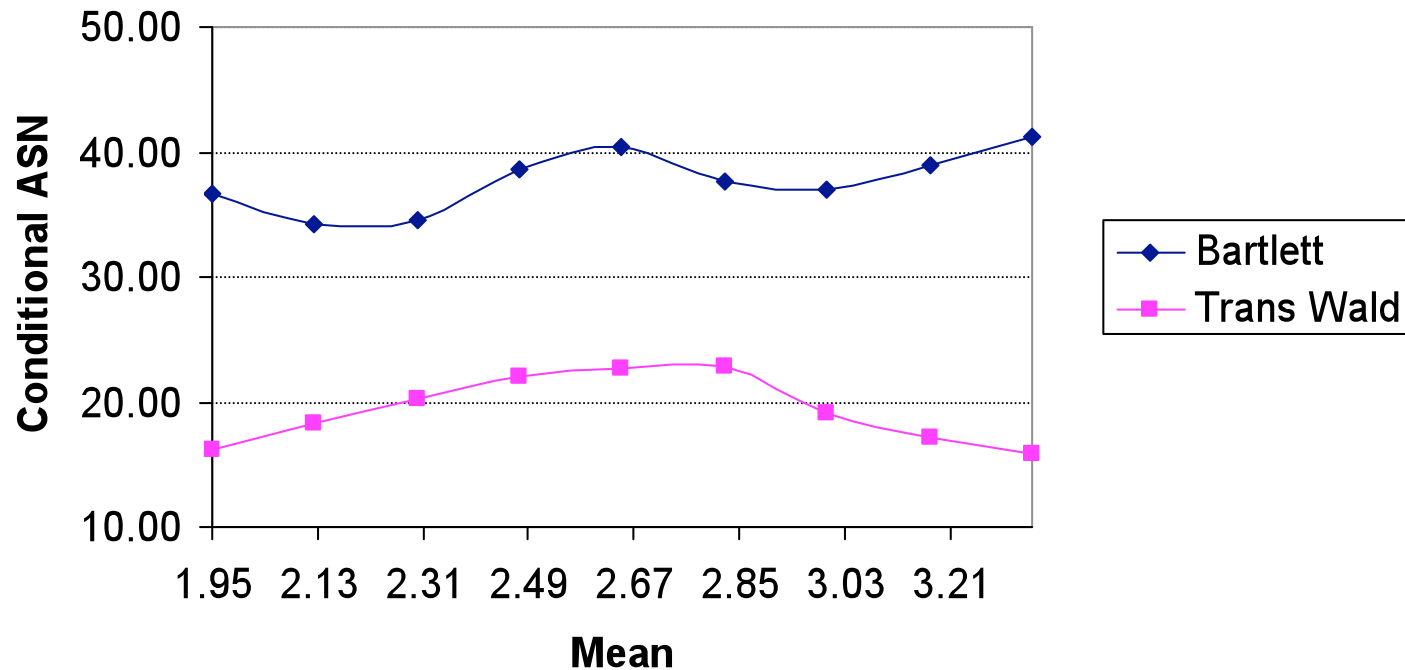
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Simulation Results of Average Sample Number



The transformed Wald test solves the tails problem and also achieve smaller ASN values



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Conclusion and Future Work

Conclusion

- The transformed Wald procedure has satisfactory OC curve and the best ASN curve

Future Work

- Consider fixed sample size determination in the spatial GLMM context
- Consider adapting close boundary sequential hypothesis test to spatial models
- Consider about model with covariates and other spatial covariance structure

References



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Thank You!



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Pseudo Likelihood Approach

In order to adapt sequential hypothesis test to GLMM model, we use pseudo model to approximate GLMM (Wolfinger and O'Connell, 2003)

Consider a data vector of Z length n satisfying:

$$\underline{Z} = \underline{\lambda} + \underline{e} \text{ with link function: } \log(\underline{\lambda}) = \underline{\mu} + \underline{G}$$

$$G(s) \sim MVN(0, \Sigma(\sigma^2, \theta))$$

e is a vector of unobserved errors with $E[\underline{e} | \underline{G}] = 0, Var[\underline{e} | \underline{G}] = \underline{\lambda}$

Let $\hat{\underline{\mu}}$ and $\hat{\underline{G}}$ be the known estimates of $\underline{\mu}$ and \underline{G} , and $\hat{\underline{\lambda}} = \exp(\hat{\underline{\mu}} + \hat{\underline{G}})$

1. Analytic Approximation

Let \tilde{e} denote the Taylor series approximation to $\underline{e} = \underline{Z} - \underline{\lambda}$, then

$$\tilde{e} = \underline{Z} - \hat{\underline{\lambda}} - (g^{-1})'(\hat{\underline{\mu}} + \hat{\underline{G}})(\underline{\mu} - \hat{\underline{\mu}} + \underline{G} - \hat{\underline{G}})$$

Where $(g^{-1})'(\hat{\underline{\mu}} + \hat{\underline{G}})$ is a diagonal matrix with elements consisting of evaluations of the first derivative of g^{-1}



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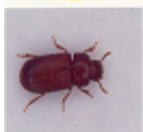
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Pseudo Likelihood Approach (Cont)

2. Probability Approximation

Approximate $\tilde{z} | \tilde{G}$ with a Gaussian distribution having the same moments as $z | \tilde{G}$:

$$\tilde{z} | \tilde{G} \sim \text{MVN}(0, \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix})$$

3. Analytic Approximation

Substitute $\hat{\lambda}$ for λ in the variance matrix, then

$$\underline{z} - \hat{\lambda} - (g^{-1})'(\hat{\mu} + \hat{G})(\underline{\mu} - \hat{\mu} + \underline{G} - \hat{G}) \sim \text{MVN}(0, \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix})$$

Since $(g^{-1})'(\hat{\mu} + \hat{G}) = \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}$

$$\begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} (\underline{z} - \hat{\lambda}) - (\underline{\mu} - \hat{\mu} + \underline{G} - \hat{G}) \sim \text{MVN}(0, \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1})$$



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Pseudo Likelihood Approach (Cont)

Conditional on G :

$$\hat{\mu} + \hat{G} + \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} (\underline{Z} - \hat{\lambda}) \sim \text{MVN}(\underline{\mu} + \underline{G}, \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1})$$

$$\text{Define } \underline{V} = \hat{\mu} + \hat{G} + \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} (\underline{Z} - \hat{\lambda})$$

then,

$\underline{V} \sim \text{MVN}(\underline{\mu}, \Sigma^*)$ is the pseudo data with

$$\Sigma^* = \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} + \Sigma(\sigma^2, \theta)$$

Now the parameters can be estimated based on the Linear Mixed Model (LMM)

Iteration Algorithms

1. Obtain an initial estimate of λ , $\hat{\lambda}$.

2. Compute pseudo data V_{\sim}

$$V_{\sim} = \hat{\mu} + \hat{G} + \begin{pmatrix} e^{\hat{\lambda}_1} & \cdots & 0 \\ 0 & \cdots & e^{\hat{\lambda}_n} \end{pmatrix}^{-1} (Z - \hat{\lambda})$$

3. Fit a linear mixed model with response variable V_{\sim} and obtain ML estimations of unknown parameters

4. Compare the old estimates of the unknown parameters (σ^2 and θ) with the new ones. If the difference is sufficiently small, then stop; otherwise, go to the next step

5. Solve the mixed equations for $\hat{\mu}$ and \hat{G}

6. compute the new estimate of λ by substituting $\hat{\mu}$ and \hat{G} in

$$\hat{\lambda} = \exp(\hat{\mu} + \hat{G}) \text{ and go to step 2}$$



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