Chain Binomial Models
and
Binomial Autoregressive Processes

TECHNISCHE UNIVERSITÄT DARMSTADT

Christian H. Weiß

Department of Mathematics,

Darmstadt University of Technology

Fachbereich Mathematik

Philip K. Pollett

Department of Mathematics,

University of Queensland

Background

This talk is based on the article

Weiß, C.H., Pollett, P.K. (2011).
Chain binomial models and binomial autoregressive processes.
Biometrics, to appear.

All references mentioned in this talk
correspond to the references in this article.

Binomial AR(1) Processes

Review & New Results

Binomial AR(1) Processes

Gaussian AR(1) process:

$Z_{t+1} \ = \ \rho \cdot Z_t + \epsilon_t,$ where (ϵ_t) i.i.d. N$(\mu_\epsilon, \sigma_\epsilon^2)$.

Discrete-valued counterpart to multiplication:

Binomial thinning operator (Steutel & van Harn, 1979):

$$p \circ x := \sum_{i=1}^{x} y_i, \qquad \text{where } y_i \text{ are i.i.d. Bin}(1, p),$$

i. e., $p \circ x \ \sim \ $ Bin(x, p) and has range $\{0, \ldots, x\}$.

Binomial AR(1) Processes

Fix $N \in \mathbb{N}$.

Parameters $\pi \in (0;1)$, $\quad \rho \in \Big(\max\{-\frac{\pi}{1-\pi}, -\frac{1-\pi}{\pi}\}\ ;\ 1\Big)$.

Define thinning probabilities $\beta := \pi\,(1-\rho)$ and $\alpha := \beta + \rho$.

Binomial AR(1) process $(n_t)_{\mathbb{N}_0}$ with range $\{0,\ldots,N\}$ defined by the recursion

$$n_{t+1} \;=\; \underbrace{\alpha \circ n_t}_{\text{survivors}} + \underbrace{\beta \circ (N - n_t)}_{\text{newly occupied}} \qquad \text{for } t \geq 0,$$

thinnings performed independently, independent of $(n_s)_{s<t}$.

(McKenzie, 1985)

Binomial AR(1) Processes

Well-known properties:

Ergodic Markov chain, transition probabilities

$$P(k|l) \;:=\; P(n_{t+1}=k \mid n_t=l) \;=$$

$$\sum_{m=\max\{0,k+l-N\}}^{\min\{k,l\}} \binom{l}{m}\binom{N-l}{k-m}\,\alpha^m(1-\alpha)^{l-m}\,\beta^{k-m}(1-\beta)^{N-l+m-k},$$

uniquely determined stationary distribution: $\text{Bin}(N,\pi)$.

Autocorrelation function: $\rho(k)=\rho^k$ for $k\geq 0$.

Regression properties:

$$\begin{aligned}\mathbb{E}(n_{t+1}\mid n_t) \;&=\; \rho\cdot n_t \;+\; N\beta,\\ \text{Var}(n_{t+1}\mid n_t) \;&=\; \rho(1-\rho)(1-2\pi)\cdot n_t \;+\; N\beta(1-\beta).\end{aligned}$$

Binomial AR(1) Processes

Parameter estimation from $n_0, \ldots, n_T$:

Maximum Likelihood (ML) approach:

$$(\hat{\pi}_{\mathrm{ML}}, \hat{\rho}_{\mathrm{ML}}) \ := \ \arg\max_{(\pi,\rho)} \ \ln L(\pi,\rho), \qquad \text{where}$$

$$L(\pi,\rho) \ := \ P_{\pi,\rho}(n_0) \cdot \prod_{t=1}^{T} \ P_{\pi,\rho}(n_t|n_{t-1}).$$

Conditional Least Squares (CLS) approach:

$$(\hat{\pi}_{\mathrm{CLS}}, \hat{\rho}_{\mathrm{CLS}}) \ := \ \arg\min_{(\pi,\rho)} \ S(\pi,\rho), \qquad \text{where}$$

$$S(\pi,\rho) \ := \ \sum_{t=1}^{T} \ \left\{n_t - \mathbb{E}_{\pi,\rho}(n_t \mid n_{t-1})\right\}^2.$$

Binomial AR(1) Processes

h-step regression properties:

Define $\beta_h = \pi(1-\rho^h)$ and $\alpha_h = \beta_h + \rho^h$ for $h \geq 1$.

Then

$$P^{(h)}(k|l) \;:=\; P(n_{t+h}=k \mid n_t = l) \;=\;$$

$$\sum_{m=\max\{0,k+l-N\}}^{\min\{k,l\}} \binom{l}{m}\binom{N-l}{k-m}\,\alpha_h^m(1-\alpha_h)^{l-m}\,\beta_h^{k-m}(1-\beta_h)^{N-l+m-k},$$

$$\mathbb{E}(n_{t+h} \mid n_t) \;=\; \rho^h\cdot n_t \;+\; N\beta_h,$$

$$\mathrm{Var}(n_{t+h} \mid n_t) \;=\; \rho^h(1-\rho^h)(1-2\pi)\cdot n_t \;+\; N\beta_h(1-\beta_h).$$

Proof: See article, Section 2.

Binomial AR(1) Processes

Application:

Parameter estimation from incomplete data $n_{t_0}, \ldots, n_{t_K}$:

Modified ML approach:

$$(\hat{\pi}_{\mathrm{ML}}, \hat{\rho}_{\mathrm{ML}}) \;:=\; \arg\max\nolimits_{(\pi,\rho)} \;\ln \tilde{L}(\pi,\rho), \qquad \text{where}$$

$$\tilde{L}(\pi,\rho) \;:=\; P_{\pi,\rho}(n_{t_0}) \cdot \prod\nolimits_{k=1}^{K} \; P_{\pi,\rho}^{(t_k - t_{k-1})}(n_{t_k} | n_{t_{k-1}}).$$

Modified CLS approach:

$$(\hat{\pi}_{\mathrm{CLS}}, \hat{\rho}_{\mathrm{CLS}}) \;:=\; \arg\min\nolimits_{(\pi,\rho)} \;\tilde{S}(\pi,\rho), \qquad \text{where}$$

$$\tilde{S}(\pi,\rho) \;:=\; \sum\nolimits_{k=1}^{K} \; \big\{ n_{t_k} - \mathbb{E}_{\pi,\rho}(n_{t_k} \mid n_{t_{k-1}}) \big\}^2.$$

Binomial AR(1) Processes

Normal Approximation for Large N:

Let $Z_t^N = \sqrt{N}(n_t/N - \pi)$. If $Z_0^N \overset{\mathsf{D}}{\to} z_0$,

(Z_t^N) converges weakly to Gaussian AR(1) process (Z_t), defined by

$$Z_{t+1} \;=\; \rho \cdot Z_t + \epsilon_t, \qquad\qquad Z_0 = z_0,$$

with (ϵ_t) i.i.d. $\mathsf{N}\big(0,\ \pi(1-\pi)(1-\rho^2)\big)$.

Proof: See article, Section 4.

Binomial AR(1) Processes

Application:

Approximate (n_t/N) by Gaussian AR(1) model

$$X_t - \pi \;=\; \rho\cdot(X_{t-1} - \pi) + \epsilon_t, \quad \text{where } \epsilon_t \sim \mathsf{N}\Big(0,\ \tfrac{\pi(1-\pi)}{N}(1-\rho^2)\Big).$$

Examples:

- Simplified asymptotics of CLS estimators (see article, Web Appendix B),
- apply tests for stationarity/unit roots originally developed for Gaussian AR(1) model (see article, Section 5).

Chain Binomial Population Models

Background & Relations

Chain Binomial Population Models

Metapopulation = "population of populations" (Hanski & Gilpin, 1991), consists of N habitat patches, which are either occupied or not.

Example: N islands, occupied by certain species.

Metapopulation dynamics = behaviour over time.

We assume successive phases of inflation and deflation, e. g., patch colonisation and extinction.

Chain Binomial Population Models

Metapopulation structure may be hierarchical, e. g.,

large central population

surrounded by N small local populations

→ **mainland-island model** (Hanski & Gilpin, 1991).

Mainland never suffers extinction,

islands may become extinct.

Mainland is source of colonists for islands.

Chain Binomial Population Models

EC model: census after colonisation phases, i. e., first extinction, then (re-)colonisation, then census.

CE model: vice versa.

Chain-binomial models:

EC model:

$$n_{t+1} \overset{\mathsf{D}}{=} \tilde{n}_t + \mathsf{Bin}(N - \tilde{n}_t, c) \qquad \tilde{n}_t \overset{\mathsf{D}}{=} n_t - \mathsf{Bin}(n_t, e);$$

CE model:

$$n_{t+1} \overset{\mathsf{D}}{=} \tilde{n}_t - \mathsf{Bin}(\tilde{n}_t, e) \qquad \tilde{n}_t \overset{\mathsf{D}}{=} n_t + \mathsf{Bin}(N - n_t, c).$$

Patches go extinct independently, probability $0 < e < 1$.

Patches are colonised independently,
with same probability $0 < c < 1$ because of mainland.

Relation to binomial AR(1) models:

$$n_{t+1} \overset{\mathsf{D}}{=} \alpha \circ n_t + \beta \circ (N - n_t) \quad \text{for } t \geq 0,$$

where α and β are given by

EC model: $\alpha = 1 - e(1-c)$, $\beta = c$.

CE model: $\alpha = 1 - e$, $\beta = (1-e)c$.

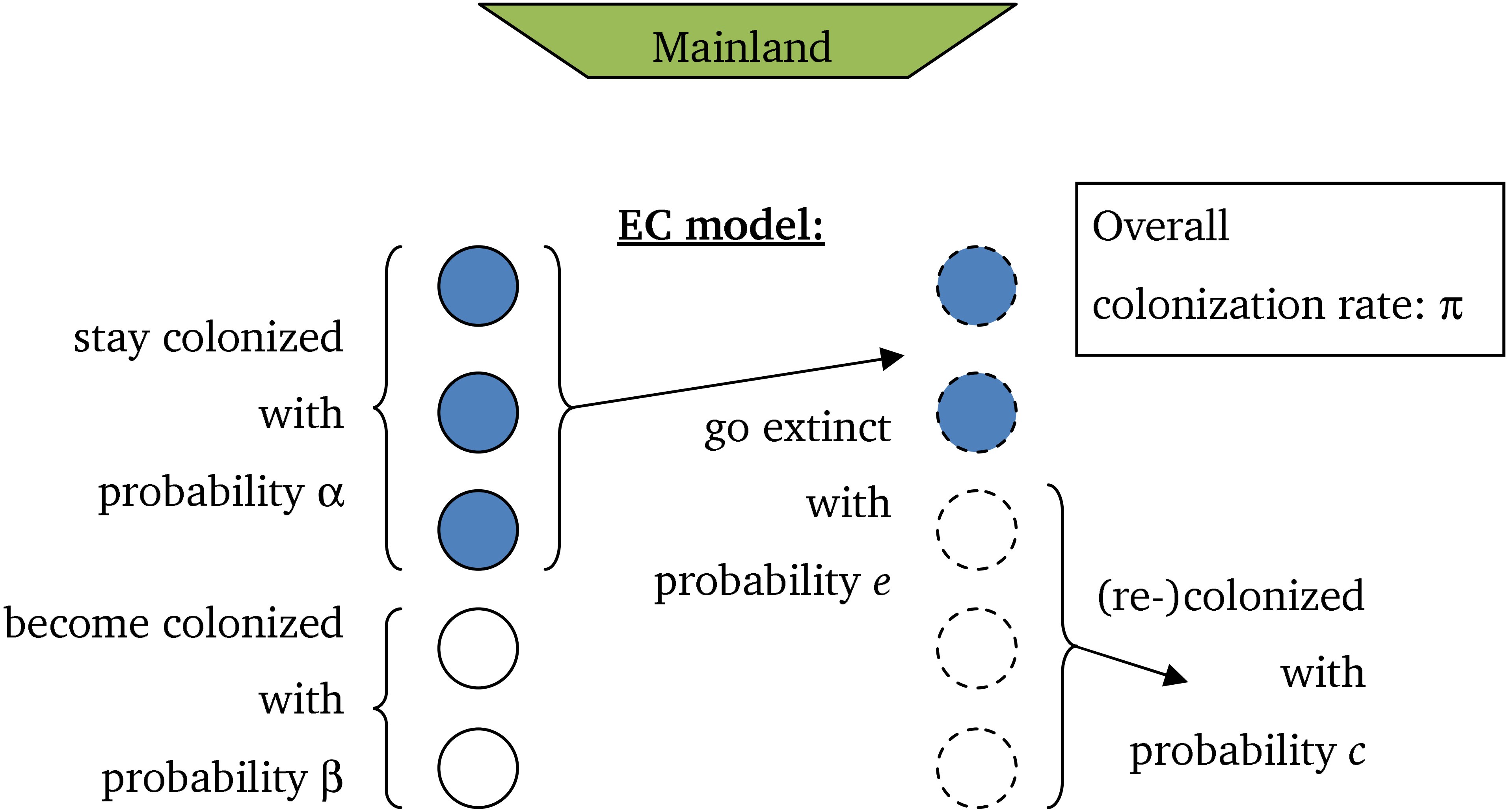
Proof: See article, Section 2.

For both models, $\rho = (1-e)(1-c) \in (0;1)$.

EC model: $\pi = c/(c+e-ec)$,

CE model: $\pi = (1-e)\cdot c/(c+e-ec)$ ($\rightarrow$ reduced π).

For both models, $(c,e) = (0,0)$ is essential singularity.



Mainland

EC model:

Overall

colonization rate: π

stay colonized

with

probability α

become colonized

with

probability β

go extinct

with

probability e

(re-)colonized

with

probability c

Chain Binomial Population Models

In a nutshell:

Both chain-binomial models

(with state-independent

colonisation and extinction probabilities)

are distributed like particular binomial AR(1) models.

⇒ Stochastic properties known,

we can apply established methods,

e. g., for parameter estimation.

Approaches for Parameter Estimation

... and a Real-Data Example

Chain Binomial Models: Parameter Estimation

ML estimation: likelihood function

$$L(c,e) \;=\; P_{c,e}(n_0)\,\prod_{t=1}^{T}\,P_{c,e}(n_t|n_{t-1}), \quad \text{where}$$

EC model: $c = \pi(1-\rho), \quad e = (1-\pi)(1-\rho)/\big\{1-\pi(1-\rho)\big\}$,

CE model: $c = \pi(1-\rho)/(\pi+\rho-\pi\rho), \quad e = (1-\pi)(1-\rho)$.

Theorem: (Proof: See article, Section 3.1)

ML estimators $\hat{c}_{\mathrm{ML}}, \hat{e}_{\mathrm{ML}}$ exist and are consistent.

If $\mathbf{I}_1(c,e) := E\big[\mathbf{J}_1(c,e)\big]$ denotes expected Fisher information, then

$$\sqrt{T}(\hat{c}_{\mathrm{ML}}-c,\ \hat{e}_{\mathrm{ML}}-e)^\top \ \overset{\mathrm{D}}{\to}\ N\big(\mathbf{0},\ \mathbf{I}_1^{-1}(c,e)\big) \quad \text{for } T\to\infty.$$

Chain Binomial Models: Parameter Estimation

CLS estimation:

In Section 3.2 of article,
we derive closed-form expressions for the
estimators and their asymptotic covariance matrix.
(not shown here due to complexity)

For both models, the
estimators are consistent and
asymptotically normally distributed.

Chain Binomial Models: Parameter Estimation

Performance of estimators:

Simulation study in Section 3.3 of article:

CLS performes worse than ML, especially for
small T (such as $T = 50$) or large ρ (such as $\rho = 0.75$).

Approximate normal distributions work rather well.

Section 6 of article:

Robustness of estimators w.r.t. inhomogeneous patches,
i. e., where patch i has probabilities (c_i, e_i),
i. e., (c, e) ≈ “effective” colonization/extinction rates.

$\rightarrow$ CLS more robust than ML.

Chain Binomial Models: Data Example

Ragwort population data

of Van der Meijden & van der Veen-van Wijk (1997).

Chain Binomial Models: Data Example

Ragwort (Senecio jacobaea, “Jakobs-Greiskraut”)

(Source: Christian Fischer resp. Kurt Stueber, Wikimedia Commons)

Chain Binomial Models: Data Example

Ragwort population data

of Van der Meijden & van der Veen-van Wijk (1997).

Ragwort occupies spatially separated sand dune patches in coastal areas of The Netherlands.

Occupancy recorded from 1974 to 1994 (i. e., $T = 21$) for particular patch network comprising $N = 102$ patches.

Local population declared extinct in year t if no living plants during census period (May to August).

Chain Binomial Models: Data Example

Ragwort population data:

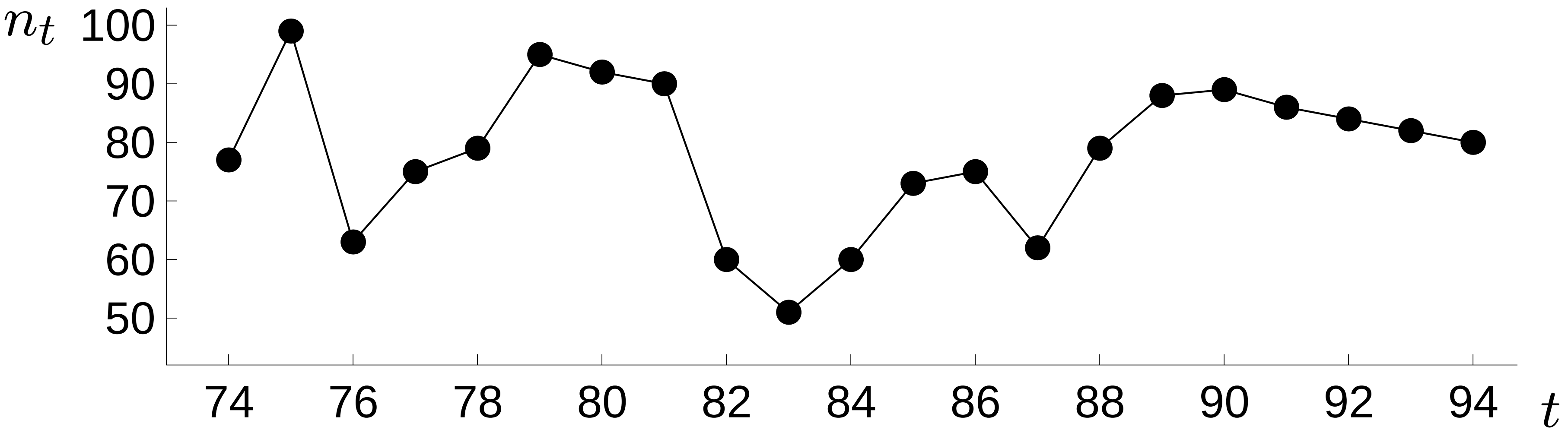
Possibly extinction during winter,
possibly recolonisation during spring, then census
⇒ EC transition structure seems most appropriate.

Recolonisation mainly due to presence of
effective seed bank (≈ mainland),
so state-independent colonisation mechanism reasonable.

Chain Binomial Models: Data Example

Ragwort population data:

Yearly number n_t of extant ragwort populations ($N = 102$) from 1974 to 1994.



Mean value ≈ 78.0, $\quad \widehat{\rho}(1) \approx 0.395$.

Chain Binomial Models: Data Example

Ragwort population data:

ML-calibrated EC model:

$\hat{e}_{\mathsf{ML}} \approx 0.455 \quad (0.081)$, $\hat{c}_{\mathsf{ML}} \approx 0.598 \quad (0.044)$.

So local population of ragwort on a sand dune
becomes extinct with probability ≈ 45 %,
empty patches available after extinction phase
recolonized with probability ≈ 60 %,
confirming its “spectacular powers of regeneration”
(Van der Meijden and van der Veen-van Wijk, 1997, p. 395).

Limiting proportion of patches occupied about 77 %.

Future Work

- **Work in progress:**

  Generalized binomial AR(1) models

  by allowing for density-dependent parameters

  $\rightarrow$ binomial overdispersion or underdispersion.

- **Further research issue:**

  Adapt framework to the Poisson INAR(1) model

  with its infinite range of counts.

Thank You

for Your Interest!

TECHNISCHE
UNIVERSITÄT
DARMSTADT

Fachbereich
Mathematik

Christian H. Weiß

Department of Mathematics

Darmstadt University of Technology

`weiss@mathematik.tu-darmstadt.de`