Bayesian Genetic Mark-Recapture Methods For Estimating Seasonal River Run Size Of Stock **Populations**

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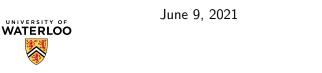




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Figure: Sockeye Salmon (Photo by Kevin Phillips)



Figure: Taku River (Photo by Paul Vecsei)

Genetic Mark-Recapture (GMR) Method

Genetic Data:

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Genetic Data: Estimated Proportions for species of interest

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Counts for some species

 $(\mu_1, ..., \mu_K)$ $(\sigma_1, ..., \sigma_K)$

Genetic Mark-Recapture (GMR) Method

Genetic Data: Count Data:

Estimated Proportions for species Counts for some species of interest

$$(\mu_1, ..., \mu_K)$$

 $(\sigma_1, ..., \sigma_K)$ N_1

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Estimated Proportions for species Counts for some species of interest

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 $(\sigma_1, ..., \sigma_K)$ N_1

$$N = \frac{N_1}{\mu_1}$$

Genetic Stock Identification (GSI) Data

```
n_t, t=1,...,T: Sample size of genetic tissues in week t (\mu_{k,t}): In-sample posterior stock proportion estimate in week t for stock k (\sigma_{k,t}): In-sample posterior standard deviation in week t for stock k
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Run Weight Data

 w_t : The Sockeye Salmon run weight (relative abundance) in week t, with $\sum_{t=1}^{T} w_t = 1$

Method of Moments (MM)

In 2001, W. J. Gazey developed a method of moments estimator to estimate total abundance of specific Salmon stocks in the Alsek River system[2]. This method has been used to estimate the abundance of Sockeye Salmon in the Taku River system by Pestal et al.[1]:

$$\hat{N} = \frac{N_1}{\sum_{t=1}^{T} w_t \mu_{1,t}},\tag{1}$$

with

$$\widehat{\mathsf{Var}}(\widehat{N}) = \sum_{t=1}^{T} (w_t \sigma_{1,t})^2 \left[\frac{\widehat{N}}{\sum_{i=1}^{T} w_i \mu_{1,i}} \right]^2. \tag{2}$$

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The variance may be significantly underestimated.

Proposed Model

• Let $X_{k,t}$ denote the number of fish of stock k in the GSI sample in week t, then:

$$(X_{1,t}, X_{2,t}, ..., X_{K,t}) \sim \text{Multinom}(n_t; \pi_{1,t}, \pi_{2,t}, ..., \pi_{K,t}),$$
 (3)

where $\pi_{k,t}$ is the true proportion of stock k in the population in week t.

② The observed GSI proportions $\mu_{k,t}$ are described as

$$\mu_{k,t} \sim TN\left(\frac{X_{k,t}}{n_t}, \sigma_{k,t}^2\right)$$
 (4)

where TN represents a truncated normal distribution with a range of $[0,\infty)$. The choice of the normal distribution is motivated by the Bernstein-von Mises theorem.

Proposed Model

We can then derive the total number of Sockeye Salmon as

$$N = \frac{N_1}{\sum_{t=1}^{T} w_t \pi_{1,t}}$$
 (5)

and stock-specific abundances as $N_k = N \sum_{t=1}^T w_t \pi_{k,t}$, for k = 2, ..., K.

Choice of Prior

Conjugate Dirichlet Prior (CDP)

$$(\pi_{1,t},...,\pi_{K,t}) \sim \mathsf{Dirichlet}(\theta_1,...,\theta_K) \tag{6}$$

When $\theta_k = 1$, it is a uniform prior; when $\theta_k = \frac{1}{2}$, it is a Jeffreys prior[3].



Choice of Prior

Transformed Normal Prior (TNP)[4]

$$\pi_{k,t} = \frac{\exp(\tau_{k,t})}{\sum_{i=1}^{K} \exp(\tau_{i,t})}$$
 (7)

$$\tau_{k,t} \stackrel{ind}{\sim} N(0,\xi^2).$$
 (8)

We consider various values for ξ : 0.5, 1, 2, ..., 5 as well as a uniform hyperprior $\xi \sim U(0, 10)$.



Choice of Prior

Time Series Prior (TSP)

$$\tau_{k,t} = \rho \tau_{k,t-1} + \epsilon_{k,t} \tag{9}$$

$$au_{k,1} \sim N\left(0, rac{s^2}{1-
ho^2}
ight)$$
 (10)

$$\epsilon_{k,t} \sim N(0,s^2) \tag{11}$$

$$\rho \sim \mathsf{Unif}(-1,1) \tag{12}$$

For s, we consider the values 0.5, 1, 2, ..., 5 as well as a uniform hyperprior $s \sim U(0,5)$. We also consider the case where s and ρ vary per stock and week with independent priors.

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Simple Simulation

- Settings:
 - ▶ 5 weeks, 3 stocks.
 - ▶ 500 GSI datasets with arbitrary preset values of $\pi_{k,t}$.
 - ▶ The true value of N was set as 80,000 and the weir count data N_1 was calculated from

$$N = \frac{N_1}{\sum_{t=1}^T w_t \pi_{1,t}}$$

as a function of N, $\pi_{k,t}$ and w_t , where $w_t = 0.2$ for t = 1, ..., 5.

Simple Simulation

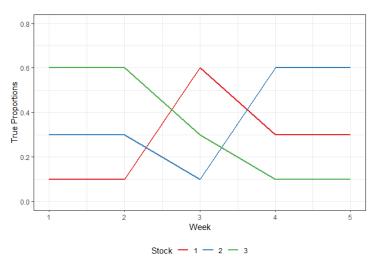


Figure: Parameter values $(\pi_{k,t})$ of the simple simulation.

Simple Simulation

- Results:
 - ► Close to the true value: absolute RBs< 0.01, RRMSEs< 0.07.
 - ► CP: 34.2% (MM) vs. 94.6% ~ 96% (Proposed)
 - ▶ SD of \hat{N} : Proposed = 4 × MM
- The MM estimator underestimates the amount of uncertainty in the estimate.
- The MM estimator does not account for the fact that $\mu_{k,t}$ is the stock proportion in the GSI samples, instead of in the population.

Settings:

- ▶ 12 weeks, 17 stocks (4 lake-types vs. 13 river-types).
- ▶ 500 GSI datasets with the observed $\mu_{k,t}$ in the GSI data as the values of $\pi_{k,t}$.
- ▶ The true value of *N* was set as 60,000 based on the MM estimator in the PSC report[1].
- ▶ The values of w_t and $\sigma_{k,t}$ were set as the observed values from the Taku River dataset.

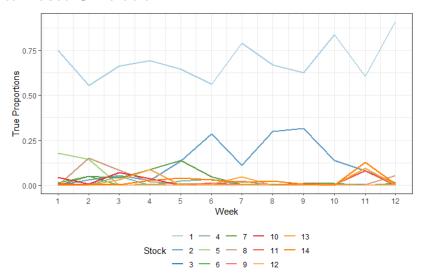


Figure: Parameter values $(\pi_{k,t})$ of the data-based simulation.

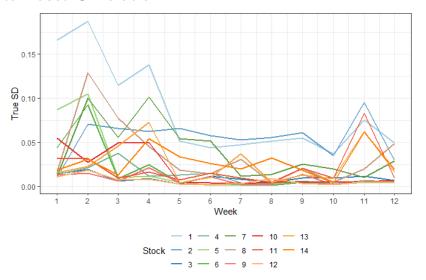


Figure: Standard deviation values $(\sigma_{k,t})$ of the data-based simulation.

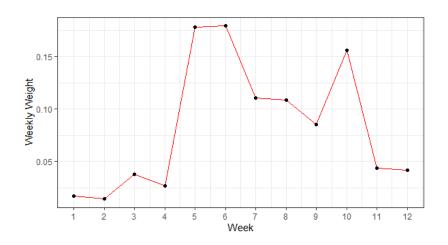


Figure: Run weights (w_t) of the data-based simulation.

Table 1: Results of the data-based simulation.

Setting	Relative Bias	RRMSE	SD	CP
MM	0.00	0.032	1,570	0.88
\Box DCP $\theta_k = 1$	0.18	0.1868	2,334	0.00
DCP $\theta_k = 0.5$	0.09	0.092	2,042	0.18
TNP $\xi = 0.5$	0.25	0.253	2,621	0.00
TNP $\xi = 1$	0.06	0.064	1,983	0.58
TNP $\xi = 2$	-0.01	0.030	1,760	0.93
TNP $\xi = 3$	-0.03	0.038	1,694	0.85
TNP $\xi = 4$	-0.03	0.045	1,658	0.78
TNP $\xi = 5$	-0.04	0.049	1,634	0.69
TNP $\xi \sim U(0,10)$	-0.05	0.054	1,633	0.63
TSP $s \sim U(0,5)$	-0.04	0.052	1,640	0.64

Discussion

- The proposed method is particularly sensitive to the choice of prior, may due to some of the $\pi_{k,t}$'s being very close to zero.
- One possible explanation could be that when simulating the data, we did not constrain $\sum_{k=1}^{K} \mu_{k,t} = 1$ for t = 1, ..., T.
- The TNP model may still be reasonable to use if various values of ξ are considered and model selection criteria such as the DIC or cross-validation are applied.
- Future Work:
 - Propose priors that would not be so sensitive.
 - Use spline method to explore the dynamics through time.
 - **...**



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Thank You