

Chinook salmon run reconstruction for the Skeena River aggregate and six Conservation Units

Luke Warkentin - DFO North Coast Stock Assessment

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1 Introduction

This document provides an update to the run reconstruction for Skeena River Chinook salmon originally described in Winther et al. (2024). These methods for run reconstruction include the Skeena River aggregate and six Conservation Units of summer run timing Chinook upstream of the Skeena River Tyee test fishery (Lower Skeena, Kitsumkalum, Zymoetz-Fiddler, Middle Skeena, Large Lakes, and Upper Skeena, Figure 1). We updated the run reconstruction using best practices for math notation, such as using single letter variable names, as much as possible (Edwards and Auger-Méthé 2019). This makes equations shorter and easier to understand. This document goes hand in hand with the R package `skrunchy` (Warkentin 2025). To make the methods easier to understand, we kept the notation of this document and the code for the `skrunchy` package similar. Our goal is to make the methods transparent, reproducible, and easy to update and adapt over time.

2 Methods

This run reconstruction relies on taking tissue samples from an aggregate population and using these samples to estimate the proportions P_i of its component populations, i , using genetic stock identification. It also relies on a reasonably accurate and precise estimate of the abundance X of one

of these component populations, which we will call population K . Thus, the number of fish X_K of a known population K is equal to the aggregate population $X_{aggregate}$ times the fraction of that population in the aggregate, P_K :

$$X_K = X_{aggregate} \cdot P_K \quad (1)$$

Rearranging this equation allows us to estimate the aggregate population size:

$$X_{aggregate} = \frac{X_K}{P_K} \quad (2)$$

Then, the abundance X_i of other populations can be estimated using their genetic proportions P_i :

$$X_i = X_{aggregate} \cdot P_i \quad (3)$$

After that, the salmon run can be “reconstructed”. Working backwards from age-specific wild spawner abundance, all mortalities (brood stock removals, fishery harvest, incidental mortality) are added back in, to estimate total recruits produced from each brood year. This produces estimates of spawners and recruits by brood year, which can then be use to model productivity.

2.1 Notation

Table 1 provides a detailed explanation of all variables used in the run reconstruction. Note that italic lower case subscripts denote indexing of variables (population i , week w , year y , age a , brood year b), and capital normal font subscripts denote different variables (e.g., U=upper, L=lower). Dots above variables indicate a rate. A star (*) indicates that a new variable has been created by adding age a as a dimension to the original variable (e.g., E and E^*). The Greek letter “tau” τ is used for terminal mortality variables, and “phi” φ is used for preterminal mortality variables. “Sigma” σ is used for standard deviation or standard error. As is typical, variance σ_x^2 of a variable x is equal to the standard deviation σ_x of x squared:

$$\sigma_x^2 = (\sigma_x)^2 \quad (4)$$

2.2 Escapement and wild spawners

2.2.1 Age Proportions

The proportion of age specific returns, Ω , for each population i was the number of aged fish n of age a divided by the total number of aged fish in a given year that were assigned to population i .

For $a = 4, 5, 6, 7$:

$$\Omega_{i,y,a} = \frac{n_{i,y,a}}{\sum_{a=4}^7 n_{i,y,a}} \quad (5)$$

Note that in some years and CUs, n was very small.

Age proportions including jacks, $\Omega_{J,i,y,a}$, for $a = 3, 4, 5, 6, 7$:

$$\Omega_{J,i,y,a} = \frac{n_{i,y,a}}{\sum_{a=3}^7 n_{i,y,a}} \quad (6)$$

2.2.2 Proportions of different populations

To calculate the total yearly gillnet test fishery catch (G),

$$G_y = \sum_{w=1}^{\dots} G_{w,y} \quad (7)$$

where $w = 1$ and \dots are the first and last weeks of test fishing in year y , respectively.

To calculate the annual proportion of population i caught in the gillnet test fishery, estimated catch of each population was calculated for each statistical week, summed across weeks, and then divided by the total catch in year y .

$$\tilde{P}_{i,y} = \frac{\sum_{w=1}^{\dots} \left(\frac{P_{i,w}}{100} \cdot G_{w,y} \right)}{G_y} \quad (8)$$

Estimation of the standard error of the annual proportions was estimated as follows:

$$\sigma_{\tilde{P}_{i,y}} = \frac{\sqrt{\sum_{w=1}^{\dots} \left(\left(\frac{\sigma_{P_{i,w}}}{100} \cdot G_{w,y} \right)^2 \right)}}{G_y} \quad (9)$$

2.2.3 Return to Terrace

The Skeena River aggregate return to Terrace was estimated from Kitsumkalum escapement and the proportion of Kitsumkalum fish in the aggregate (Figure 2):

$$X_{i=\text{Skeena},y} = \frac{K_y}{\tilde{P}_{i=\text{Kitsumkalum},y}} \quad (10)$$

Standard deviation of return to Terrace for the Skeena aggregate was as follows (see Chinook Technical Committee 1999, page 6, third equation):

$$\sigma_{X_{i=\text{Skeena},y}} = \sqrt{(X_{i=\text{Skeena},y})^2 \cdot \left(\frac{\sigma_{K_y}^2}{(K_y)^2} + \frac{\sigma_{\tilde{P}_{i=\text{Kitsumkalum},y}}^2}{(\tilde{P}_{i=\text{Kitsumkalum},y})^2} \right)} \quad (11)$$

Return to Terrace and its standard deviation for $i = \text{Kitsumkalum}$ was the same as the estimate of spawners in the Kitsumkalum River from the mark-recapture study:

$$X_{i=\text{Kitsumkalum},y} = K_y \quad (12)$$

$$\sigma_{X_{i=\text{Kitsumkalum},y}} = \sigma_{K_y} \quad (13)$$

For all other populations (not the Skeena aggregate or Kitsumkalum), the return to Terrace $X_{i,y}$ was equal to the Skeena aggregate return to Terrace times the population's proportion:

$$X_{i,y} = X_{i=\text{Skeena},y} \cdot \tilde{P}_{i,y} \quad (14)$$

Standard deviation of return to Terrace, $\sigma_{X_{i,y}}$, for populations besides Skeena and Kitsumkalum was as follows (see Chinook Technical Committee 1999, page 6, second equation):

$$\sigma_{X_{i,y}} = \sqrt{X_{i=\text{Skeena},y}^2 \sigma_{\tilde{P}_{i,y}}^2 + \tilde{P}_{i,y}^2 \sigma_{X_{i=\text{Skeena},y}}^2 - \sigma_{\tilde{P}_{i,y}}^2 \sigma_{X_{i=\text{Skeena},y}}^2} \quad (15)$$

2.2.4 Escapement

Calculating escapement depended on the population. For Kitsumkalum, escapement was equal to the Kitsumkalum River mark-recapture POPAN estimate. For populations downstream or near Terrace (Lower Skeena, Zymoetz-Fiddler), escapement was equal to the return to Terrace. For populations upstream of Terrace (Upper Skeena, Middle Skeena, Large Lakes), escapement was equal to the return to Terrace minus the mortality from in-river fishing (total mortality due to in-river fishing upstream of Terrace, T_U , times the fraction that population i makes up in the total return to Terrace of the three Conservation Units upstream of Terrace). See Section 2.3.1 for T_U calculations. For the Skeena aggregate, the terminal freshwater mortalities upstream of Terrace are subtracted from the return to Terrace.

$$E_{i,y} = \begin{cases} K_y & \text{if } i = \text{Kitsumkalum,} \\ X_{i,y} & \text{if } i = \text{Lower Skeena or Zymoetz-Fiddler,} \\ X_{i,y} - \left(T_{U,y} \cdot \frac{X_{i,y}}{X_{U,y}}\right) & \text{if } i = \text{Upper Skeena, Middle Skeena, or Large Lakes,} \\ X_{i,y} - T_{U,y} & \text{if } i = \text{Skeena.} \end{cases} \quad (16)$$

where the total return to Terrace for the three Conservation Units upstream of Terrace (Upper Skeena, Middle Skeena, Large Lakes) was

$$X_{U,y} = X_{i=\text{Upper Skeena},y} + X_{i=\text{Middle Skeena},y} + X_{i=\text{Large Lakes},y} \quad (17)$$

Age-specific escapement E^* for all populations except Kitsumkalum were equal to escapement E multiplied by age proportion Ω . Note that age 7 fish (very low proportions) were added to age 6 fish by return year.

$$E_{i,y,a}^* = \begin{cases} E_{i,y} \cdot \Omega_{i,y,a} & \text{if } a = 4, 5 \\ E_{i,y} \cdot \Omega_{i,y,a=6} + E_{i,y} \cdot \Omega_{i,y,a=7} & \text{if } a = 6 \end{cases} \quad (18)$$

Age-specific escapement for Kitsumkalum was based on age data from spawning grounds and expansions based on male/female age proportions (not from ages from samples at Tyee test fishery). Note that for Kitsumkalum, age 7 fish are added to age 6 fish by return year as well.

$$E_{i=\text{Kitsumkalum},y,a}^* = K_{y,a}^* \quad (19)$$

Hatchery origin spawners, $H_{y,a}^*$, was the estimated CWT tagged and adipose fin clipped fish in Kitsumkalum escapement, *escape*, (column ‘escape’ in new 2025 CWT ERA outfiles) by return year, age, and stock (KLM or KLY), multiplied by an expansion factor to account for untagged releases, $\frac{total.release}{CWT.release}$, and then summed across the two stocks:

$$H_{y,a}^* = \sum_{s=KLM}^{KLY} \left(escape_{y,a,s} \frac{total.release_{y,s}}{CWT.release_{y,s}} \right) \quad (20)$$

This was summed by return year to get hatchery origin spawners by return year:

$$H_y = \sum_{a=4}^7 H_{y,a}^* \quad (21)$$

K^* was calculated as follows:

$$K_{y,a}^* = \Omega_{KM,y,a} \left(K_{M,y} - H_y \frac{K_{M,y}}{K_y} \right) + \Omega_{KF,y,a} \left(K_{F,y} - H_y \frac{K_{F,y}}{K_y} \right) + H_{y,a}^* \quad (22)$$

where we assumed that the overall hatchery contribution by return year had the same sex ratio as the POPAN escapement estimates for males and females.

2.2.5 Spawners and Wild Spawners

To calculate the number of spawners for population i and age a , brood stock removals (B) were removed from Kitsumkalum and the Skeena aggregate. For the other populations, spawners were equal to escapement:

$$S_{i,y,a}^* = \begin{cases} E_{i,y,a}^* - B_{y,a}^* & \text{if } i = \text{Kitsumkalum or Skeena,} \\ E_{i,y,a}^* & \text{otherwise.} \end{cases} \quad (23)$$

Spawners were then summed by return year to get total spawners by return year.

$$S_{i,y} = \sum_{a=4}^7 S_{i,y,a}^* \quad (24)$$

To calculate wild (natural origin) spawners, hatchery origin spawners were subtracted from Kitsumkalum and the Skeena aggregate. For all other populations, wild spawners were equal to spawners.

$$W_{i,y,a}^* = \begin{cases} S_{i,y,a}^* - H_{y,a}^* & \text{if } i = \text{Kitsumkalum or Skeena,} \\ S_{i,y,a}^* & \text{otherwise.} \end{cases} \quad (25)$$

Wild spawners were then summed by return year to get total wild spawners by return year.

$$W_{i,y} = \sum_{a=4}^7 W_{i,y,a}^* \quad (26)$$

The proportion of wild spawners (p) for Kitsumkalum and the Skeena aggregate was the sum of wild spawners and brood removals (since brood are unclipped and assumed to be wild fish) divided by escapement. This is to get the proportion of wild spawners in the escapement, which is then applied to terminal freshwater mortalities to estimate wild terminal mortalities. For all other populations, proportion wild spawners was 1. Note that this is slightly different than Winther et al. 2024 equation 12, which did not include brood removals.

$$p_{i,y,a} = \begin{cases} \frac{W_{i,y,a}^* + B_{i,y,a}^*}{E_{i,y,a}^*} & \text{if } i = \text{Kitsumkalum or Skeena,} \\ 1 & \text{otherwise.} \end{cases} \quad (27)$$

Note that for p , if both $W_{i,y,a}^*$ and $E_{i,y,a}^*$ were 0 (e.g., Kitsumkalum age 4 for year 1995), then $p = 1$. This was so that if there were terminal mortalities τ for Kitsumkalum (due to catch of age 4 at Tyee but no age 4 in Kitsumkalum escapement), the terminal mortalities τ would be retained. This is different than Winther et al. 2024, which set $p = 0$ for this case.

2.3 Estimating mortality and run size

Once wild spawners are estimated, sources of mortality were added to reconstruct each cohort of Chinook salmon (Figure 3).

2.3.1 Terminal mortality (freshwater, and marine near the Skeena River mouth)

2.3.1.1 Freshwater terminal mortality

Freshwater terminal mortality for the lower river (below Terrace) and the upper river (above Terrace) were calculated separately as T_L and T_U , respectively. Because jack estimates at the Tyee test fishery, First Nations FSC, and recreational fisheries included a large portion of age 4 fish, jacks and adults for these fisheries were first combined. Then age 3 fish were removed to give terminal mortalities for only age 4-7 fish.

Terminal mortality downstream of Terrace, including jacks, was:

$$T_{L,y} = \sum_{a=4}^7 \Omega_{J,i=\text{Skeena},y,a} \times (1.046 \cdot \text{tyee}_y + 1.069 \cdot \text{rec.catch}_{L,y} + 0.05 \cdot \text{rec.release}_{L,y} + 1.046 \cdot \text{FN.catch}_{L,y}) \quad (28)$$

Terminal mortality upstream of Terrace, including jacks, was (no recreational release data):

$$T_{U,y} = \sum_{a=4}^7 \Omega_{J,i=\text{Skeena},y,a} (1.069 \cdot \text{rec.catch}_{U,y} + 1.046 \cdot \text{FN.catch}_{U,y}) \quad (29)$$

After terminal mortalities by year were calculated, age-specific freshwater terminal mortality of age 4+ fish for the upper and lower river (τ_U and τ_L) were calculated by applying the age proportions of age 4-7 fish.

Total freshwater terminal mortality for the lower Skeena River (downstream of Terrace) τ_L , for population i ,

$$\hat{\tau}_{L,i,y,a} = \begin{cases} T_{L,y} \cdot \Omega_{i,y,a} & \text{if } i = \text{Skeena}, \\ T_{L,y} \cdot \Omega_{i,y,a} \cdot \frac{\tilde{P}_{i,y}}{\sum_{i=1}^6 \tilde{P}_{i,y}} & \text{otherwise.} \end{cases} \quad (30)$$

Where $\sum_{i=1}^6 \tilde{P}_{i,y}$ indicates the sum of \tilde{P} for the six summer run populations upstream of Tyee (Lower Skeena, Kitsumkalum, Zymoetz-Fiddler, Middle Skeena, Large Lakes, Upper Skeena). This excludes Skeena Estuary, Ecstall, Early Cedar, and Upper Bulkley.

Note that recreational catch below Terrace in past years could be biased towards Kitsumkalum fish as these were targeted in the Skeena mainstem just downstream of the Kitsumkalum confluence. River morphology has changed in this location.

Then, terminal mortalities for age 7 fish were added to mortalities for age 6 fish from the same brood year. In other words, age 7 mortalities were moved to their return year -1:

$$\tau_{L,i,y,a} = \begin{cases} \hat{\tau}_{L,i,y,a} & \text{if } a = 4 \text{ and } 5, \\ \hat{\tau}_{L,i,y,a=6} + \hat{\tau}_{L,i,y+1,a=7} & \text{if } a = 6. \end{cases} \quad (31)$$

Total freshwater terminal mortalities upstream of Terrace for population i :

$$\hat{\tau}_{U,i,y,a} = \begin{cases} T_{U,y} \cdot \Omega_{i,y,a} & \text{if } i = \text{Skeena}, \\ T_{U,y} \cdot \Omega_{i,y,a} \cdot \frac{\tilde{P}_{i,y}}{\tilde{P}_{U,y}} & \text{if } i = \text{Middle Skeena, Large Lakes, or Upper Skeena}, \\ 0 & \text{if } i = \text{Lower Skeena, Kitsumkalum, or Zymoetz-Fiddler}. \end{cases} \quad (32)$$

where $\tilde{P}_{U,y}$ is

$$\tilde{P}_{U,y} = \tilde{P}_{i=\text{Upper Skeena},y} + \tilde{P}_{i=\text{Middle Skeena},y} + \tilde{P}_{i=\text{Large Lakes},y} \quad (33)$$

Terminal mortalities for age 7 fish were added to mortalities for age 6 fish from the same brood year. In other words, age 7 mortalities were moved to their return year -1:

$$\tau_{U,i,y,a} = \begin{cases} \hat{\tau}_{U,i,y,a} & \text{if } a = 4 \text{ and } 5, \\ \hat{\tau}_{U,i,y,a=6} + \hat{\tau}_{U,i,y+1,a=7} & \text{if } a = 6. \end{cases} \quad (34)$$

2.3.1.2 Marine terminal mortality

Terminal mortality from marine fisheries (this would include commercial and recreational in Area 4, etc.) was:

$$\tau_{M,i,y,a} = \frac{W_{i,y,a}^*}{1 - \dot{\tau}_{M,y,a}} - W_{i,y,a}^* \quad (35)$$

2.3.1.3 Total terminal mortality

Wild total terminal mortality was the sum of terminal mortalities from freshwater and terminal marine fisheries, adjusting freshwater mortalities using proportion wild spawners:

$$\tau_{W,i,y,a} = \tau_{M,i,y,a} + p_{i,y,a} \cdot \tau_{L,i,y,a} + \tau_{U,i,y,a} \quad (36)$$

Note that in Winther et al. 2024 Excel files, p is only applied to τ_U and τ_L , not to τ_M as shown in the Winther et al. 2024 report equation 14. τ_M is derived from wild spawners only and does not need to be adjusted with p . Also note that Winther et al. 2024 applied p to τ_U and τ_L , whereas here we apply p to τ_L only. This is because τ_U is assumed to be all wild spawners, since all hatchery origin spawners in this method are Kitsumkalum origin and we assume exit the Skeena mainstem just downstream of Terrace, and thus are not encountered in freshwater fisheries upstream of Terrace. Therefore, we assume that all fish caught in freshwater fisheries upstream of Terrace (τ_U) are wild origin. We ignore the small number of Upper Bulkley hatchery origin Chinook since this population is not part of the run reconstruction (due to its early run timing), inconsistent clipping rates, and because there are no reliable estimates of hatchery origin escapement to the Upper Bulkley Conservation Unit (as in Winther et al. 2024).

2.3.2 Terminal run

The terminal run (wild) was all the wild fish that made it back to the Skeena River mouth area, including terminal mortality, wild spawners, and fish taken as brood stock:

$$TermRun_{i,y,a} = \begin{cases} \tau_{W,i,y,a} + W_{i,y,a}^* + B_{y,a}^* & \text{if } i = \text{Kitsumkalum or Skeena,} \\ \tau_{W,i,y,a} + W_{i,y,a}^* & \text{otherwise.} \end{cases} \quad (37)$$

2.3.3 Total mature run and preterminal harvest rate

The total mature run was the terminal run plus mature fish caught in ocean net fisheries:

$$MatureRun_{i,y,a} = \frac{TermRun_{i,y,a}}{1 - \dot{\varphi}_{M,y,a}} \quad (38)$$

2.3.4 Preterminal mortality for immature fish caught in the ocean

The preterminal post-fishery abundance A_φ was the abundance of the cohort after non-net fisheries (e.g., troll), after accounting for maturation rate, but before preterminal net (gillnet, seine) fishery harvest of mature fish. In other words, the preterminal post-fishery abundance is the number of fish that matured into the mature run, of the fish that survived non-net ocean fisheries.

$$A_{\varphi,i,y,a} = \frac{MatureRun_{i,y,a}}{r_{y,a}} \quad (39)$$

Ocean pre-fishery abundance, A_P was the preterminal post-fishery abundance, A_φ , plus the fish caught in preterminal non-net fisheries (e.g., troll).

$$A_{P,i,y,a} = \frac{A_{\varphi,i,y,a}}{1 - \dot{\varphi}_{E,y,a}} \quad (40)$$

The preterminal fishing mortality in nominal fish was the ocean pre-fishery abundance minus the preterminal post-fishery abundance:

$$\varphi_{N,i,y,a} = A_{P,i,y,a} - A_{\varphi,i,y,a} \quad (41)$$

Preterminal fishing mortality in adult equivalents was, of the fish caught at younger ages, how many would have hypothetically survived to become adults?

$$\varphi_{Q,i,y,a} = \varphi_{N,i,y,a} \cdot Q_{y,a} \quad (42)$$

2.4 Total recruits, including mature and immature fish

Once we know the total mature run and the preterminal fishing mortality in adult equivalents, the total recruits R can be calculated:

$$R_{i,y,a}^* = MatureRun_{i,y,a} + \varphi_{Q,i,y,a} \quad (43)$$

The brood year b of each cohort of recruits R^* was equal to their return year y minus their age at return a . Recruits R^* by brood year was:

$$R_{i,b=y-a,a}^* = R_{i,y,a}^* \quad (44)$$

Recruits by population, brood year, and age were summed to get recruits by population and brood year for each year of spawners. Note that ages 4-6 are used in this equation. Age 3 fish (jacks) are not included in the run reconstruction, and age 7 fish are combined with age 6 fish in previous equations.

$$R_{i,b} = \sum_{a=4}^6 R_{i,b,a}^* \quad (45)$$

References

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Table 1: Variables and notation used in run reconstruction.

Value	Description
$n_{i,y,a}$	Number of fish that were both aged as age a and assigned to population i with genetic analysis in return year i .
$\Omega_{i,y,a}$	Proportion of fish caught at Tyee of age a assigned to population i using individual genetic assignment in year y , excluding jacks. Only uses Gilbert-Rich total ages 4, 5, 6, and 7. Excludes jacks because the estimation of Kitsumkalum spawners and returns to Terrace are only for ages 4+.
$\Omega_{J,i,y,a}$	Proportion of fish caught at Tyee of age a assigned to population i using individual genetic assignment in year y , including jacks. Uses total Gilbert-Rich ages 3, 4, 5, 6, and 7. Used to remove jacks from freshwater terminal mortality.
$\Omega_{KM,y,a}$	Age proportions of male Kitsumkalum Chinook collected on the Kitsumkalum River, of age a in year y . Uses total Gilbert-Rich ages 4, 5, 6, and 7.
$\Omega_{KF,y,a}$	Age proportions of female Kitsumkalum Chinook collected on the Kitsumkalum River, of age a in year y . Uses total Gilbert-Rich ages 4, 5, 6, and 7.
K_y	Number of Kitsumkalum Chinook returns (escapement) in year y , estimated with POPAN mark-recapture (Gilbert-Rich total ages 4, 5, 6, and 7, no jacks). Includes wild and hatchery origin fish, and fish that were removed for brood stock.
$K_{M,y}$	Number of male Kitsumkalum Chinook returns (escapement) in year y , estimated with POPAN mark-recapture (Gilbert-Rich total ages 4, 5, 6, and 7, no jacks). Includes wild and hatchery origin fish.
$K_{F,y}$	Number of female Kitsumkalum Chinook returns (escapement) in year y , estimated with POPAN mark-recapture (Gilbert-Rich total ages 4, 5, 6, and 7, no jacks). Includes wild and hatchery origin fish, and fish that were removed for brood stock.

Table 1: Variables and notation used in run reconstruction.

Value	Description
$K_{y,a}^*$	Number of Kitsumkalum Chinook returns (escapement) in year y of age a , estimated with POPAN mark-recapture (ages 4, 5, 6, and 7, no jacks) and age sampling from the Kitsumkalum River (not Tyee test fishery). Age proportions applied separately to female and male fish. Includes hatchery origin fish and fish that were removed for brood stock.
σ_{K_y}	Standard error of K_y .
$G_{w,y}$	Number of adult Chinook (based on length cutoff at Tyee) caught in gillnet Skeena River Tyee Test Fishery in statistical week w and year y . Note that this was revised in some years due to inconsistent sampling methods in past years (e.g., fish sampled for genetics the day after being caught), and thus may not always match Fishery Operations System (FOS) weekly counts.
G_y	Number of adult Chinook (based on length cutoff at Tyee) caught in gillnet Skeena River Tyee Test Fishery in year y (sum of $G_{w,y}$).
i	Index for population. Includes six Conservation Units (Lower Skeena, Kitsumkalum, Zymoetz-Fiddler, Middle Skeena, Large Lakes, and Upper Skeena) as well as the Skeena River aggregate ($i = \text{Skeena}$).
y	Index for return year.
a	Index for fish age at return (Gilbert Rich total age).
w	Index for week (statistical fishing week). Note that this is Sunday-Saturday.
b	Index for brood year
$P_{i,w,y}$	Proportion P of catch G_w in week w and year y belonging to population i based on genetic stock identification mixture analysis (ages 4, 5, 6, and 7, no jacks). Expressed as a proportion of 100 to be consistent with Molecular Genetics Lab outputs (e.g., 50 = 50% or 0.5)
$\sigma_{P_{i,w,y}}$	Standard Deviation of $P_{i,w,y}$, expressed as a proportion of 100 to be consistent with Molecular Genetics Lab outputs (e.g., 10 is a standard deviation of 10% or 0.1)

Table 1: Variables and notation used in run reconstruction.

Value	Description
$\tilde{P}_{i,y}$	Proportion \tilde{P} of catch G_y in year y belonging to population i based on aggregating weekly genetic stock identification mixture analyses and weekly catch (weekly expansions). Different than results of annual mixture analysis, which does not account for change in sampling rate or population proportions over the season. Expressed as a decimal (e.g., 0.5) for concise notation.
$\sigma_{\tilde{P}_{i,y}}$	Standard Deviation of $\tilde{P}_{i,w}$. Expressed as a decimal (e.g., 0.1) for concise notation.
$X_{i,y}$	Return to Terrace of large Chinook for population i in year y (ages 4, 5, 6, and 7, no jacks), estimated from genetic proportion of catch at Tyee Test Fishery and Kitsumkalum POPAN mark-recapture estimate.
$\sigma_{X_{i,y}}$	Standard deviation of $X_{i,y}$.
$X_{U,y}$	Sum of return to Terrace of large Chinook for populations upstream of Terrace (Upper Skeena, Middle Skeena, and Large Lakes Conservation Units) in year y .
$E_{i,y}$	Escapement of Chinook in population i in year y .
$E_{i,y,a}^*$	Escapement of Chinook in population i in year y , of age a .
$S_{i,y}$	Number of spawners for population i in year y .
$S_{i,y,a}^*$	Number of spawners for population i in year y , of age a .
$W_{i,y}$	Wild (natural origin) spawners in population i in year y .
$W_{i,y,a}^*$	Wild (natural origin) spawners in population i in year y , of age a .
B_y	Number of adult Chinook broodstock taken in the Kitsumkalum River in year y .
$B_{y,a}^*$	Number of adult Chinook broodstock taken in the Kitsumkalum River in year y , of age a .

Table 1: Variables and notation used in run reconstruction.

Value	Description
H_y	Hatchery origin escapement to Kitsumkalum River in year y . Older data: sum of CTC model output column Esc_exp by return year, for KLM (fry) and KLY (yearlings) combined. I think this should be ages 4-7 only
$H_{y,a}^*$	Hatchery origin escapement to Kitsumkalum River in year y , of age a . Older data: sum of CTC model output column Esc_exp by return year and age, for KLM (fry) and KLY (yearlings) combined. From new CTC ERA outfile, ‘escape’, expanded for untagged releases (expansion factor is CWT releases divided by total releases by brood year). I think this should be ages 4-7 only
$p_{i,y,a}$	Proportion wild spawners (natural production) for population i in year y .
$tyee_y$	Total catch of Chinook at Tyee Test Fishery in year y , including adults and jacks.
$rec.catch_{L,y}$	Recreational catch of all Chinook in year y below Terrace, including jacks.
$rec.release_{L,y}$	Recreational release of all Chinook in year y below Terrace, including jacks.
$rec.catch_{U,y}$	Recreational catch of all Chinook in year y upstream of Terrace, including jacks.
$FN.catch_{L,y}$	First Nations FSC catch of all Chinook in year y below Terrace, including jacks.
$FN.catch_{U,y}$	First Nations FSC catch of all Chinook in year y upstream of Terrace, including jacks.
$T_{U,y}$	Terminal mortalities from freshwater fisheries, upstream of Terrace, by year. Includes recreational and First Nations FSC catch plus incidental mortalities. Called Tau in R code to avoid T variable name (which stands for TRUE in R).
$\tau_{U,i,y,a}$	Terminal mortalities from freshwater fisheries, upstream of Terrace, by population, year, and age. Age 7 mortalities are added to age 6 mortalities of the same brood year.

Table 1: Variables and notation used in run reconstruction.

Value	Description
$T_{L,y}$	Terminal mortalities from freshwater fisheries, below Terrace, by year. Includes recreational, First Nations FSC, Tyee Test Fishery, and incidental mortalities. Called Tau in R code to avoid T variable name (which stands for TRUE in R).
$\tau_{L,i,y,a}$	Terminal mortalities from freshwater fisheries, below Terrace, by population, year, and age. Age 7 mortalities are added to age 6 mortalities of the same brood year.
$\dot{\tau}_{M,y,a}$	Terminal marine exploitation rate. Sum of exploitation rate for terminal marine net fisheries and exploitation rate for terminal marine sport fisheries (coded <i>TNBC TERM N</i> and <i>TNBC TERM S</i> by the Chinook Technical Committee, respectively), which are outputs from the Kitsumkalum CWT analysis. Confirm whether TNBC TERM N includes Tyee.
$\tau_{M,i,y,a}$	Terminal mortalities from marine fisheries, recreational and commercial (near the Skeena River mouth and surrounding near-shore areas, including Area 4).
$\tau_{i,y,a}$	Total terminal mortalities: mortalities from in-river fishing (recreational and First Nations FSC) and terminal marine fisheries plus incidental mortality (recreational plus Area 4).
$\tau_{W,i,y,a}$	Wild terminal mortalities (natural origin).
$TermRun_{i,y,a}$	Wild terminal run (natural origin) consists of fish making it back to the terminal area. Includes fish caught in terminal fisheries (including freshwater fisheries and marine commercial and marine recreational catch in Area 4) and the fish that make it past terminal fisheries to spawn.
$MatureRun_{i,y,a}$	Total mature run, includes terminal run plus mature adult fish harvested in the ocean in net fisheries (preterminal).

Table 1: Variables and notation used in run reconstruction.

Value	Description
$\dot{\varphi}_{M,i,y}$	Preterminal net total mortality harvest rate of mature fish. Used to calculate preterminal ocean harvest of mature fish and total mature run. An output of the CTC Chinook model equal to seine and gillnet catch and incidental mortalities in areas seaward of the terminal area divided by the sum of catch and incidental mortalities in terminal fisheries plus escapement for the cohort. Called <i>MatureOceanNetER</i> in Winther et al. analysis. Sum of 2020 CTC ERA model output values. Called <i>PTNetTMHR</i> in Winther et al. 2024. For updating: In Winther et al. 2024, this was 0 for age 3 and 4, and sum of ALASKA N and CENTRL N for age 5 and 6.
$A_{\varphi,i,y,a}$	Preterminal post fishery abundance. Abundance of cohort after non-net fisheries (e.g., troll), after accounting for maturation rate but before preterminal net (gillnet, seine) fishery harvest of mature fish. Of the fish that survived non-net ocean fisheries, the number of fish that matured into the mature run, <i>MatureRun</i> .
$r_{y,a}$	Maturation rate by year y and age a , from CTC Chinook model output for Kitsumkalum fry releases (code KLM). This is fraction of preterminal post-fishery abundance A_{φ} (survived preterminal non-net fisheries, e.g., troll) that matured into mature run <i>MatureRun</i> . Always equals 1 for age 6 fish.
A_P,i,y,a	Ocean pre-fishery abundance
$\dot{\varphi}_{E,y,a}$	Preterminal total mortality exploitation rate. Output of CTC Chinook model equal to the number of fish caught plus incidental mortalities for non-net fisheries (e.g., troll), in areas seaward of the terminal area, divided by total stock for the cohort, in nominal fish (not adjusted for AEQs). Troll catch is a major part of this. Called <i>PretermER</i> in Winther et al. 2024 analysis, which is a sum of CTC ERA model output values. Called <i>PTTMER</i> in Winther et al. 2024 text. In Winther et al. 2024, for age 5, 6 fish this was the sum of ER for all other fisheries (excludes ALASKA N and CENTRL N). For age 3, 4 fish this was the sum of ER for all other fisheries and ALASKA N and CENTRL N.
$\varphi_{N,i,y,a}$	Preterminal fishing mortality in nominal fish.

Table 1: Variables and notation used in run reconstruction.

Value	Description
$\varphi_{Q,i,y,a}$	Preterminal fishing mortality in adult equivalents.
$Q_{y,a}$	Adult equivalency rate, from the CTC model output from Kitsumkalum fry releases. Always equal to 1 for age 6 fish.
$R_{i,y,a}^*$	Total recruits for population i , return year y and age a .
$R_{i,b,a}^*$	Total recruits for population i , brood year b and age a .
$R_{i,y}$ or $R_{i,b}$	Total recruits for population i and either return year y or brood year b .

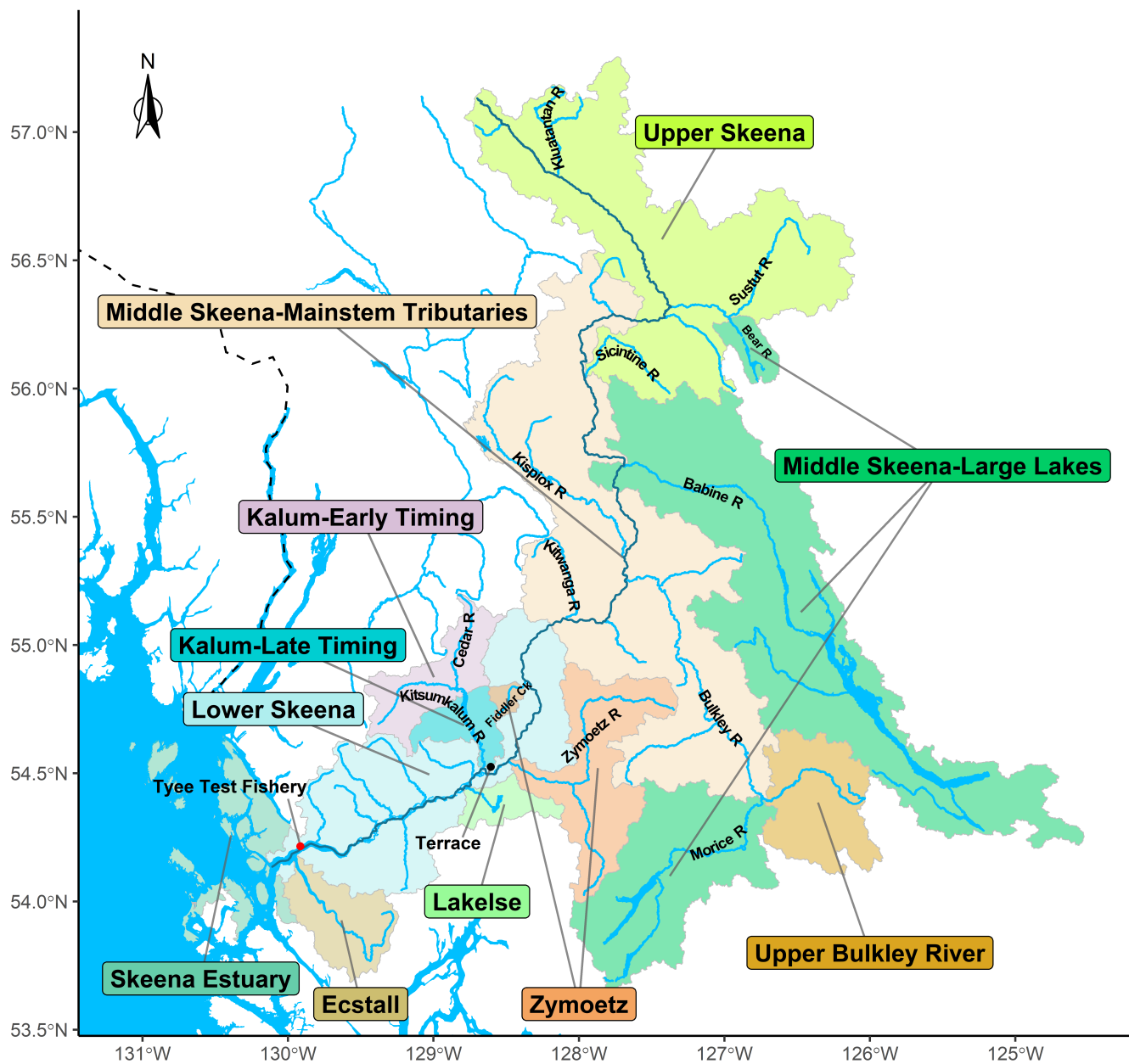


Figure 1: Chinook salmon Conservation Units in the Skeena River watershed. The run reconstruction is for six: Lower Skeena, Kalum-Late Timing (Kitsumkalum), Zymoetz (Zymoetz-Fiddler), Middle Skeena-Mainstem Tributaries (Middle Skeena), Middle Skeena-Large Lakes (Large Lakes), and Upper Skeena. Modified from Figure 2 in Winther et al. 2024.

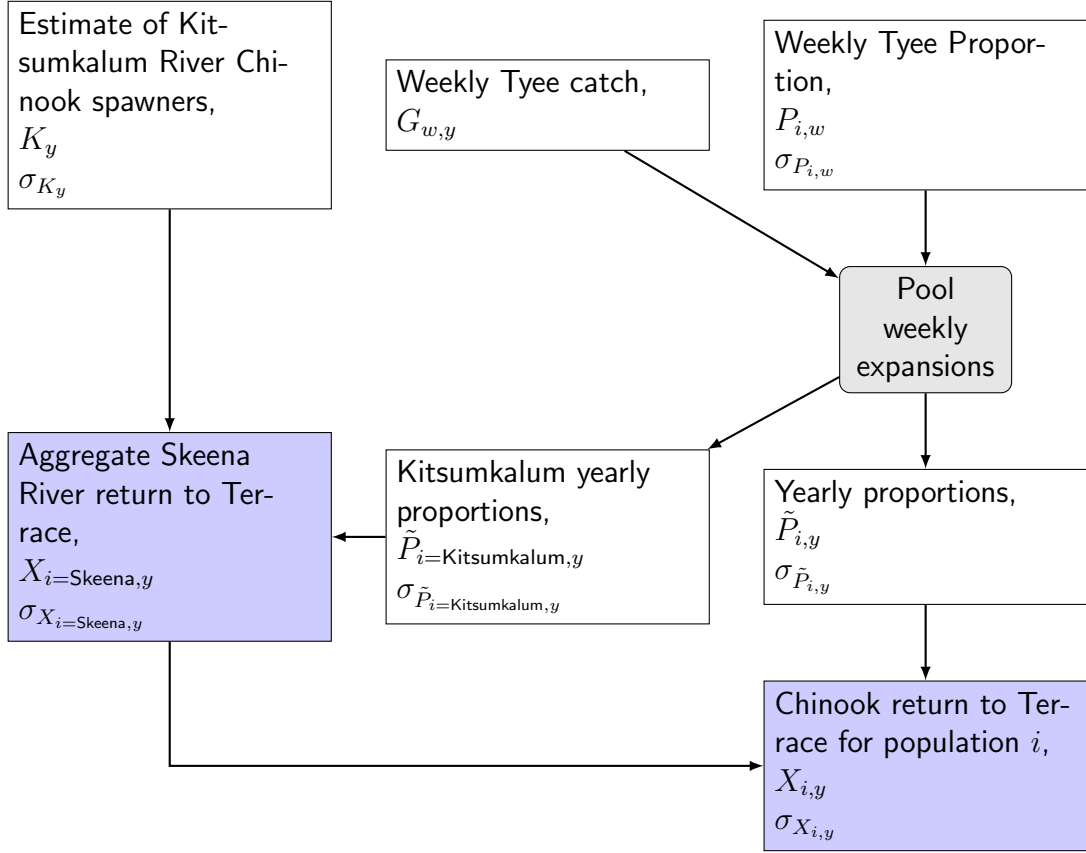


Figure 2: Data sources and methods for estimating the Chinook return to Terrace (and uncertainty) for the Skeena River aggregate and for the component Conservation Units.

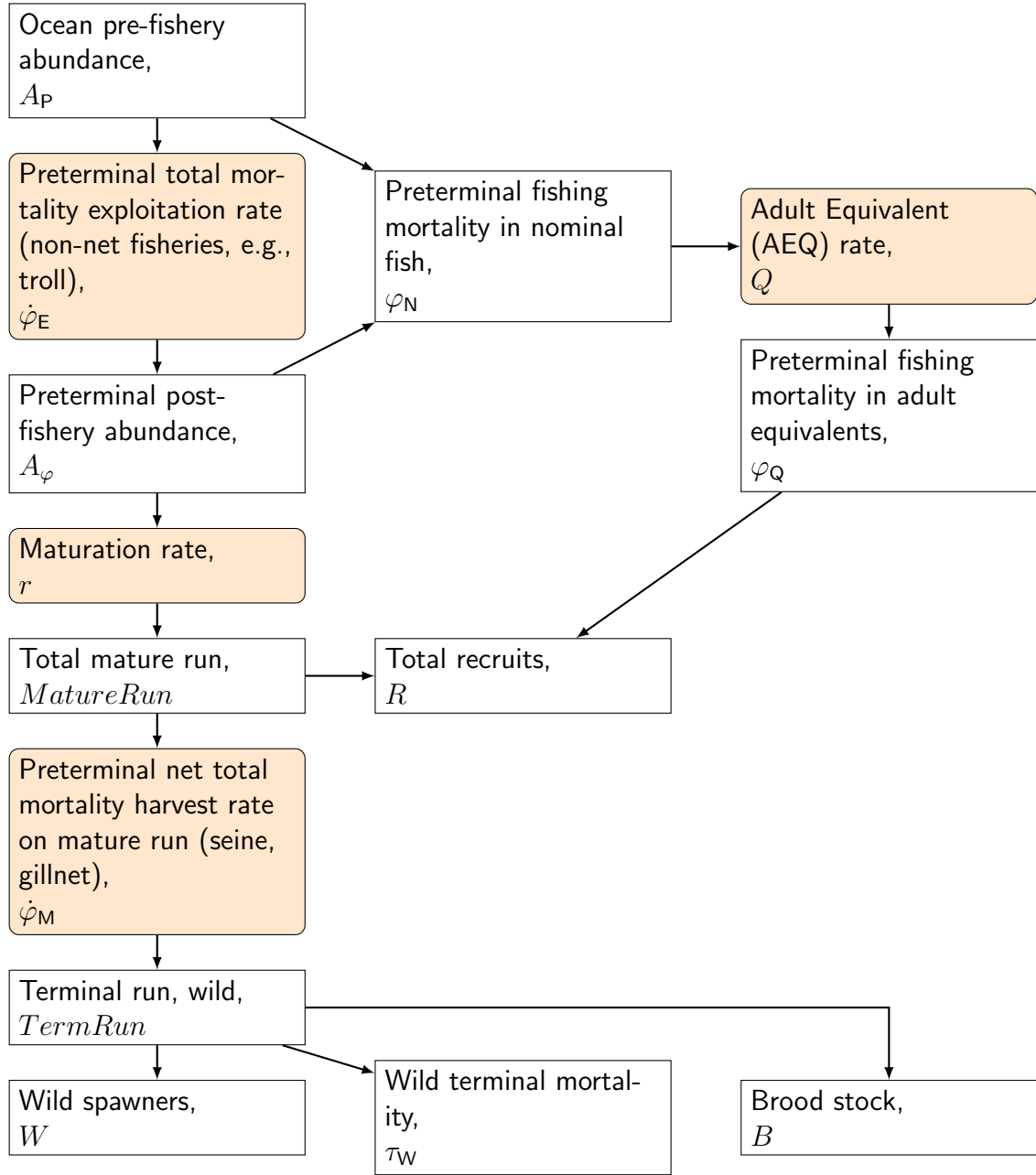


Figure 3: Flow diagram showing the sources of mortality throughout the life of Chinook cohorts from ocean pre-fishery abundance, showing how wild spawners and total recruits are estimated. Note that the run reconstruction equations presented in the Methods section work backwards (upwards) according to this diagram. Rates are shown in orange.