

Salmonid Redd Superimposition in the Feather River, CA: the Association Between Spawning Habitat Characteristics and Salmonid Species

Dani Hartwigsen

Scott Herren

Chinook Salmon and Steelhead Trout are an essential part of the riverine and ocean ecosystem. Unfortunately, they are a species of concern with declining wild populations. This is partially caused by decreased spawning habitat due to anthropological disturbances, and potentially leading to redd superimposition. It is unknown whether Steelhead spawning habitat characteristics in the Feather River overlaps sufficiently with that of Chinook to make redd superimposition likely to occur. This study aims to fill that knowledge gap by studying the Steelhead trout and Chinook salmon populations' redd characteristics in the Feather River, CA. Although we found large overlap in spawning habitat characteristics on the bivariate level implying superimposition is likely to occur, we concluded from multivariate analysis using logistic regression that this overlap is minimal of nature and not of management concern due to the abundance of different channel widths available in the Feather River. Understanding spawning timing, habitat characteristics, and the overlapping of spawning habitat can help researchers and land managers make sound decisions relating to habitat restoration and hatchery efforts to improve these salmonid populations - listed as threatened species under the Endangered Species Act - in managed river systems.

Introduction and Background

Chinook Salmon and Steelhead Trout are of cultural, economic, and recreational importance, as well as being an essential part of the riverine and ocean ecosystem. Unfortunately, they are a species of concern with declining wild populations. This can be attributed to a myriad of reasons, one being decreasing in-river spawning success due to anthropological disturbances such as: the large scale reduction of salmonid (salmon and trout) spawning grounds due to Oroville Dam construction ([Volk, Boughton, and Harrison 2020](#)); limited natural spawning-sized gravel influx below the Dam, causing armoring of the substrate ([Sommer, McEwan, and Brown 2001](#)); leading to impacted spawning grounds below the Dam where Steelhead and

Chinook spawn in the same small area (Cook, n.d.). This results in known Chinook redd (egg-nests in the gravel) superimposition (Cavallo, Brown, and Lee 2009). It is however unknown whether Steelhead, who spawn when Chinook eggs are still in the gravel, also superimpose on Chinook redds.

A study by Togaki et al. (2023) suggests that there is a direct correlation between spawning succession and success; when two species of salmonids utilize the same spawning habitat, the later spawning species may be more successful due to superimposition disturbing the earlier spawning salmonids' redds. This study focused on two trout species in small streams, but no literature was found directly comparing trout and salmon spawning habitat in a larger river system. This study aims to fill that knowledge gap by studying the Steelhead Trout and Chinook Salmon populations' redd characteristics in the Feather River. Understanding the timing of spawning, spawning behavior, and the overlapping of spawning habitat can help researchers and land managers make sound decisions relating to habitat restoration and hatchery efforts to improve these salmonid populations - listed as threatened species under the Endangered Species Act - in the Feather River, CA.

The major factors determining spawning habitat suitability are gravel size (Kondolf et al. 2008), water velocity, water depth (Kammel et al. 2016). From Togaki et al. (2023) can be deduced that availability of streams with different channel widths may be of importance as well. To analyze the possibility of Steelhead superimposition on Chinook redds, this study examines these most influential variables with regard to salmonid spawning habitat suitability and how these variables compare between species. Specifically, a multivariate comparison of these spawning habitat characteristics in regards to Chinook and Steelhead redds will be conducted, hypothesizing that there is sufficient difference in spawning habitat that a model can accurately determine which of these salmonid species a redd belongs to.

Study Design and Data Collection

The dataset used for this study is unpublished salmonid redd observations in the Feather River CA, 2014 - 2025 (Cook et al., 2025, Department of Water Resources) from an observational study on Chinook Salmon and Steelhead Trout. Data was collected during yearly redd surveys (wading through the river to visually identify redds and record data) from fall 2014 through winter in early 2025 in the Feather River from river mile 66 to 48. Chinook redds (n=37,571) were surveyed from September through December, and Steelhead redds (n = 1502) from December through March - each depending on when the first- and last new redds were observed. Only 'new' redds were counted as new observations, using the following criteria: 1. Completeness of redd ("test-digs" are excluded); and 2. "newness" of redd (to prevent recounting redds, those that are algaed over were excluded). Steelhead redd observations are nearly comprehensive. For Chinook redds, the sheer number of observations posed a limitation to data collection and resulted in the taking of random subsamples on high-volume days. During subsampling, all redds were geologged and a random subsample was taken measurements on. Water velocity (m/s, OTT MF pro Velocity meter) and depth (m, 1.5 m

measurement rod, 10 cm increments) were both measured directly upstream from the redd. Relative substrate size classes were denoted in an estimated percentage of total observed in a redd. River conditions restricted surveyors to collect data in areas too swift/deep for wading - these redds were only geologged. Some years no or less data was collected due to a lack of personnel or extreme river conditions.

Methods

Data Preparation

The variables of interest; species (Chinook Salmon or Steelhead Trout), depth (m), velocity (m/s), and the substrate size classes (all in % of total: 'mud silt and sand'(<1.9 mm) , 'gravel' (2-49mm), 'pebble' (50-149mm), 'cobble'(150-300mm), and 'boulder' (>300mm)) were isolated and checked for outliers. Species contained 1 NA value, which was removed from the dataset. Depth outliers were identified as values at- or below zero, and over 1.5 m. These values were transformed to NA in the dataset. Velocity outliers were identified using 1.5IQR, and transformed to NA values together with any observations containing negative values, zeros, and no values. The substrate variables 'mud silt and sand', 'gravel', 'cobble', and 'boulder' were log transformed to ensure data normality. The variable 'channel width' (Very narrow (0-15m wide), Narrow (16-50m wide), Medium (51-100m wide), Broad (>100m wide)) was created by measuring the broadest part of the river section a redd was found in using arcGIS. Only observations containing data on all variables of interest were analyzed (n=4,910). All other observations were removed from the dataset prior to statistical analysis.

Statistical Analysis

All analyses were performed using R statistical Software (version 4.4.3 (2025-02-28 ucrt)). To compare the means between species redd locations and water depth, water velocity, and substrate size class percentages, Two-Sample T-Tests for a difference in means was conducted. The assumptions of independence, normality, and equal variance were verified. To compare the means between species redd locations and channel width, a chi squared test was conducted. The assumptions were verified prior to analysis.

A multivariable logistic regression model was used to model the likelihood the redd was made by a Steelhead based on the variables of interest. Water velocity and depth were identified as the factors of primary interest. Channel width was identified as a potential confounder since Togaki et al. (2023) indicated that channel width is a predictor for species spawning. Substrate size class was identified as a possible predictor. To build the model, variables were added or removed based on model fit and ANOVA results to create new models. For example: 'CobbleLog' was found to not be significantly predicting which species made a redd, and could be removed from the model. Boulder was added to the model instead of 'CobbleLog' and was found to be a significant predictor of which species a redd was associated with though ANOVA. Models were compared using AIC and BIC, and the model with the lowest scores was chosen.

Table 1: Summary table of the redds dataset

Characteristic	N = 4,910 ¹
Species	
Chinook	3,853 / 4,910 (78%)
Steelhead	1,057 / 4,910 (22%)
Velocity	0.49 (0.22)
Depth	0.43 (0.18)
ChannelWidth	
Medium	1,793 / 4,910 (37%)
Broad	1,348 / 4,910 (27%)
Narrow	1,009 / 4,910 (21%)
VeryNarrow	760 / 4,910 (15%)
MudSiltSand	8 (10)
Pebble	41 (16)
Gravel	32 (17)
Cobble	16 (16)
Boulder	3.1 (6.8)

¹n / N (%); Mean (SD)

pROC was used to find the best threshold using Youden’s J. The corresponding performance measures (sensitivity, specificity, positive and negative predictive values) were calculated using the specific threshold outcome.

Results

Descriptive Statistics

Table 1 shows the characteristics of redds included in this dataset (n=4910), where Chinook redds make up over three-quarters of all observations (78%, n=3853). Average water velocity across species is 0.49m/s (sd=0.22) and the average water depth across species is 0.43 m (sd=0.18). The highest proportion of redds were found in channels of medium width (37%, n=1793), while the lowest proportion of redds was found in very narrow channels (15%, n=760). On average, the largest proportion of substrate in a redd is pebble (41%, sd=16%), and the lowest proportion is boulder (3.1%, sd=6.8%). In Figure 1, the relative density of substrate sizes is displayed per species. Although most substrate size classes overlap heavily, the means of ‘MudSiltSand’ and ‘Cobble’ differ the most between Steelhead (10%, sd=11% and 13%, sd=13% respectively) and Chinook (7%, sd=9% and 17%, sd=16% respectively).

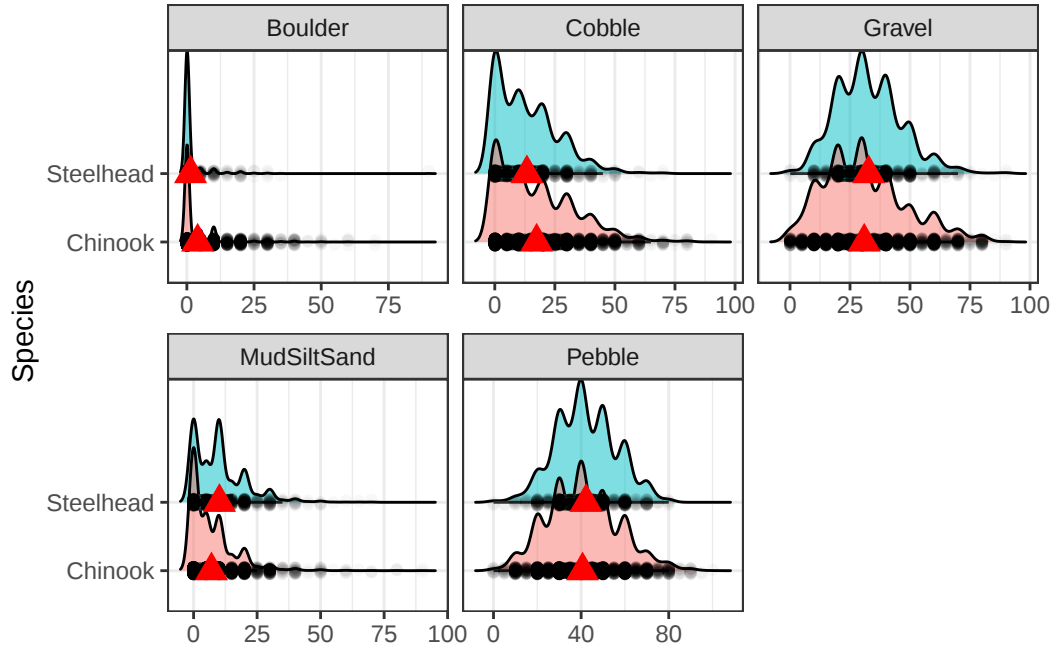


Figure 1: Density plot of substrate at redds per species of salmon

Figure 2 shows the relative abundance of redds per channel width per species. Almost half of all Chinook redds were found in medium width channels (47.1%, $n=17,322$), while the least were found in very narrow channels (8.1%, $n=2,962$). In contrast, most Steelhead redds were found in very narrow channels (39.2%, $n=493$), while only 21.2% ($n=266$) of Steelhead redds were found in medium width channels. Figure 3 illustrates the dominance of Chinook redds in the river system regardless of channel width: even in very narrow channels, where most Steelhead spawn, they only make up 14.3% ($n=493$) of all redds found.

Inferential Statistics

Table 2 shows descriptive statistics per species of salmonid, showing significant differences between Chinook and Steelhead in water velocity (0.5, 0.23 vs 0.45, 0.21 respectively, $p<0.001$) and depth (0.45, 0.18 vs 0.34, 0.14 respectively, $p<0.001$), and all substrate size classes ($p<0.001$) except pebble (41, 16 vs 42, 14 respectively, $p=0.2$), and channel width. A relatively high proportion of Chinook spawn in medium channels (40%, $n=1557$) in comparison to Steelhead (22%, $n=236$). The opposite is true for very narrow channels, where a larger proportion of Steelhead spawn (35%, $n=370$) compared to Chinook (10%, $n=390$). Approximately equal proportions of Chinook and Steelhead spawn in broad channels (27% vs 28% respectively).

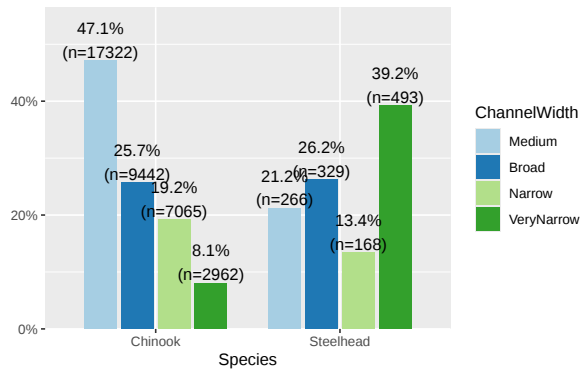


Figure 2: Frequency of Redds in Channel Width Category per Species

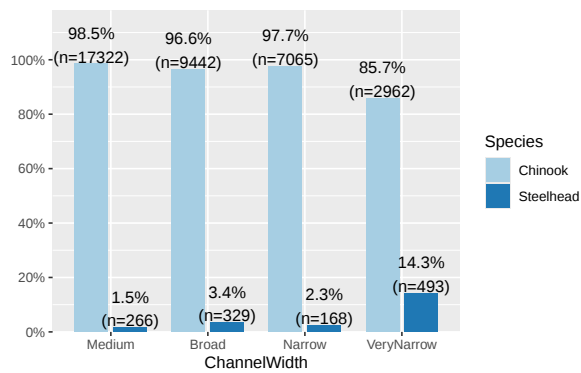


Figure 3: Frequency of Steelhead and Chinook Redds per Channel Width Category

Table 2: Spawning Habitat Characteristic Differences per Species of Salmonid

Characteristic	Chinook N = 3,853 ¹	Steelhead N = 1,057 ¹	p-value ²
Velocity	0.50 (0.23)	0.45 (0.21)	<0.001
Depth	0.45 (0.18)	0.34 (0.14)	<0.001
ChannelWidth			<0.001
Medium	1,557 (40%)	236 (22%)	
Broad	1,054 (27%)	294 (28%)	
Narrow	852 (22%)	157 (15%)	
VeryNarrow	390 (10%)	370 (35%)	
MudSiltSand	7 (9)	10 (11)	<0.001
Pebble	41 (16)	42 (14)	0.2
Gravel	31 (18)	34 (13)	<0.001
Cobble	17 (16)	13 (13)	<0.001
Boulder	3.5 (7.1)	1.5 (5.1)	<0.001

¹Mean (SD); n (%)

²Two Sample t-test; Pearson's Chi-squared test

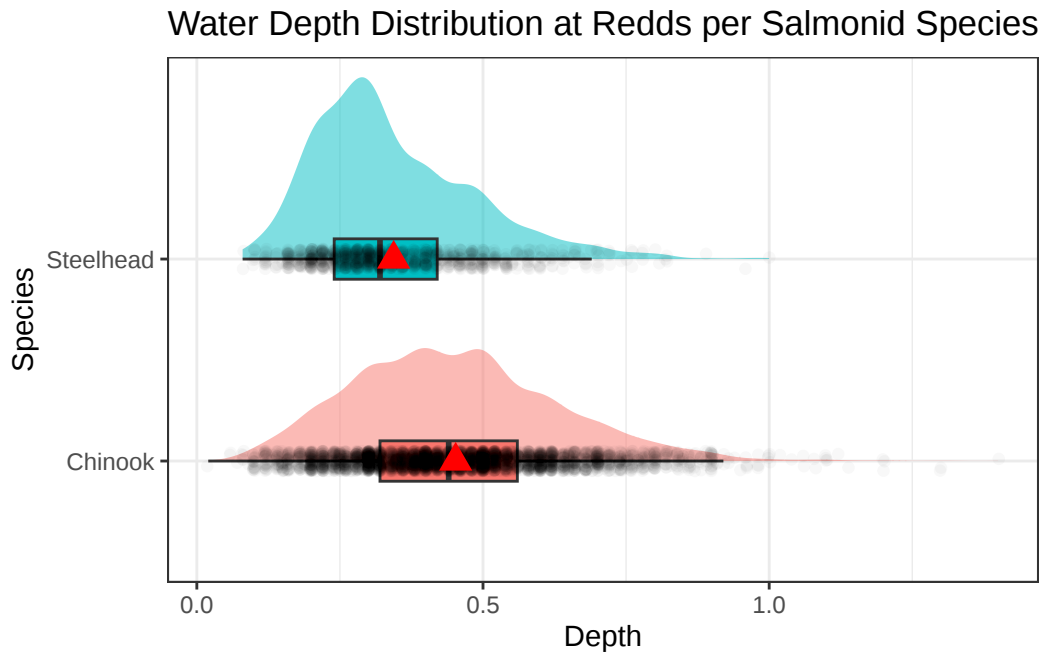


Figure 4: Density Plot of Redd Depth per Species of Salmonid

Table 3: Mean Redd Depth per Species per Channel Width

ChannelWidth	Chinook	Steelhead	p_value
Medium	0.49 (0.48, 0.50)	0.40 (0.38, 0.41)	<0.001
Broad	0.42 (0.41, 0.43)	0.34 (0.33, 0.36)	<0.001
Narrow	0.49 (0.47, 0.50)	0.42 (0.40, 0.45)	<0.001
VeryNarrow	0.30 (0.28, 0.31)	0.28 (0.27, 0.29)	0.038

Figure 4 shows overlap in redd depths across species. Chinook however redds are, on average, 0.12m (CI 0.09, 0.11; $p < 0.0001$) deeper than Steelhead redds (0.44 and 0.32 m respectively). Chinook redd depths are also more varied than Steelhead redds ($sd = 0.18$ and 0.14 respectively). The variances are roughly equal. This holds true when examining the mean depth per species in channels of different widths (Table 3) Thus, there is strong evidence to suspect spawning depths of Chinook and Steelhead are statistically different.

Logistic Regression Model

Table 4 shows the regression table for the best fitted model. Water ‘velocity’, ‘depth’, ‘channel width’, ‘Mud Silt and Sand’ (MSSlog), ‘gravel’ (GravelLog), and ‘boulder’ (BoulderLog) were significantly associated with the outcome. Interestingly, although ‘Pebble’ was not significantly associated with the outcome, the model fit was better when this variable was included. Two other variables that stood out were ‘depth’ and ‘very narrow’ channel width. After controlling for velocity, substrate, and channel width, every additional meter a redd is deep is associated with 0.07 (0.04, 0.12) times the odds that the redd was made by a Steelhead ($p < 0.001$). After controlling for depth, velocity, and substrate, redds in very narrow channels have 3.24 (2.61, 4.03) times the odds of being made by a Steelhead compared to redds in a medium width channel ($p < 0.001$).

In Figure 5, the model predicted probability of a redd being made by a Chinook Salmon or Steelhead is on the y-axis and the true outcome category is on the x-axis. There seems to be somewhat of a separation of outcome category based on predicted probability.

More of the redd observations with low predicted probabilities correspond with Chinook Salmon. Steelhead redd observations exhibit probabilities between near 0 to 0.7, and are more evenly distributed than Chinook redd observations. This indicates the model may be slightly better at predicting whether or not a redd belongs to a Chinook than it is at predicting a redd belongs to a Steelhead.

From table 5 can be deduced that 67.3% of true Steelhead and 69.0% of true Chinook were correctly classified as their respective species at a threshold of 0.212. The model predicts Steelhead right 37.4% of the time, yet predicts Chinook right about 88.5% of the time. Only 11.5% of salmonids predicted to be Chinook are actually Steelhead.

Table 4: Regression Table

Characteristic	OR	95% CI	p-value
(Intercept)	0.23	0.12, 0.43	<0.001
Depth	0.07	0.04, 0.12	<0.001
Velocity	0.69	0.49, 0.98	0.036
MSSlog	1.09	1.05, 1.12	<0.001
Pebble	1.00	1.00, 1.01	0.079
GravelLog	1.20	1.06, 1.37	0.007
BoulderLog	0.85	0.80, 0.90	<0.001
ChannelWidth			
Medium	—	—	
Broad	1.44	1.18, 1.75	<0.001
Narrow	1.16	0.92, 1.45	0.2
VeryNarrow	3.25	2.61, 4.04	<0.001

Abbreviations: CI = Confidence Interval, OR = Odds Ratio

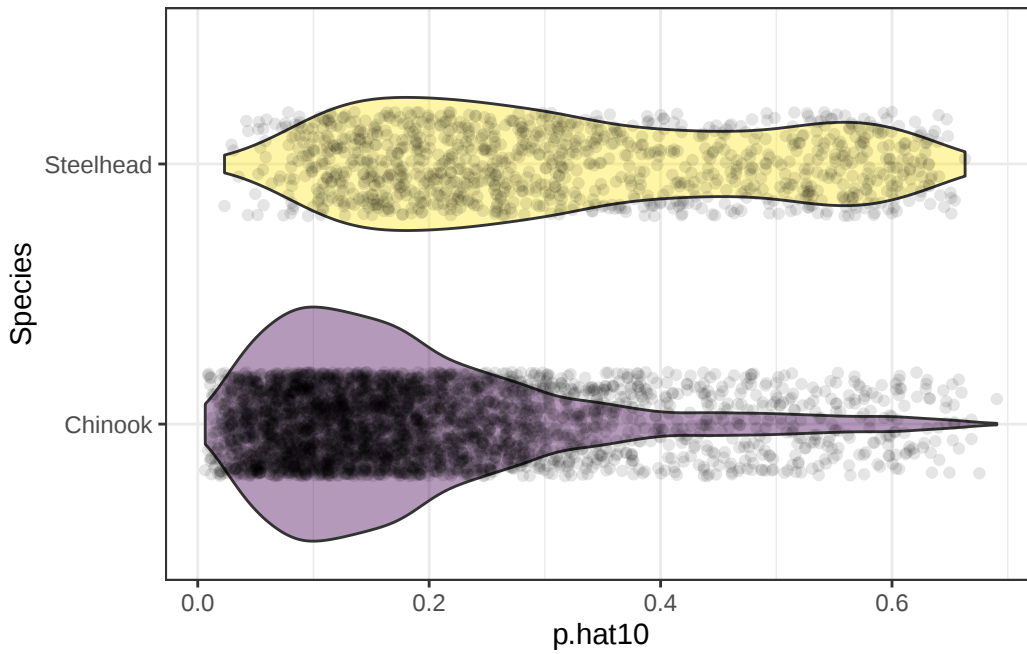


Figure 5: Predictive Model Performance

Table 5: pROC Values

Metric	Value
threshold	0.212
sensitivity	0.673
specificity	0.691
ppv	0.374
npv	0.885

Conclusion

The model is more accurate at predicting whether a redd belongs to a Chinook than to a Steelhead. This may have resulted from the large proportion of observations belonging to Chinook Salmon (78%). Although the preferred habitat characteristics of Chinook and Steelhead differ based on water velocity, depth, channel width, and substrate, there is overlap in the model. This means that there may indeed be superimposition happening of Steelhead on Chinook redds in the shallower, slower moving environments with more gravel and less boulder in its substrate constitution. This is especially true in very narrow channels. Given the relative abundance of medium and broad channels in the study area when compared to very narrow channels, the impact of Steelhead redd superimposition on Chinook redds is likely to be minimal enough to not be a management concern in the Feather River, CA. This outcome reinforces the findings of Togaki et. al (2023) , who concluded that superimposition is likely to occur in the narrower channels that were studied. For river systems with predominantly very narrow channels, management action by means of increasing Chinook-optimized spawning habitat may positively impact the Chinook runs.

Limitations to this study include the large difference in observations between Chinook and Steelhead and different degrees of data collection. For example, Steelhead observations included more environmental variables such as distance from bank, in-stream cover, and overhead cover. Chinook observations lacking this information limited the number of variables that could be added to the predictive model. Additionally, geo-spatial data associated with the redds was not utilized and could provide further clarity on the likelihood of inter-species redd superimposition in shared spawning gravel. Conservation biologists working on river systems with both Steelhead and Chinook runs may use this information to determine whether redd superimposition may be affecting their in river spawning population.

To improve the model and understanding of differences between optimal Steelhead and Chinook spawning habitat, future research may focus on the distance of redds from the bank, in-stream cover (logs, small woody debris, obstructions), overhead cover (obstructions for predation by birds of prey and/or birds feeding on juveniles), and which ‘river section’ a redd is found in (riffle, run, glide, pool). These variables can help zero in on salmonid spawning habitat preference differences.

References

- Attali, Dean, and Christopher Baker. 2025. *ggExtra: Add Marginal Histograms to 'Ggplot2', and More 'Ggplot2' Enhancements*. <https://doi.org/10.32614/CRAN.package.ggExtra>.
- Auguie, Baptiste. 2017. *gridExtra: Miscellaneous Functions for "Grid" Graphics*. <https://doi.org/10.32614/CRAN.package.gridExtra>.
- Cavallo, Bradley, Randy Brown, and Dennis Lee. 2009. "Hatchery and Genetic Management Plan for Feather River Hatchery Spring-Run Chinook Salmon Program." *Feather River Hatchery and Genetic Management Plan*.
- Cook, Call, C. n.d. "Salmonid Redd Observations in the Feather River, CA - 2014 Through 2025 (V1)."
- Kammel, Leah E, Gregory B Pasternack, Duane A Massa, and Paul M Bratovich. 2016. "Near-Census Ecohydraulics Bioverification of Oncorhynchus Mykiss Spawning Microhabitat Preferences." *Journal of Ecohydraulics* 1 (1-2): 62–78.
- Kassambara, Alboukadel. 2025. *Ggpubr: 'Ggplot2' Based Publication Ready Plots*. <https://doi.org/10.32614/CRAN.package.ggpubr>.
- Kay, Matthew. 2025. *ggdist: Visualizations of Distributions and Uncertainty*. <https://doi.org/10.5281/zenodo.3879620>.
- Kondolf, G Mathias, John G Williams, Timothy C Horner, and David Milan. 2008. "Assessing Physical Quality of Spawning Habitat." In *American Fisheries Society Symposium*, 65:000–000. American Fisheries Society Bethesda, Maryland.
- Lüdtke, Daniel. 2025. *sjPlot: Data Visualization for Statistics in Social Science*. <https://CRAN.R-project.org/package=sjPlot>.
- Lüdtke, Daniel, Mattan S. Ben-Shachar, Indrajeet Patil, Philip Waggoner, and Dominique Makowski. 2021. "performance: An R Package for Assessment, Comparison and Testing of Statistical Models." *Journal of Open Source Software* 6 (60): 3139. <https://doi.org/10.21105/joss.03139>.
- Posit team. 2025. *RStudio: Integrated Development Environment for r*. Boston, MA: Posit Software, PBC. <http://www.posit.co/>.
- R Core Team. 2021. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.
- Robin, Xavier, Natacha Turck, Alexandre Hainard, Natalia Tiberti, Frédérique Lisacek, Jean-Charles Sanchez, and Markus Müller. 2011. "pROC: An Open-Source Package for r and s+ to Analyze and Compare ROC Curves." *BMC Bioinformatics* 12: 77.
- Robinson, David, Alex Hayes, and Simon Couch. 2025. *Broom: Convert Statistical Objects into Tidy Tibbles*. <https://doi.org/10.32614/CRAN.package.broom>.
- Sjöberg, Daniel D., Karissa Whiting, Michael Curry, Jessica A. Lavery, and Joseph Larmarange. 2021. "Reproducible Summary Tables with the Gtsummary Package." *The R Journal* 13: 570–80. <https://doi.org/10.32614/RJ-2021-053>.
- Sommer, Ted, Debbie McEwan, and Randall Brown. 2001. "Factors Affecting Chinook Salmon Spawning in the Lower Feather River." *Fish Bulletin* 179.
- Togaki, Daisuke, Ayaka Sunohara, and Mikio Inoue. 2023. "Overlap in Spawning Habitat

- Characteristics Between Two Salmonids in Relation to Stream Size: Redd Superimposition Hypothesis on Longitudinal Species Replacement.” *Canadian Journal of Fisheries and Aquatic Sciences* 80 (5): 840–50.
- Volk, Carol, David Alan Boughton, and Lee R Harrison. 2020. “Estimating Habitat Capacity for Spring-Run Chinook Salmon and Steelhead in the North Fork Feather River Watershed.”
- Wickham, Hadley. 2016. *Ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. <https://ggplot2.tidyverse.org>.
- Wickham, Hadley, Mara Averick, Jennifer Bryan, Winston Chang, Lucy D’Agostino McGowan, Romain François, Garrett Grolmund, et al. 2019. “Welcome to the tidyverse.” *Journal of Open Source Software* 4 (43): 1686. <https://doi.org/10.21105/joss.01686>.
- Wilke, Claus O. 2025. *Ggridges: Ridgeline Plots in 'Ggplot2'*. <https://doi.org/10.32614/CRAN.package.ggridges>.

Appendix

The following programs and packages where used: R Core Team (2021), Posit team (2025), Wickham et al. (2019), Kay (2025), Lüdecke (2025), Sjoberg et al. (2021), Kassambara (2025), Robinson, Hayes, and Couch (2025), Lüdecke et al. (2021), Wickham (2016), Attali and Baker (2025), Robin et al. (2011), Auguie (2017), Wilke (2025)

Table 1

Table 1

```
b %>%
  tbl_summary(Statistic = list(
    all_continuous() ~ "{mean} ({sd})",
    all_categorical() ~ "{n} / {N} ({p}%)"
```

Figure 1

Figure 1

```
redds_long <- redds %>%
  select(Species, MudSiltSand, Pebble, Gravel, Cobble, Boulder) %>%
  pivot_longer(
    cols = c(MudSiltSand, Pebble, Gravel, Cobble, Boulder),
    names_to = "Substrate",
    values_to = "Value"
  ) %>%
```

```

filter(!is.na(Value), !is.na(Species))

ggplot(redds_long, aes(x = Value, y = Species, fill = Species)) +
  geom_density_ridges(alpha=.5)+
  geom_boxplot(width = .2, outlier.shape = NA) +
  geom_jitter(alpha = 0.03, height = 0.05) +
  stat_summary(fun = "mean", geom = "point", col = "red", size = 4, pch = 17) +
  facet_wrap(~ Substrate, scales = "free_x") +
  theme_bw() +
  labs(x = NULL, y = "Species") +
  theme(legend.position = "none")

```

Figure 2

Figure 2

```

plot_xtab(redds$Species, grp=redds$ChannelWidth,
          margin = "row", show.total = FALSE)

```

Figure 3

Figure 3

```

plot_xtab(redds$ChannelWidth, grp=redds$Species,
          margin = "row", show.total = FALSE)

```

Table 2

Table 2

```

b %>%
  tbl_summary(
    by = Species,
    type = list(ChannelWidth ~ "categorical"), # force categorical
    statistic = list(all_continuous() ~ "{mean} ({sd})")
  ) %>%
  add_p(
    test = list(
      all_continuous() ~ "t.test",

```

```

    all_categorical() ~ "chisq.test"
  ),
  test.args = list(
    all_tests("t.test") ~ list(var.equal = TRUE)
  )
)

```

Table 3

Table 3

```

# Compute mean + 95% CI for Depth by ChannelWidth * Species
depth_summ <- b %>%
  filter(
    ChannelWidth %in% c("VeryNarrow", "Narrow", "Medium", "Broad"),
    !is.na(Depth),
    !is.na(Species)
  ) %>%
  group_by(ChannelWidth, Species) %>%
  summarise(
    n          = n(),
    mean_depth = mean(Depth),
    sd_depth   = sd(Depth),
    se_depth   = sd_depth / sqrt(n),
    t_crit     = qt(0.975, df = n - 1),
    ci_low     = mean_depth - t_crit * se_depth,
    ci_high    = mean_depth + t_crit * se_depth,
    .groups    = "drop"
  ) %>%
  mutate(
    mean_ci = sprintf("%.2f (%.2f, %.2f)", mean_depth, ci_low, ci_high)
  )

# Get t-test p-values for Depth ~ Species within each ChannelWidth
pvals <- b %>%
  filter(
    ChannelWidth %in% c("VeryNarrow", "Narrow", "Medium", "Broad"),
    !is.na(Depth),
    !is.na(Species)
  ) %>%
  group_by(ChannelWidth) %>%

```

```

summarise(
  p_value = t.test(Depth ~ Species, var.equal = TRUE)$p.value,
  .groups = "drop"
) %>%
mutate(
  p_value = ifelse(p_value < 0.001, "<0.001", sprintf("%.3f", p_value))
)

# Put Species in columns, ChannelWidth in rows, and add p-values
depth_table <- depth_summ %>%
  select(ChannelWidth, Species, mean_ci) %>%
  pivot_wider(
    names_from = Species,
    values_from = mean_ci
  ) %>%
  left_join(pvals, by = "ChannelWidth")

# output table
depth_table %>%
  gt()

```

Figure 4

Figure 4

```

ggplot(b, aes(x=Depth, y=Species, fill=Species)) +
  ggtitle("Water Depth Distribution at Redds per Salmonid Species") +
  stat_slab(alpha=.5, justification = 0) +
  geom_boxplot(width = .2, outlier.shape = NA) +
  geom_jitter(alpha = 0.03, height = 0.05) +
  stat_summary(fun="mean", geom="point", col="red", size=4, pch=17) +
  theme_bw() +
  labs(x="Depth", y = "Species") +
  theme(legend.position = "none")

```

Table 4

Table 4

```
# isolate model data
data.for.model10 <- redds %>%
  mutate(MSSlog = log(MudSiltSand+.05)) %>%
  mutate(GravelLog = log(Gravel+.05)) %>%
  mutate(BoulderLog = log(Boulder+.05)) %>%
  select(Depth, Velocity, MSSlog, Pebble, GravelLog, BoulderLog, ChannelWidth,
         Species) %>% na.omit() %>%
  mutate(Species01 = ifelse(Species == "Chinook", 0, 1))

# Fit the model and create a summary table.
model10 <- glm(Species01~Depth + Velocity + MSSlog + Pebble + GravelLog +
              BoulderLog + ChannelWidth,
              data=data.for.model10, family = 'binomial')

tbl_regression(model10, exponentiate = TRUE, intercept = TRUE)
```

Figure 5

Figure 5

```
p.hat10 <- predict(model10, type = "response")
model.pred.data10 <- cbind(data.for.model10, p.hat10)

ggplot(model.pred.data10, aes(x = Species, y = p.hat10, fill = Species)) +
  geom_violin(alpha = 0.4) +
  geom_jitter(alpha = 0.1, width = 0.2) +
  scale_fill_viridis_d(guide = FALSE) +
  coord_flip() +           # rotate 90 degrees
  theme_bw()               # remove grey background
```

Table 5

Table 5

```
roc_obj <- roc(data.for.model10$Species01, predict(model10, type="response"), levels = c(0,1))

# Best Youden threshold + key metrics
metrics <- coords(roc_obj, "best", best.method = "youden",
  ret = c("threshold","sensitivity","specificity","ppv","npv"))
```

```
#turn metrics into a table
metrics_table <- as.data.frame(t(metrics))
metrics_table <- data.frame(
  Metric = rownames(metrics_table),
  Value = round(as.numeric(metrics_table[, 1]), 3),
  row.names = NULL
)

metrics_table %>%
  gt()
```