## Study location

The study consisted of two reach pairs on five replicate streams in the western Cascade Mountains of Oregon. Each reach pair consisted of one treatment reach and one reference reach. Two of the reach pairs (W-100, W-113) are located on private Weyerhaeuser Co. land, and three (LOON, CHUCK, MCTE) were located on U.S. Forest Service land, one of which (MCTE) was situated in the HJ Andrews Experimental Forest. Stream reaches were 90 meters in length and treatment gaps were 20 to 40 meters in diameter and situated approximately around meter thirty of treatment reaches. Sites had a buffer between stream reach pairs to limit any effects of the upstream reach on downstream conditions.

All of the streams are wadeable, fish-bearing streams with bankfull widths of 1-6 meters. Fish-bearing streams were purposefully selected to provide management-relevant results for key species such as salmonids. Additionally, streams of this size comprise roughly 70% of total stream length in forested catchments. The streams run through 40-60-year-old riparian forests regenerating from previous harvest. These forests have a homogenous canopy structure with heavy understory shading, as defined by their early to mid-seral stage. Small streams also provide ease of sampling and maximize the effect of a canopy opening manipulation since small streams may be completely shaded by overhead vegetation due to their high edge to area ratio.

## Study Design

The before-after, control-impact (BACI) study design lends itself to experimental field studies by accounting for natural variations between sites. By taking the difference of a given variable between the paired reaches and comparing the change in the difference from pre to post-treatment years, we account for both spatial and temporal variation. For the BACI analyses, a sample unit refers to a whole stream including both treatment and reference reaches because the metric of interest for BACI is the difference between the two reaches. Therefore, we have five sample units with two repeated measures, pre and post-treatment. To test for effects of the gap treatment, we quantify and assess changes in the reach differences between the two years. Pre-treatment data or Samples were collected during summer 2017 and post-treatment data were gathered summer 2018. Canopy gaps were cut in the treatment reach during the winter of 2017-18 to permit adequate time for response to the canopy manipulation at all sites besides MCTE. At MCTE gaps were cut at the end of summer 2017 after data collection.

## Data Collection

### Light

Daily, photosynthetically active radiation (PAR) was estimated from fluorescein decay over a twenty-four hour period following methods in Warren et al. Fluorescein dyes were prepared by diluting to 400 g L-1 with DI water and buffering with 40 g L-1 of aquarium salt. Once the dye was prepared, we filled 3.7 mL glass vials and stored them in the dark until deployment. At each study reach three replicate vials were deployed every five meters on the stream bed, and retrieved twenty-four hours later. Because fluorescence of fluorescein changes with temperature (Bechtold, Rosi-Marshall, Warren, & Cole ([2012](#ref-Bechtold2012))), vials were left in the dark until they reached room temperature. Fluorescence was then measured using a fluorometer (Turner Designs, San Jose, California), and the twenty-four hour decay rate was converted to daily photosynthetically active radiation (PAR) using the relationship in (D. R. Warren, Collins, Purvis, Kaylor, & Bechtold ([2017](#ref-Warren2017))).

### Chlorophyll *a*

In each study reach, three ceramic tiles (15 cm x 15cm) were placed every 10 meters and left for 4 weeks before they were collected to allow periphyton communities to establish. Tiles were placed in riffle sections at a depth of 10-25 cm to keep them from silting over. All tiles were deployed in mid-July, and the tiles were deployed at the control and treatment reaches of each stream at the same time to keep within unit measures consistent. After collection, tiles were kept in the dark, submerged in water for two hours to avoid potential photosaturation issues with the *in situ* chlorophyll *a* measurements. Chlorophyll *a* (abbreviated as Chla for the remainder of this text) concentrations were then quantified using a BenthoTorchTM (BBE Moldaenke GmbH), a portable field instrument used for the quantification of chlorophyll *a* fluorescence.

### Benthic Invertebrate Sampling

Three benthic invertebrate samples were taken at each stream reach at meters 15, 45 and 75, or the closest area with non-boulder substrate. Samples were collected once per year over the course of one week using a Surber sampler with a 0.09 m2 sampling area. Substrate was disturbed to a depth of approximately four inches for one minute. The sample was then preserved in 95% ethanol for identification and enumeration in the lab.

In the lab, the three benthic samples per reach were combined into a single pooled sample for each reach. The pooled sample was then subsampled using a Caton tray. Squares of? the area of the Caton tray were randomly sampled until the cutoff of 300 individuals or greater was reached. Benthic invertebrates were then identified down to genus or the lowest taxonomic unit (LTU) for cryptic taxa such as Chironomidae primarily following Merritt, Cummins, & Berg ([2008](#ref-Merritt2008)). Counts from subsamples were then converted to densities using the following formula:

where is the fraction subsampled, 0.09 is the area of the Surber sampler in square meters, and the result is divided by three because three samples from meters 15, 45 and 75 were pooled.

For community analyses, singleton taxa (taxa occurring in only one reach) were removed from the original matrix and density values were log transformed to reduce the effect of abundant taxa (Chironomidae, *Baetis*, *Micrasema*) on community relationships by applying the formula

where is the density value per square meter for a given taxon. The resulting matrix of benthic invertebrates at the LTU level of identification (20 reaches by 64 taxa) was then used for analysis. Functional feeding groups (FFG) were assigned using the feeding habits of each taxon as identified in Merritt et al. ([2008](#ref-Merritt2008)), and raw density values were used for FFG analyses because sparse or hyper abundant groups were less of a concern with aggregate functional groups.

During Chla tile collection at the two streams with snails as the dominant scraper, the number of snails (Juga) and cased caddisfly (observed taxa being primarily Uenoidae and Glossosomatidae) on each tile were recorded and then removed before taking chlorophyll readings with a BenthoTorchTM.

### Trout Diets

Trout diets were collected during the post-treatment year. Trout diets were collected during three-pass depletion for fish population estimates and were only taken from a subset of fish greater than 100 mm in length. Fish were anesthetized AQUI-S and gastric lavaged. Stomach contents were evacuated by injecting water into the fish stomach using a piece of small plastic tubing attached to a syringe. Diet samples were collected in filter paper and preserved in 95% ethanol for lab processing.

All trout diets were processed (9 to 13 diets per reach) with aquatic invertebrates identified down to the family level and terrestrial invertebrates identified to order. Because the number of fish dieted in each reach varied, the average of all fish diets was used. The resulting matrix was then filtered for aquatic species and appended to a matrix of 2018 stream benthic invertebrate families (10 reaches by 38 families), producing a matrix of 20 sample units (SU’s) by 40 families consisting of both fish diets and benthic samples. Singleton taxa were then removed to create a matrix of combined diet and benthic families of 20 SU’s by 36 families. At this point, the combined matrix was relativized by row maxima to compensate for the difference between benthic sampling—measured in density per m2—and fish diets.

## Data Analysis

### BACI Analysis

The BACI analysis was performed in R (R Core Team ([2018](#ref-R-base))), and consisted of calculating reach-pair differences by subtracting the control reach value from the treatment reach value. Reach differences were calculated for light, Chla, invertebrate richness, Ephemeroptera, Trichoptera, Plecoptera (EPT) index (Wallace, Grubaugh, & Whiles ([1996](#ref-Wallace1996))), total invertebrate density and invertebrate densities by functional feeding group. A paired t-test with 4 degrees of freedom was then performed for each metric by subtracting the reach difference from the pre-treatment year from the difference value in the post-treatment year for each stream assuming the difference between the two reach ratios should be zero if there is no effect of the treatment.

### Community Analysis

Community analyses were performed in PC-ORD (McCune & Mefford ([2016](#ref-PC-ORD))) and R (R Core Team ([2018](#ref-R-base))) using the Vegan package (Oksanen et al. ([2018](#ref-vegan))). Blocked multi-response permutation procedure (MRBP) was used to assess differences between treatment and control reaches in the pre and post-treatment years. MRBP was followed up with blocked indicator species analysis (ISA) to determine underlying taxa driving any grouping detected by MRBP. The combined benthic and diet community matrix was subsequently tested for any differences between treatment and control reaches and benthic versus diet taxa representation using the same MRBP and ISA methods.

To test for any pre-treatment reach differences in 2017, MRBP was run on 2017 data only with *treatment* and *reference* as the two *a priori* groups and blocked by *stream*. The 2018 post-treatment data were then assessed using the same MRBP grouping and blocking. MRBP is a nonparametric method used to test for differences between groups. This method accommodates paired or blocked study designs by accounting for variation related to study design variables that have little bearing on the question being addressed. In this case, MRBP accounts for any between-stream variation. MRBP outputs a p-value for the observed within-group distance (smaller distances constituting stronger grouping) by shuffling SU’s between groups to generate a distribution of possible within-group distances (McCune, Grace, & Urban ([2002](#ref-McCune2002))).

The follow-up ISA calculates an indicator value (IV) for each species. The IV is a composite of a taxon’s fidelity and exclusivity to a group. A taxon consistently abundant in one group and never present in any other, would receive a high IV. Conversely, a taxon rarely abundant in SU’s of one group and present in other groups would receive a low IV (McCune et al. ([2002](#ref-McCune2002))). A Monte Carlo test of 1,000 permutations of the taxa matrix was used to generate a p-value for each taxon’s IV.

Nonmetric multidimensional scaling (Kruskal ([1964](#ref-Kruskal1964))) was used to assess residual variation in the treatment and control reach communities, and quantify the relationship between the synthetic community variables extracted from the ordination axes and environmental variables such as Chla. Sorensen distance was used for both ordinations to reduce the impact of outliers. The ordination was rotated to maximize the environmental variable Chla along axis 1. A random start was used and the real data were run 250 times to ensure an absolute stress minima was reached. A Monte Carlo test with 100 permutations was used to generate a p-value for the probability that the final ordination has a lower than expected stress value than? based on chance alone.

### Analysis of Trout Diets

Trout diets were collected in the post-treatment year, which limits analysis to a comparison of reference versus treatment reaches without the control on inherent reach differences. We performed paired t-tests for the abundance of each functional feeding group represented in the diets of trout in the reference and the treatment reach, and on the modified Ivlev’s selectivity index (as defined in Jacobs ([1974](#ref-Jacobs1974))) for each FFG.