

**Bear River Watershed Water Quality and Benthic Macroinvertebrates:
trends, sites and contaminants of concern, and targets for future monitoring**

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INTRODUCTION

The following report contains results from analysis of water quality, algae, and benthic macroinvertebrate (BMI) communities sampled in the Bear River watershed from 2016-2019. It includes analysis of water quality parameters sampled monthly from 2016-2019 and BMI communities sampled in 2018 and 2019. We performed quantitative analysis and interpretation where possible given sampling fidelity, but only report qualitative results where sample sizes were insufficient to glean quantitative relationships (e.g. algal biomass). We first present an analysis of water quality and BMI community variation in relation to variation in water quality. We then provide a brief outlook for specific sites of concern and identify future sampling needs.

METHODS

We performed all statistical analyses in R version 3.5.2 (R Development Core Team 2017). We first explored variation in water quality across the watershed over time via simple line plots and boxplots to identify sites of concern, parameters that vary significantly spatially or temporally, and to identify underlying trends. Because NO_3 and PO_4 were not continuously sampled, comparing concentrations over time was not feasible, and we instead explored spatial variation via boxplots.

We quantified BMI community differences across space and time and examined the effect of changes in water quality on benthic health. BMI communities are often strong indicators of water quality and overall stream health, as different BMI taxa respond differently to various water quality parameters. For example, predator taxa, which represent a top level of a healthy faunal food web, often only occur in locations with clear, cool water with variable substrate habitats (Ode 2003). Response of BMI communities to water quality can also be assessed using taxon-specific tolerance values or multi-metric indicators. Tolerance values are numerical approximations of how tolerant various taxa are to degraded stream quality; high tolerance values are associated with presence in degraded habitats, while low values are associated with taxon presence in pristine aquatic environments (Ode 2003). We calculated a weighted tolerance value for each sample by averaging the tolerance value of each taxon multiplied by the proportion of the total sample made up by each taxon. Multi-metric indicators (MMI), however, further quantify BMI communities by comparing observed faunal composition to “expected” composition, with expected proportions of various taxa derived via intensive sampling of comparable habitats over large regional scales. Here we use the Family Level Index (FLI) developed by that California Surface Water Ambient Monitoring Program (SWAMP), which calculates a single value representing likelihood of stream degradation based on proportional representation of BMI families in our total sample. The method is roughly akin to the standard California Stream Condition Index (Rehn et al. 2015).

To compare communities both spatially and temporally, we used non-metric multidimensional scaling (NMDS). NMDS is a multivariate ordination technique that compares whole sample units (i.e. a group of taxa taken from one site at one sampling date) by total

community composition. It creates a synthetic multidimensional space derived entirely from differences in the data itself. For example, if two samples are very different from each other in terms of their community composition, they will be very far apart on multiple axes, with the axes representing total abundance of each taxon. If two samples are similar in composition, they will be close together on multiple axes. This analysis allows us to compare whole samples as opposed to single values, and subsequently overlay vectors representing environmental parameters (such as water quality) to test how differences in community composition may be driven by observed variation in the environment. We performed NMDS using the vegan package (Oksanen 2007). We used sorensen (bray-curtis) distance to quantify differences between samples, and tested NMDS fit by visually tracking stress versus number of final dimensions. We chose a three-dimensional final ordination based on decreasing explanation of variance between three and four-dimensional solutions (**Figure S1**). We ran two NMDS ordinations because algae data was incompletely sampled across all locations. The first NMDS included all sites that were sampled for BMI and water quality collectively (hereafter referred to as BMI-WQ ordination), which included June and October of 2018 and June of 2019. The second ordination included sites that had all BMI and algae biomass (hereafter referred to as BMI-Alg ordination), which included less overall sites over the same sampling period.

Finally, to assess taxon-specific drivers of differences in community composition and how composition changes relative to water quality, we performed Kruskal-wallis tests (a non-parametric alternative to analysis of variance, ANOVA) on all taxa to test for significant differences in taxon density by sampling month, year, and site. To quantitatively test how water quality controls benthic communities, we built generalized linear models (GLMs) using FLI, MMI, and weighted tolerance as response variables and site, year, month, and all water quality parameters as predictors. We ran raw models with all variables, then used step-wise reduction via comparison of Akaike's Information Criterion (AIC) to select final models. Final models were then used to derive predicted values of FLI given changes in significant environmental parameters. We built models using the `glm()` function in R, and fit predicted model values using `predict()`.

RESULTS

Water Quality

Conductivity, pH, water temperature, dissolved oxygen (DO), turbidity, and both Total Coliform and *E.coli* concentration were the only parameters that were successfully continuously across all sample dates. Nitrate (NO³), and phosphate (PO⁴) had multiple missing datapoints throughout the sampling period, but general trends were still explorable.

Conductivity varied significantly among sites and over time (**Figure 1A**). Sites lower in the watershed and on tributaries consistently had higher conductivity than sites at higher elevations and on the main river stem, with the highest conductivity observed in sites 11-13

and lowest conductivity observed in sites 1-7 (**Figure 1B**). Sites 11-13 (which are all tributaries to the main stem) were also significantly different from all other sites and represent a distinct conductivity group. The highest observed conductivity was 496.7 $\mu\text{S}/\text{cm}$, recorded at site 13 in August of 2017. Site 13 consistently had the highest conductivity of all sampled sites for a given sampling period, with exceptions in Fall of 2017 and early Winter 2018 when sites 11 and 12 surpassed site 13 in peak conductivity.

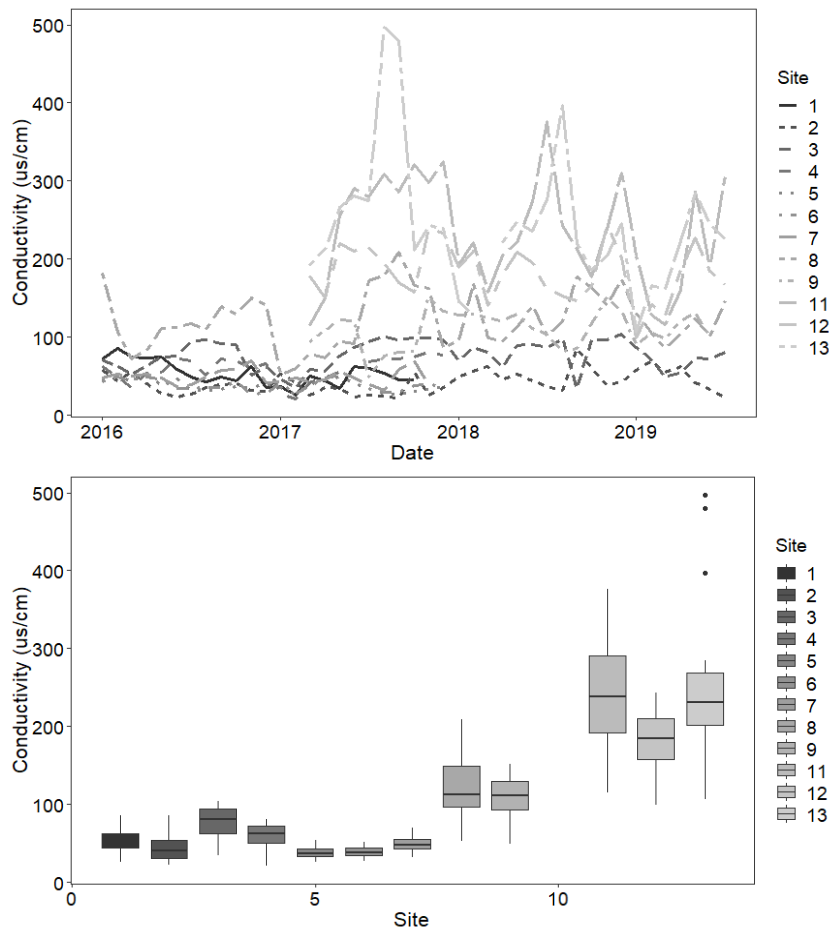


Figure 1. Conductivity ($\mu\text{S}/\text{cm}$) of all sites sampled in Bear River watershed from 2016-2019. A) Conductivity over time across all sites. B) Boxplot of conductivity for all sample dates per site; horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (± 1.5 SD) outliers. Site numbers increase with decreasing elevation, on average, with sites 9-13 also being on lower elevation tributaries.

Spatial trends in pH across the watershed were similar to conductivity but not as significant (**Figure 2**), with sites higher in the watershed having lower pH and sites lower in the watershed having higher pH, on average (**Figure 2B**). However, extreme low pH (acidic) outliers were observed in sites 4-7, primarily in late 2016 and early 2017 (**Figure 2A**).

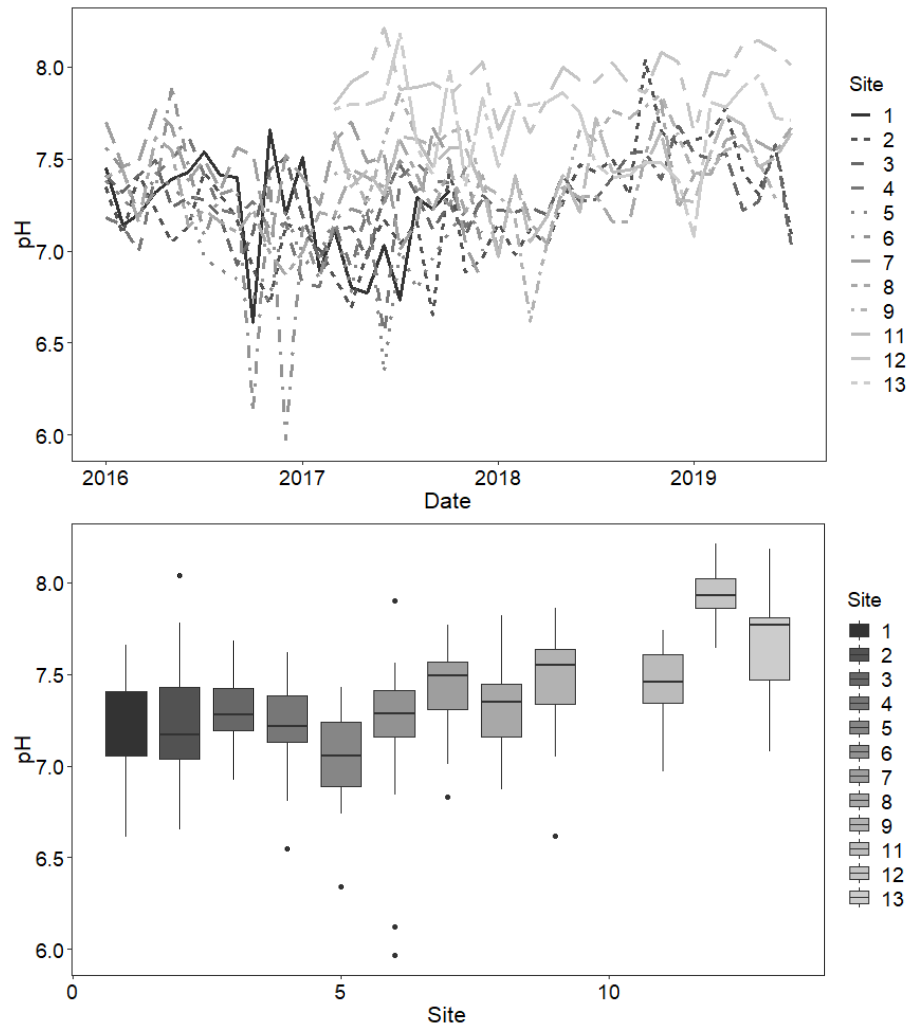


Figure 2. Recorded pH of all sites sampled in Bear River watershed from 2016-2019. A) pH over time across all sites. B)) Boxplot of pH for all sample dates per site; horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (± 1.5 SD) outliers.

Water temperature again followed similar spatial trends to conductivity and pH; sites higher in the upper watershed were cooler on average, while lower elevation sites were warmer (**Figure 3B**). Variance in lower elevation sites was also greater than high elevation sites,

with a greater difference between site minimum and maximum at lower sites, on average. The highest temperatures and greatest variance were observed in site 11-13, again representing a distinct site group, as well as in site 8.

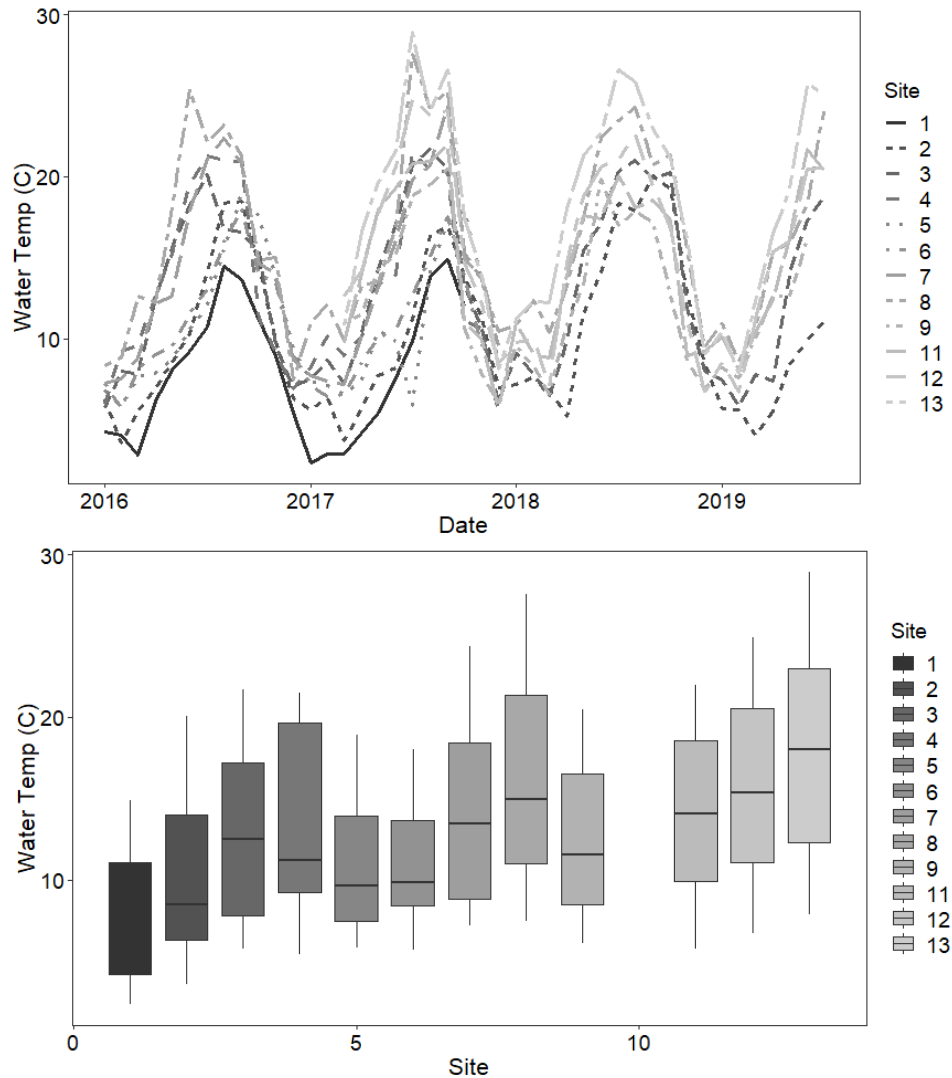


Figure 3. Recorded water temperature (°C) of all sites sampled in Bear River watershed from 2016-2019. A) Temperature over time across all sites. B) Boxplot of temperature for all sample dates per site; horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (+/- 1.5 SD) outliers.

Examinations of NO^3 and PO^4 trends across space show similar spatial trends to other measured variables; both NO^3 and PO^4 increase lower in the watershed. However, highest observed values and highest variance are observed in sites 9, 11, and 13 for NO^3 (**Figure 4A**),

and site 11 for PO_4 (**Figure 4B**). Sites 9-13 are all on tributaries to the main river stem. This demonstrates that the majority of high concentration NO_3 and PO_4 inputs are from tributaries in the lower watershed.

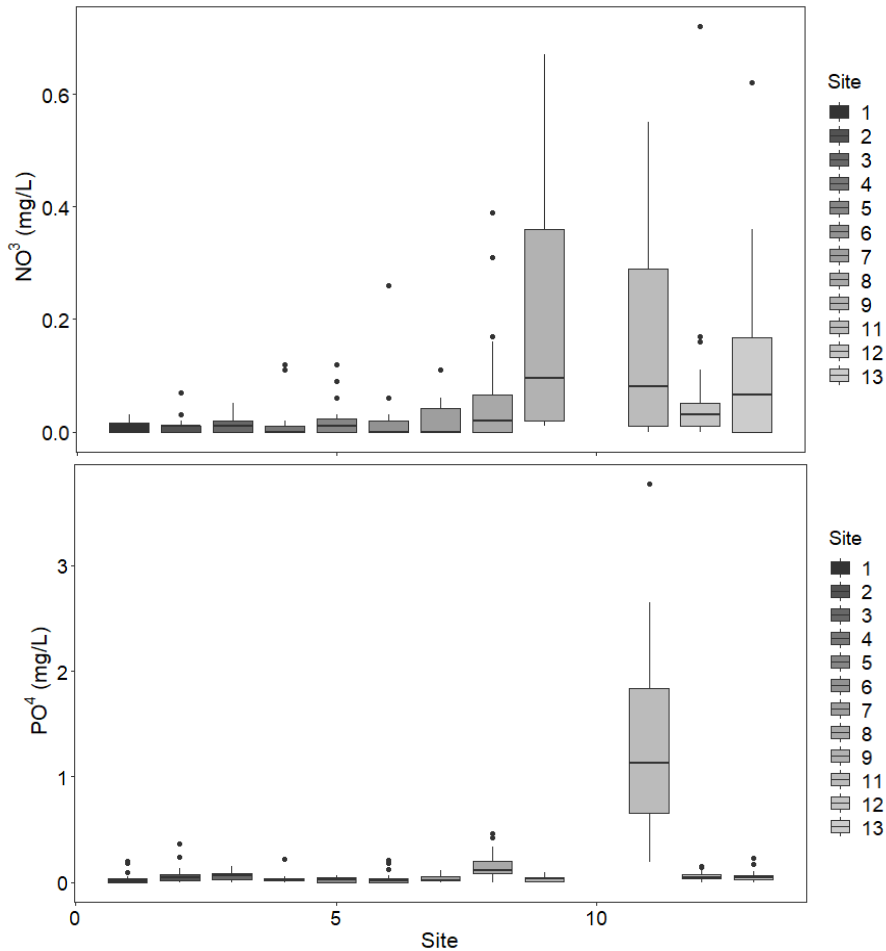


Figure 4. Boxplots of NO_3 (A) and PO_4 (B) from all sampled sites in Bear River watershed from 2016-2019. Horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (± 1.5 SD) outliers.

Total coliform and *E.coli* concentrations varied significantly both spatially and temporally (Figure 5 and Figure 6, respectively). Because of the high range of observed values,

we further examined variation in concentration above the third quartile (75th percentile) of each measurement. Further, to ease interpretation of highly variable line plots, barplots of concentration were used to explore variation in unpartitioned Total coliform (**Figure 5A**).

The highest observed average total coliform measurements were in low elevation tributary sites (primarily in sites 11-13) (**Figure 5A**). However, site 4 (an upper elevation tributary) also contained the highest recorded concentrations in the watershed in 2016, early 2017, and early 2018. All sites showed spikes in concentration in late 2018 (**Figure 5A**). Concentrations of *E. coli* were highest in sites 9-13, all of which are lower watershed tributaries (**Figure 6**), with spikes in early 2016 and late 2018.

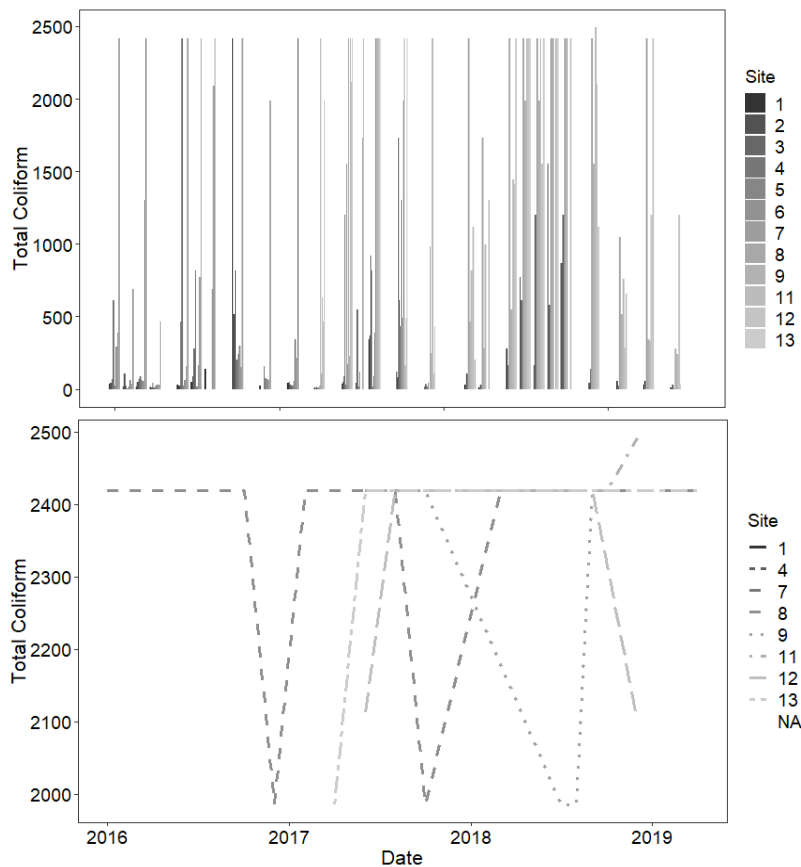


Figure 5. Total Coliform concentration over time and across all sampled sites in Bear River watershed from 2016-2019. A) concentration across all sample dates and locations. B) Concentration only in sites with concentrations above the 3rd quartile of all observations.

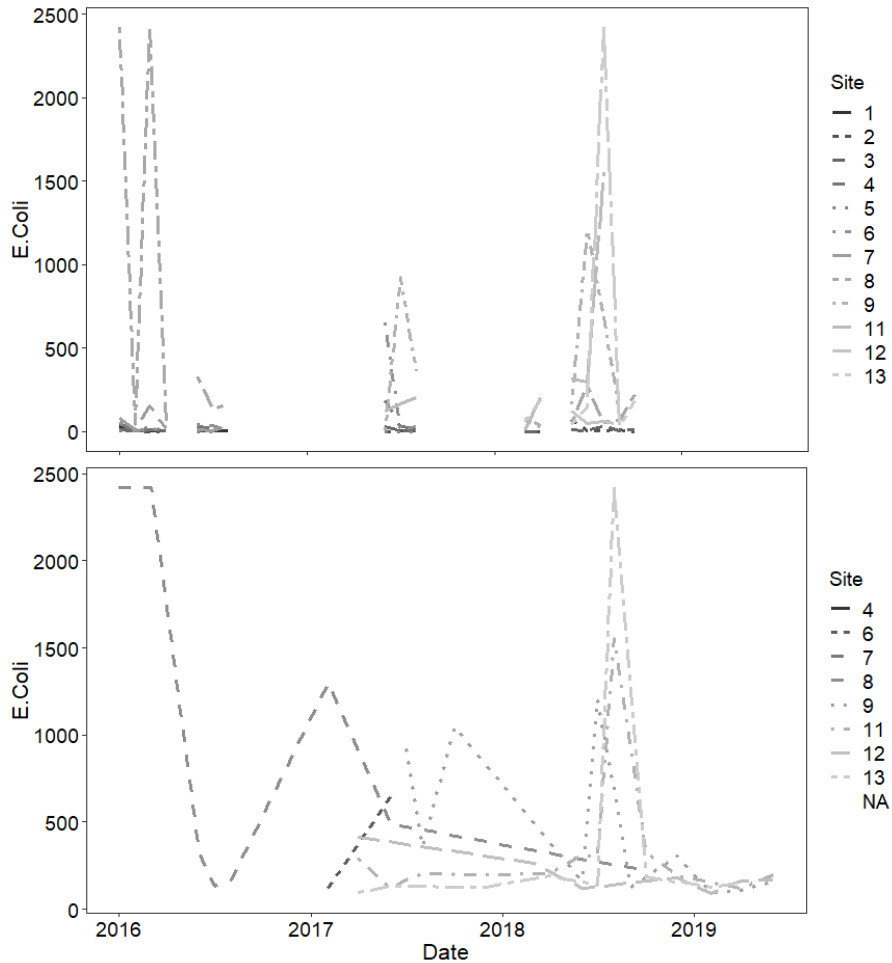


Figure 6. Total *E. coli* concentration over time and across all sampled sites in Bear River watershed from 2016-2019. A) concentration across all sample dates and locations. B) Concentration only in sites with concentrations above the 3rd quartile of all observations.

Dissolved oxygen varied significantly over time, but less so spatially, with a similar relationship to (but inverse relationship with) water temperature (**Figure 7A**). Dissolved oxygen was highest in high elevation sites, and lowest in low elevation sites and tributaries. The lowest observed values were seen in sites 8, 11, and 13 (**Figure 7B**). Sites 11 and 13 are low elevation tributaries, while site 8 represents the lowest elevation sampling point in the watershed.

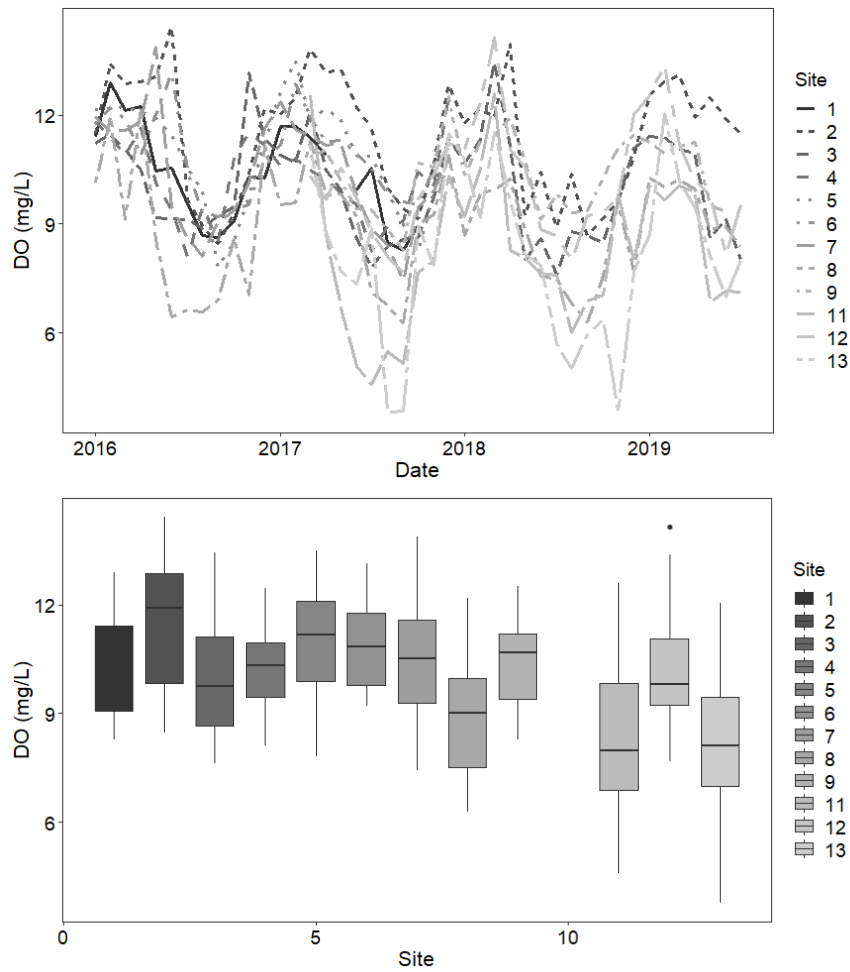


Figure 7. Dissolved oxygen (DO) concentration (mg/L) over time and across all sampled sites in Bear River watershed from 2016-2019. A) Concentration across all sample dates and locations. B) Box plots of concentrations by site across all years. Horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (± 1.5 SD) outliers.

Turbidity was extremely variable, with significant outliers observed in all sites (Figure 8). The highest turbidity was observed at site 4 in early 2017 (Figure 8A). Turbidity was highest and most variable in mid-watershed sites (4-7), the lowest site (8), and lowest at both the high elevation main stem site (1) and the low elevation tributaries (11-13) (Figure 8B).

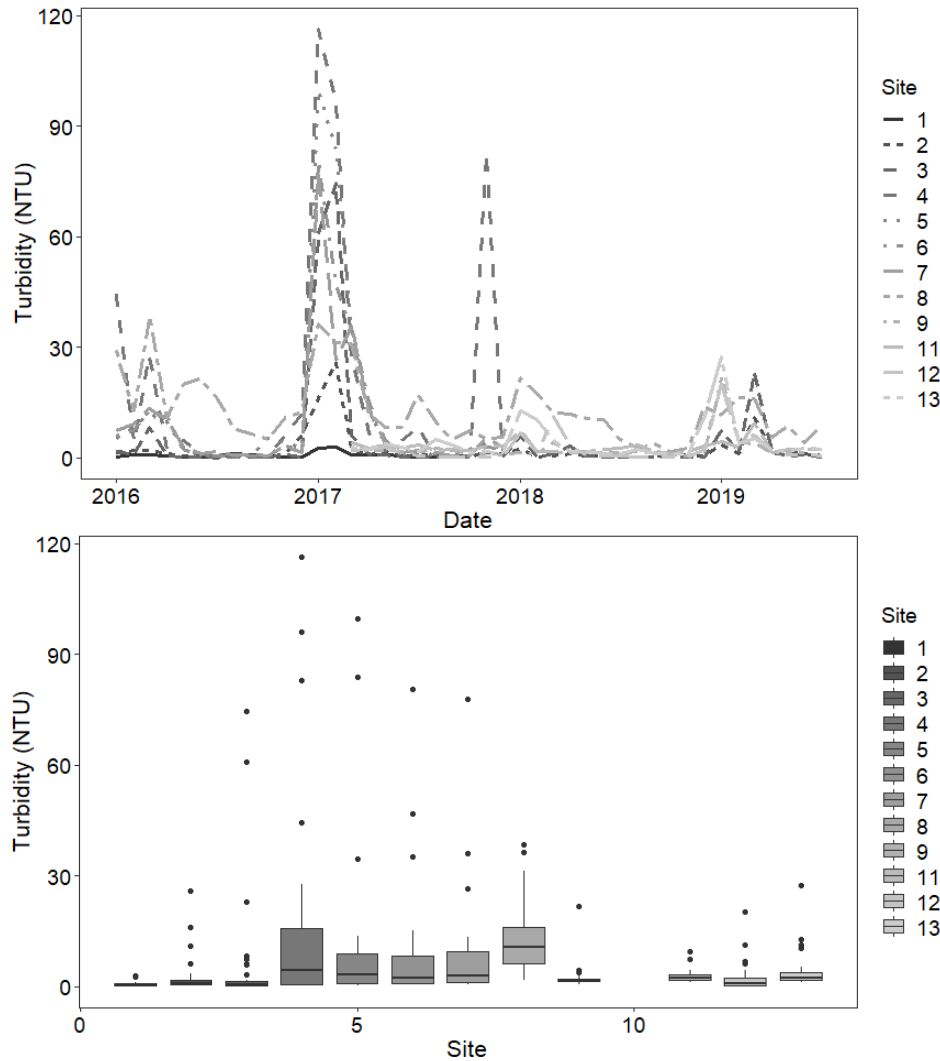


Figure 8. Turbidity (Nephelometric Turbidity Units NTU) over time and across all sampled sites in Bear River watershed from 2016-2019. A) Concentration across all sample dates and locations. B) Box plots of concentrations by site across all years. Horizontal line represents mean value, box contains first and third quartile, vertical line represents range and dots signify extreme (+/- 1.5 SD) outliers.

Benthic Fauna and Water Quality Controls on Community Composition

The BMI-WQ NMDS found a three-dimensional solution, but axes 1 and 2 explained most of the variance (29.3% and 21.1%, respectively) in the BMI community (**Figure 9**). We assessed community differences by site across sampling months (June versus October, **Figure 9**), years (2018 versus 2019, **Figure 10B**), and stream location (tributary versus main stem, **Figure S3**). BMI communities were significantly different across sites, as well as between sampling months (**Figure 9**), and sampling years (**Figure 10B**). Communities primarily diverged along NMDS axis 1, which was associated with variation in pH, dissolved oxygen, PO_4 , *E.Coli*,

and turbidity (**Figure S2**). Conductivity, water temperature, total coliform, and NO_3^- concentration were primarily associated with variation along NMDS axis 2, which represents between-site, within-year and within-month variation. However, no environmental vector had a statistically significant ($p < 0.05$) association with either axis. After paring environmental vectors to only those with slightly significant relationships (here identified as $p < 0.3$), only dissolved oxygen, PO_4^{4-} , and sampling month remained as being associated with variation in BMI community composition (**Figure 9**). Samples from tributaries were not significantly different from main stem samples, counter to observations of significant differences in water quality between tributary and main stem sites (**Figure S3**).

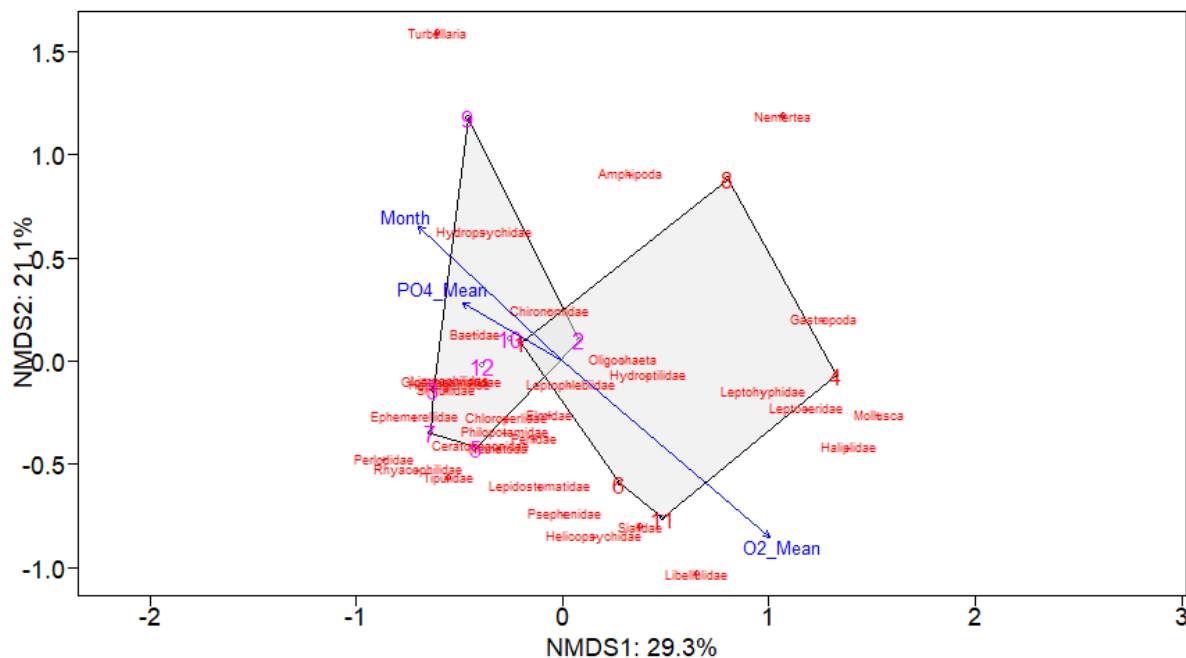


Figure 9. Non-metric multidimensional scaling (NMDS) ordination plot of benthic macroinvertebrate (BMI) communities sampled in the Bear River watershed. Large numbers represent sites. Red text denotes taxon-specific location along each axis. For example, sites further right on axis 1 contain more Mollusca, while sites higher on axis 2 have higher abundance of Turbellaria. Axis percentages represent variance explained. Grey hulls represent grouping by sampling month, with June samples on the right, and October samples on the left. Blue arrows represent linear correlations between listed environmental variables and axes 1 and 2, with arrow direction denoting positive correlation.

We then overlaid BMI MMI values such as FLI and Tolerance values onto final ordinations trimmed to only include significant water quality parameters. All MMI values, including FLI, average weighted tolerance, observed versus expected taxa (O/E), and a raw MMI were significant predictors of variation in community composition (**Figure 10**), across both sampling month (**Figure 10A**), and sampling year (**Figure 10B**). However, tolerance had the highest correlation with community differences of all overlaid vectors.

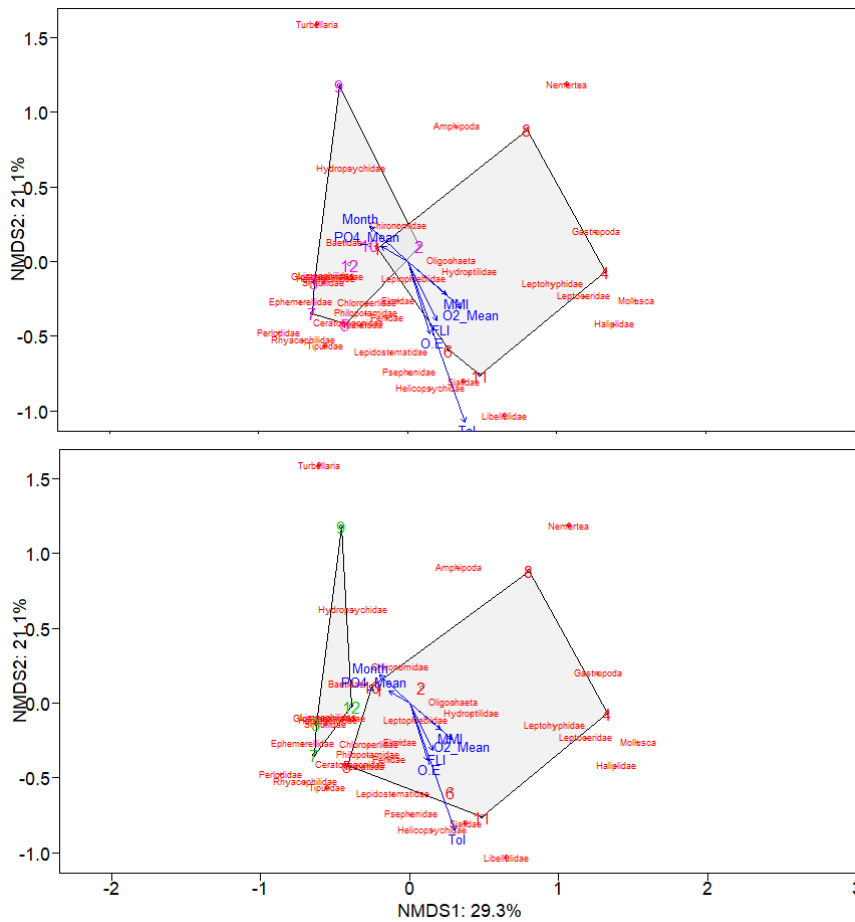


Figure 10. Non-metric multidimensional scaling (NMDS) ordination plot of benthic macroinvertebrate (BMI) communities sampled in the Bear River watershed versus environment and MMI values. Large numbers represent sites. Red text denotes taxon-specific location along each axis. See Figure 9 caption for further explanation. A) Sites separated by sampling month (June on right, October on left). B) Sites separated by sampling year (2018 on left, 2019 on right). Blue arrows represent direction of positive correlation with overlaid variable.

The BMI-Alg ordination found that differences in site composition were correlated with changes in total algal mass (**Figure 11**). However, due to the decreased sample size associated with final ordinations, any quantitative comparisons should be interpreted cautiously. Qualitatively, sites lower in the watershed appear to have both higher algal mass and different community compositions from sites higher in the watershed. Because of the small sample size, we were unable to overlay MMI values onto the BMI-Alg ordination.

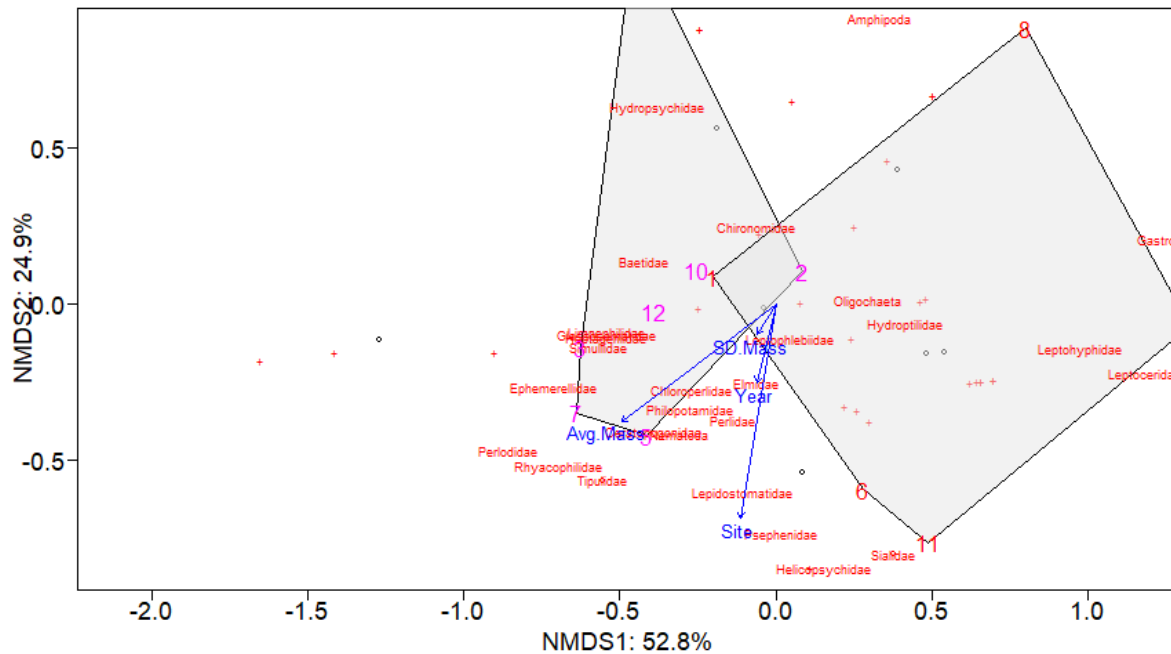


Figure 11. Non-metric multidimensional scaling (NMDS) ordination plot of benthic macroinvertebrate (BMI) communities sampled in the Bear River watershed versus algal mass. Large numbers represent sites. Red text denotes taxon-specific location along each axis. See Figure 9 caption for further explanation. Note that incomplete sampling did not allow a robust NMDS ordination, and only qualitative interpretation is possible (see text).

There was no significant differences in family abundance across sites (Kruskal-Wallis $p > 0.05$) Two families (Chironomida and Elmidae) significantly differed by year ($p < 0.05$), with both taxa decreasing in abundance in 2019 samples (**Figure 12**). Three families (Baetidae, Glossosomatidae, and Hydropsychidae) significantly differed by sampling month across both years ($p < 0.05$), with all three taxa showing higher densities in June than October (**Figure 13**). Due to the distribution of sites in the final NMDS ordination by both month and year, this demonstrates that all five of these families (Baetidae, Chironomidae, Elmidae, Glossosomatide, and Hydropsychidae) are the primary drivers of variation between sample communities.

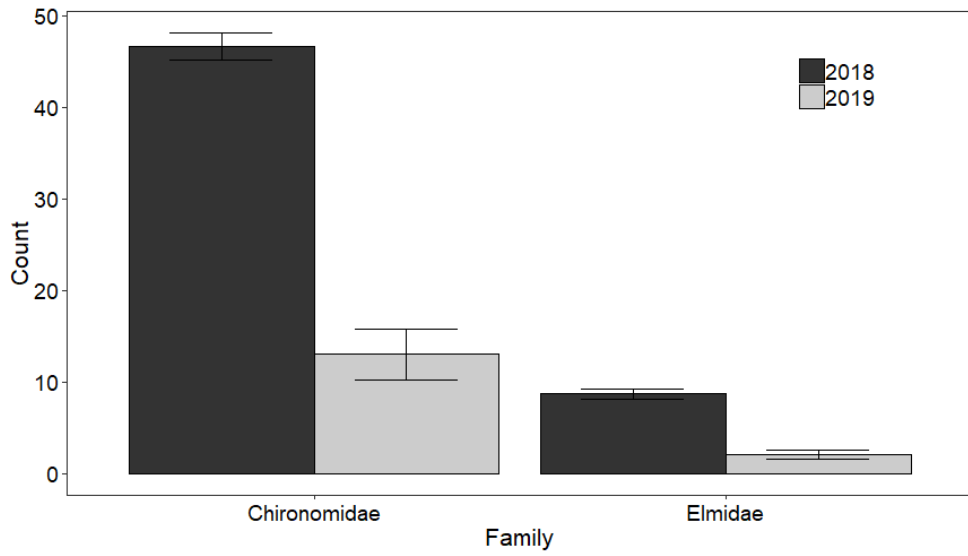


Figure 12. Raw abundance (out of 100 counted BMI) of families that significantly differed between sampling years. Error bars represent standard error of total counts.

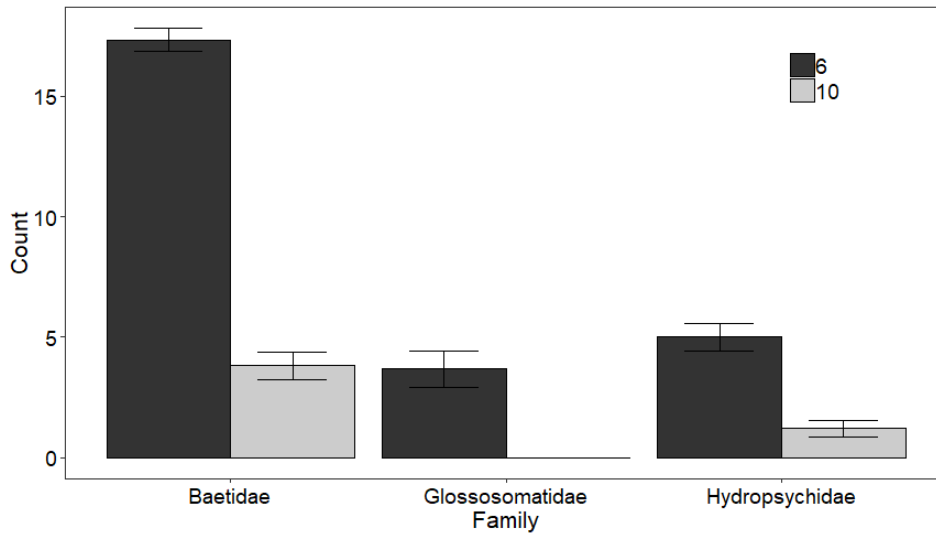


Figure 13. Raw abundance (out of 100 counted BMI) of families that significantly differed between sampling months (6 = June, 10 = October). Error bars represent standard error of total counts.

Interestingly, counter to NMDS overlays, tolerance and MMI did not significantly vary across sites, years, and months when accounting for all other variables (GLM $p > 0.5$). FLI, however, did significantly vary; the only significant GLM was for FLI, with month, NO^3 , conductivity, pH, and sample site identified as significant predictors (**Table 1**). The largest effect was by site, with site 9 having significantly higher FLI when accounting for the effect of all other environmental variation. Interestingly, site 2 (an upstream site) had the lowest FLI of all sampled sites. Out of strictly environmental variables, pH had the highest effect, with a positive relationship between pH and FLI (**Figure 14**). However, the relationship was non-linear across sites and differed between June (**Figure 14A**) and October (**Figure 14B**). Peak FLI was associated with neutral pH (~ 7) in June, and slightly more acidic values (5-7) in October. NO^3 (**Figure 15**) and conductivity (**Figure 16**) had negative effects on FLI, but effects were negligible and varied more across sites.

Table 1. Model results from GLM with family level index (FLI) as response, and all measured water quality variables as predictors. β = coefficient (effect size), SE = standard error of coefficient estimate, p = p-value. Month or site numbers listed in parentheses indicate the effect for that month or site being significant. For example, October had a lower (negative β) FLI than June, while Site 9 (positive β) had a higher FLI than other sites when accounting for all other sources of variation.

Variable	β	SE	p
Intercept	-0.805	1.19×10^{-2}	0.009
Month (Oct.)	-0.265	2.17×10^{-3}	0.005
NO^3	-0.193	4.01×10^{-3}	0.013
Conductivity	-2.97×10^{-3}	2.05×10^{-5}	0.004
pH	0.212	1.36×10^{-3}	0.004
Site (3)	4.37×10^{-2}	2.71×10^{-3}	0.039
Site (8)	0.193	2.54×10^{-3}	0.008
Site (9)	0.520	2.27×10^{-3}	0.003
Site (11)	0.201	2.85×10^{-3}	0.009
Site (12)	0.366	3.12×10^{-3}	0.005

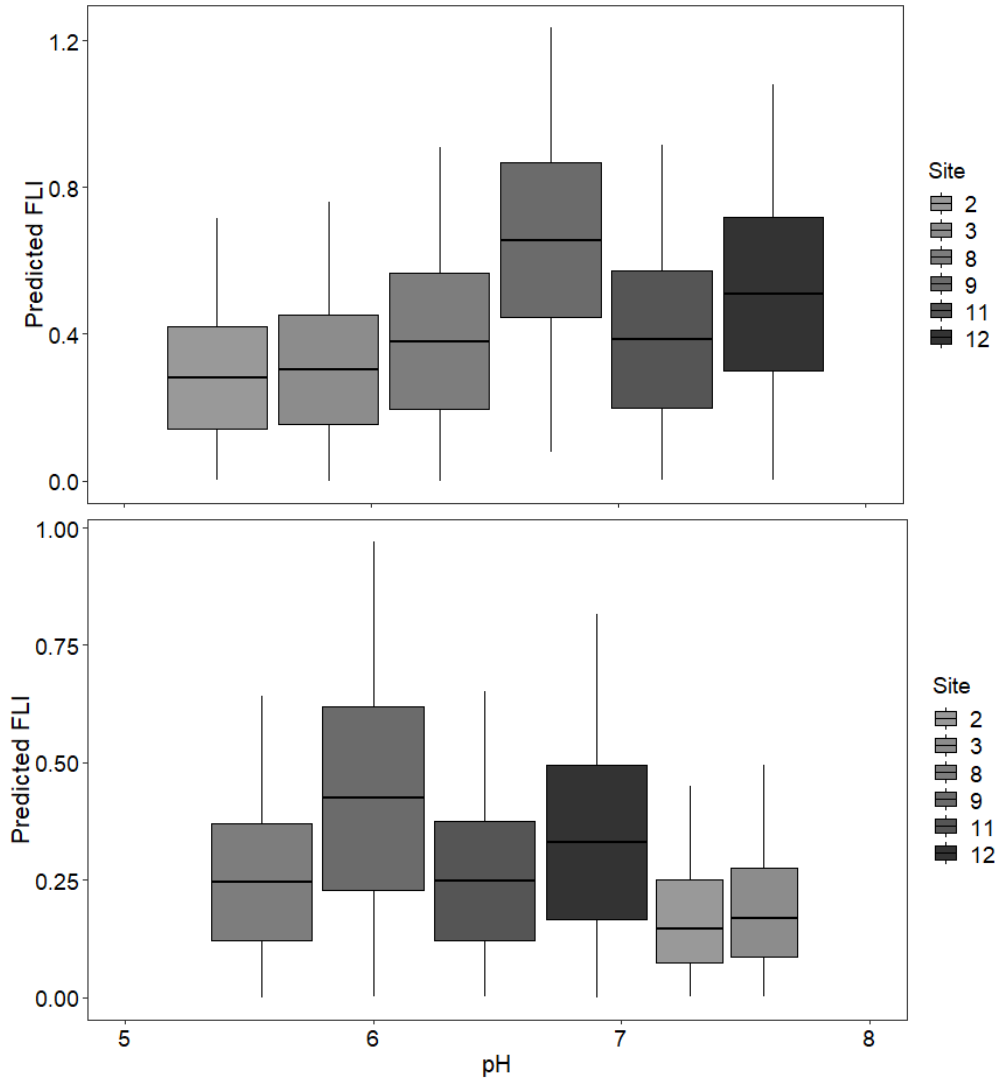


Figure 14. Boxplots of predicted BMI FLI by pH and site while accounting for variation in NO_3 and conductivity. Values predicted using a generalized linear model. A) June FLI. B) October FLI.

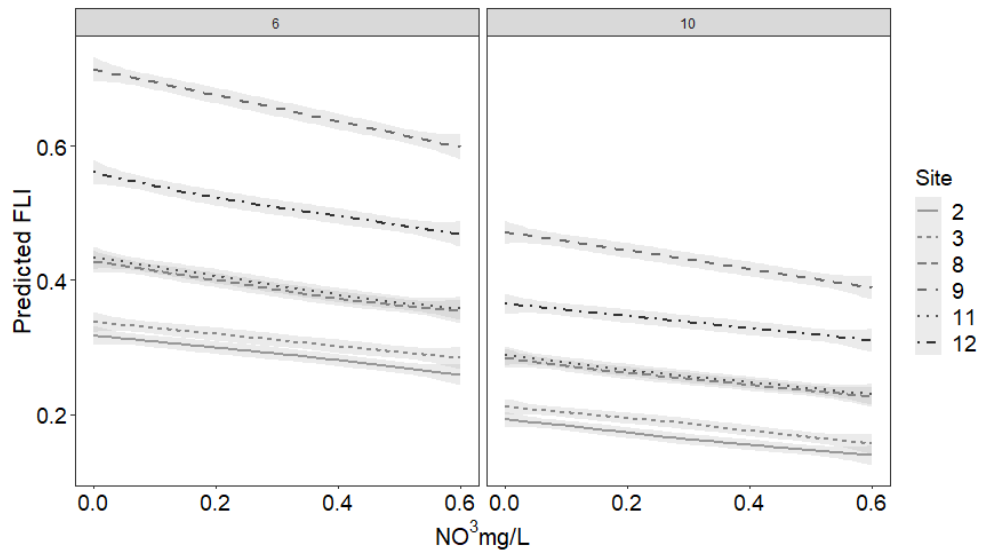


Figure 15. Predicted BMI FLI by month (6 = June, 10 = October), NO³ and site while accounting for variation in pH and conductivity. Values predicted using a generalized linear model.

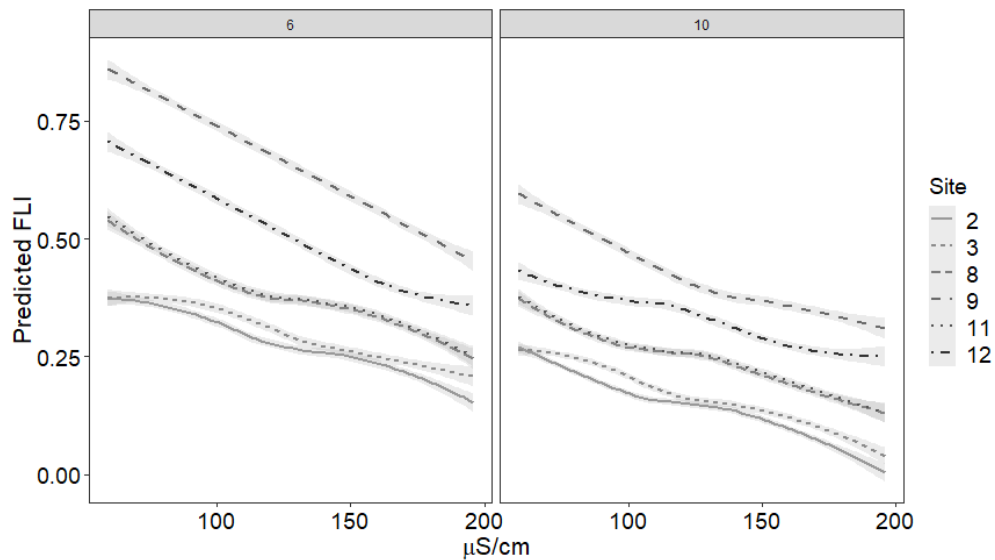


Figure 16. Predicted BMI FLI by month (6 = June, 10 = October), conductivity and site while accounting for variation in pH and NO³. Values predicted using a generalized linear model.

DISCUSSION

Sites and Contaminants of Concern

Site 9 had the highest FLI, on average, that was also very responsive to changes in water quality, but also a very high and highly variable NO_3 concentration. This site is on a short upland tributary of the main stem of the Bear River, and thus may be a fairly pristine stream habitat (in terms of elevation and BMI community) but in a degraded location with various contaminant inputs. Site 12, similarly, is highly degraded in terms of water quality but had a high FLI that was highly responsive to changes in water quality.

Lower watershed sites have higher peak temperature, NO_3 and PO_4 , and turbidity and lower dissolved oxygen, on average. This trend is particularly exaggerated in tributaries and at the lowest sampling point (site 8, which also represents a confluence of all upstream contaminants). However, three of the four sites with the highest FLI values were also on tributaries. We found that the primary families associated with differences in community composition were Baetidae, Chironomidae, Elmidae, Glossosomatidae, and Hydropsychidae, all of which were more abundant in low elevation tributary sites. Thus, low elevation sites appear degraded when examining raw water quality, but not when using FLI as a proxy for biological indication of degradation. Further, site 2, the upmost stream site sampled sufficiently for BMI community composition analysis, was shown to have the lowest FLI, but high water quality. This could be due to FLI being derived from samples that stop at 100 individuals. The FLI has not been fully tested and calibrated in the Bear River watershed to the same extent that a genus level MMI has been at larger regional scales (Mazor et al. 2016).

Endangered, threatened, rare and species of special concern

We consulted the California Natural Diversity Database (CNDDDB) to extract observation records from all quads within the Bear River watershed. We found records of 93 species with varying levels of protection status, including 4 amphibians, 20 birds, 2 crustaceans, 5 fish, 8 insects, 15 reptiles, 38 plants (including 1 bryophyte), and 1 special status vegetative community type (Table S1). Note that not all species included in the table actually occur within the watershed, particularly fish and insect species found primarily in the Central Valley which occur within the same quadrangle as the confluence of the Bear River with the X River. We provide all records here from the CNDDDB, but only refer below to those which are known to occur strictly within the Bear River proper and are likely directly or indirectly associated with variables analyzed in this report.

Endangered or threatened salmonid fish species of concern in the monitoring area are Central Valley steelhead (*Oncorhynchus mykiss irideus*) and Central Valley Spring run Chinook Salmon (*Oncorhynchus tshawytscha*), both anadromous fish that use foothill streams as spawning habitat. For both species, water temperature is of primary concern, with thresholds of

20-22C being associated with increased use of thermal refuges (Keefer et al. 2018). Turbidity has also been shown to be associated with decreased smolt swimming speed, with the lowest observed swimming speeds being seen in times of high temperature and high turbidity (Lehman et al. 2017). Thus, primary management concerns for anadromous fish include maintaining low temperature and low turbidity. Only three sites in the Bear River (8, 12, and 13) are accessible for spawning on the Bear River due to the presence of the Camp Far West Reservoir dam. All three of these sites reached or exceeded the 20-22C thresholds each summer throughout the monitoring period. Turbidity peaks as low as 7 NTU were shown to be associated with decreased swimming speed (Lehman et al. 2017), and all three of our Salmonid-accessible sites experienced turbidity well above these values. Turbidity at sites 12 and 13 was relatively low, but experienced peaks of >25 NTU, while site 8 experienced a peak of >35 NTU.

Presence of listed amphibians is primarily thought to be associated with non-native predator presence and disease, particularly *Batrachochytrium dendrobatidis* (Bd), a fungus which causes chytridiomycosis which often results in frog death (Battaglin et al. 2016). There is little evidence for direct impacts of water quality on special status frog presence. However, degraded water quality is associated with increased non-native competitor and predator presence (such as that of American Bullfrog, *Rana Catesbiana*). Bd presence does not appear to follow any particular water quality parameter, and instead may be associated with host presence and likelihood of successful spread (i.e. vector spatial distribution). However, it is worth noting that relationships among water quality, Bd presence, and listed amphibian presence is still somewhat inconclusive, and direct correlations among e.g. temperature, nutrient concentration, and Bd presence may vary from watershed to watershed and significantly within a watershed. Thus, successful monitoring and management for target listed amphibian species should be based on presence/absence surveys of targets, non-native predators, and Bd throughout the watershed to identify site-specific management targets.

Western Pond Turtle () is primarily responsive to habitat presence for refuge from predators. Water quality variables associated with their presence are...Interestingly, numerous studies have demonstrated that restoration projects focusing strictly on water quality may be associated with degradation of standing pools used as predator refuge.

Recommendations for Future Monitoring

The most noteworthy departures from average watershed conditions are in NO³ and PO⁴ concentrations at sites 9 and 11. These sites represent targets for continued monitoring and upstream expansion of monitoring sites to potentially identify contaminant sources. The high degree of biological degradation (which may or not be sufficiently recorded in FLI values; see below) observed throughout the watershed warrants concern. Low FLI values were recorded in all three major reaches of the river separated by reservoirs, while high FLI values were observed in tributaries. Future monitoring should focus on BMI collection at further upstream sites to establish if the entire watershed is degraded, or if there is point of biological degradation between site 1 and site 2. This point of biological degradation may help further

identify land use or other issues upstream that can be targeted for mitigation of whole-watershed issues.

One particularly noteworthy and time-sensitive trend is that of declining BMI abundance in important families. All five families that were significantly associated with differences in BMI community composition (Baetidae, Chironomidae, Elmidae, Glossosomatidae, and Hydropsychidae) declined significantly between 2018 and 2019. Further sampling is recommended to identify if this trend is transient or indicative of some larger on-going stress.

The complex relationships between site location, water quality, and BMI community composition outlined above warrant continued monitoring, with particular sampling attention paid to sites 1 and 2 (pristine control sites but with potentially degraded BMI communities), site 8 (downstream confluence), sites 9 and 12 (tributary sites with low water quality but high BMI biological integrity), and site 11 (highly degraded). The lack of agreement between theoretical expectation of water quality control on BMI communities and the MMIs used here demonstrate two points for continued evaluation: (1) the FLI may not sufficiently represent biological integrity in the Bear River, either due to insufficient sample size with 100 individuals, or due to a lack of calibration with comparable reference sites with communities representing true degradation in this watershed; and (2) the Bear River represents a unique watershed with complex relationships between stream location, water quality, and biological integrity that warrants further exploration and monitoring before any definitive statements about target sites for preservation or restoration can be made.

The primary water quality parameters associated with changes throughout the watershed appear to be pH, NO_3^- , and conductivity. Thus, these three parameters should continue to be monitored for temporal and spatial sources of variation. However, extreme variation spatially across the watershed demonstrates a need for continued sampling to identify specific sites of concern and further target remediation projects. Further, differences in algal biomass were significant, but statistically could not be evaluated given the limited sample size over a two-year period. In short, the results presented here demonstrate a watershed with a significantly degraded biological community, but not enough information has been gathered to target specific sources of degradation, and further monitoring is warranted, with target sites being identified above, and particular attention paid to pH, conductivity, NO_3^- , and continued sampling of algal biomass.

For target species identified in the CNDDDB, management and monitoring is taxon-specific. For anadromous fish, we recommend continued monitoring of water quality, particularly temperature, dissolved oxygen, and turbidity at sites 8, 12, and 13, paired with salmonid presence surveys. Identification of sources of variation (both spatial and temporal) in temperature, dissolved oxygen, and turbidity can assist in identification of management targets, including late season managed flows....

REFERENCES

Battaglin, W. A., K. L. Smalling, C. Anderson, D. Calhoun, T. Chestnut, and E. Muths. 2016.

Potential interactions among disease, pesticides, water quality and adjacent land cover in amphibian habitats in the United States. *The Science of the Total Environment* 566–567:320–332.

Keefer, M. L., T. S. Clabough, M. A. Jepson, E. L. Johnson, C. A. Peery, and C. C. Caudill. 2018.

Thermal exposure of adult Chinook salmon and steelhead: Diverse behavioral strategies in a large and warming river system. *PLOS ONE* 13:e0204274.

Lehman, B., D. D. Huff, S. A. Hayes, and S. T. Lindley. 2017. Relationships between Chinook

Salmon Swimming Performance and Water Quality in the San Joaquin River, California.

Transactions of the American Fisheries Society 146:349–358.

Mazor, R. D., A. C. Rehn, P. R. Ode, M. Engeln, K. C. Schiff, E. D. Stein, D. J. Gillett, D. B. Herbst,

and C. P. Hawkins. 2016. Bioassessment in complex environments: designing an index for consistent meaning in different settings. *Freshwater Science* 35:249–271.

Ode, P. 2003. List of Californian Macroinvertebrate Taxa and Standard Taxonomic Effort. CA

Department of Fish and Wildlife.

Oksanen, J. 2007. Multivariate Analysis of Ecological Communities in R: Vegan Tutorial. UR L

<http://cc.oulu.fi/~jarioksa/opetus/metodi/vegantutor.pdf> 1.

R Development Core Team. 2017. R: A language and environment for statistical computing. R

Foundation for Statistical Computing, Vienna, Austria.

Rehn, A. C., R. D. Mazor, and P. Ode. 2015. The California Stream Condition Index (CSCI): A New Statewide Biological Scoring Tool for Assessing the Health of Freshwater Streams. CA Department of Fish and Wildlife.

SUPPLEMENTARY INFORMATION

All code used in this analysis can be found in the attached .zip file in the "SSI_Rose_Report.R" script.

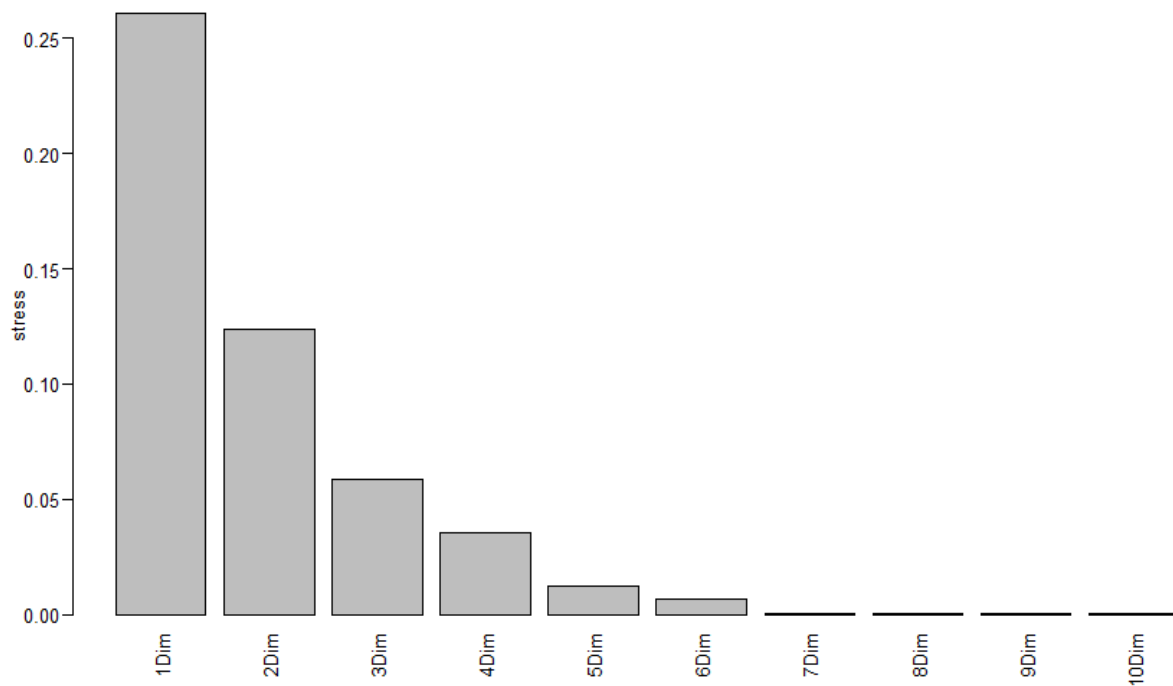


Figure S1. Plot of NMDS stress versus number of solution dimensions. The point at which exponential loss in variance explained (stress) was used to choose final dimensions (three).

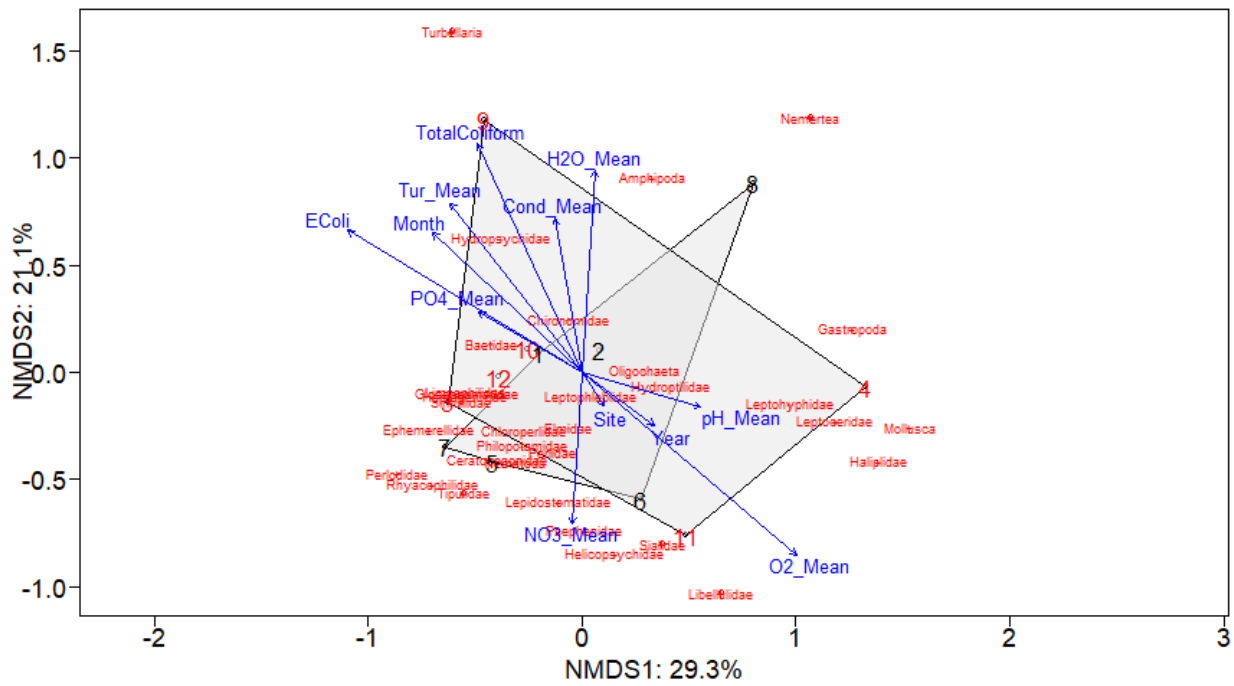


Figure S3. Non-metric multidimensional scaling (NMDS) ordination plot of benthic macroinvertebrate (BMI) communities sampled in the Bear River watershed versus environment, including all water quality variables (unconstrained by significance of correlation). Large numbers represent sites. Grey hulls represent grouping by watershed location (tributary versus mainstem), demonstrating no significant difference by location. Red text denotes taxon-specific location along each axis. See Figure 9 caption for further explanation and final ordination following variable reduction via trimming by statistical significance.

Table S1. Species listed in the California Natural Diversity Database (CNDDDB) quadrangles located on or adjacent to Bear River watershed locations. Note that presence of some species in this list does not equate to presence in the watershed due to quadrangle size. For example, numerous Central Valley-specific taxa are listed but may not be present in the lower watershed, but instead may be present immediately downstream.

Scientific_Name	Common_Name	Federal_Status	State_Status	CDFW_Status	CA_Rare_Plant_Rank
<i>Rana boylei</i>	foothill yellow-legged frog	None	Candidate Threatened	SSC	-
<i>Rana draytonii</i>	California red-legged frog	Threatened	None	SSC	-
<i>Rana muscosa</i>	southern mountain yellow-legged frog	Endangered	Endangered	WL	-
<i>Rana sierrae</i>	Sierra Nevada yellow-legged frog	Endangered	Threatened	WL	-
<i>Accipiter cooperii</i>	Cooper's hawk	None	None	WL	-
<i>Accipiter gentilis</i>	northern goshawk	None	None	SSC	-
<i>Agelaius tricolor</i>	tricolored blackbird	None	Threatened	SSC	-
<i>Aquila chrysaetos</i>	golden eagle	None	None	FP ; WL	-
<i>Ardea alba</i>	great egret	None	None	-	-
<i>Ardea herodias</i>	great blue heron	None	None	-	-
<i>Buteo swainsoni</i>	Swainson's hawk	None	Threatened	-	-
<i>Coccyzus americanus occidentalis</i>	western yellow-billed cuckoo	Threatened	Endangered	-	-
<i>Contopus cooperi</i>	olive-sided flycatcher	None	None	SSC	-
<i>Cypseloides niger</i>	black swift	None	None	SSC	-
<i>Empidonax traillii</i>	willow flycatcher	None	Endangered	-	-
<i>Haliaeetus leucocephalus</i>	bald eagle	Delisted	Endangered	FP	-
<i>Icteria virens</i>	yellow-breasted chat	None	None	SSC	-
<i>Lanius ludovicianus</i>	loggerhead shrike	None	None	SSC	-
<i>Laterallus jamaicensis coturniculus</i>	California black rail	None	Threatened	FP	-
<i>Pandion haliaetus</i>	osprey	None	None	WL	-
<i>Riparia riparia</i>	bank swallow	None	Threatened	-	-
<i>Setophaga petechia</i>	yellow warbler	None	None	SSC	-
<i>Strix nebulosa</i>	great gray owl	None	Endangered	-	-
<i>Strix occidentalis occidentalis</i>	California Spotted Owl	None	None	SSC	-

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<i>Lepidurus packardi</i>	vernal pool tadpole shrimp	Endangered	None	-	-
<i>Linderiella occidentalis</i>	California linderiella	None	None	-	-
<i>Acipenser medirostris</i>	green sturgeon	Threatened	None	SSC	-
<i>Cottus gulosus</i>	riffle sculpin	None	None	SSC	-
<i>Oncorhynchus mykiss irideus pop. 11</i>	steelhead - Central Valley DPS	Threatened	None	-	-
<i>Oncorhynchus tshawytscha pop. 6</i>	chinook salmon - Central Valley spring-run ESU	Threatened	Threatened	-	-
<i>Pogonichthys macrolepidotus</i>	Sacramento splittail	None	None	SSC	-
<i>Anthicus antiochensis</i>	Antioch Dunes anthicid beetle	None	None	-	-
<i>Anthicus sacramento</i>	Sacramento anthicid beetle	None	None	-	-
<i>Bombus caliginosus</i>	obscure bumble bee	None	None	-	-
<i>Bombus occidentalis</i>	western bumble bee	None	Candidate Endangered	-	-
<i>Cicindela hirticollis abrupta</i>	Sacramento Valley tiger beetle	None	None	-	-
<i>Desmocerus californicus dimorphus</i>	valley elderberry longhorn beetle	Threatened	None	-	-
<i>Orobittacus obscurus</i>	gold rush hanging scorpionfly	None	None	-	-
<i>Rhyacophila spinata</i>	spiny rhyacophilan caddisfly	None	None	-	-
<i>Aplodontia rufa californica</i>	Sierra Nevada mountain beaver	None	None	SSC	-
<i>Corynorhinus townsendii</i>	Townsend's big-eared bat	None	None	SSC	-
<i>Erethizon dorsatum</i>	North American porcupine	None	None	-	-
<i>Euderma maculatum</i>	spotted bat	None	None	SSC	-
<i>Lasiurus cinereus</i>	hoary bat	None	None	-	-
<i>Martes caurina sierrae</i>	Sierra marten	None	None	-	-
<i>Myotis evotis</i>	long-eared myotis	None	None	-	-
<i>Myotis thysanodes</i>	fringed myotis	None	None	-	-
<i>Myotis yumanensis</i>	Yuma myotis	None	None	-	-
<i>Pekania pennanti</i>	fisher - West Coast DPS	None	Threatened	SSC	-
<i>Vulpes vulpes necator</i>	Sierra Nevada red fox	Candidate	Threatened	-	-
<i>Margaritifera falcata</i>	western pearlshell	None	None	-	-
<i>Emys marmorata</i>	western pond turtle	None	None	SSC	-
<i>Phrynosoma blainvillii</i>	coast horned lizard	None	None	SSC	-

<i>Thamnophis gigas</i>	giant gartersnake	Threatened	Threatened	-	-
<i>Great Valley Mixed Riparian Forest</i>	Great Valley Mixed Riparian Forest	None	None	-	-
<i>Mielichhoferia elongata</i>	elongate copper moss	None	None	-	
<i>Allium sanbornii</i> var. <i>congdonii</i>	Congdon's onion	None	None	-	
<i>Allium sanbornii</i> var. <i>sanbornii</i>	Sanborn's onion	None	None	-	
<i>Antennaria flagellaris</i>	stoloniferous pussy-toes	None	None	-	
<i>Arctostaphylos mewukka</i> ssp. <i>truei</i>	True's manzanita	None	None	-	
<i>Brodiaea sierrae</i>	Sierra foothills brodiaea	None	None	-	
<i>Calystegia stebbinsii</i>	Stebbins' morning-glory	Endangered	Endangered	-	1B.1
<i>Calystegia vanzuukiae</i>	Van Zuuk's morning-glory	None	None	-	1B.3
<i>Carex sheldonii</i>	Sheldon's sedge	None	None	-	2B.2
<i>Carex xerophila</i>	chaparral sedge	None	None	-	1B.2
<i>Ceanothus fresnensis</i>	Fresno ceanothus	None	None	-	
<i>Chlorogalum grandiflorum</i>	Red Hills soaproot	None	None	-	1B.2
<i>Clarkia biloba</i> ssp. <i>brandegeae</i>	Brandegee's clarkia	None	None	-	
<i>Claytonia parviflora</i> ssp. <i>grandiflora</i>	streambank spring beauty	None	None	-	
<i>Cordylanthus tenuis</i> ssp. <i>brunneus</i>	serpentine bird's-beak	None	None	-	
<i>Cypripedium californicum</i>	California lady's-slipper	None	None	-	
<i>Cypripedium fasciculatum</i>	clustered lady's-slipper	None	None	-	
<i>Darlingtonia californica</i>	California pitcherplant	None	None	-	
<i>Eriogonum tripodum</i>	tripod buckwheat	None	None	-	
<i>Fremontodendron decumbens</i>	Pine Hill flannelbush	Endangered	Rare	-	1B.2
<i>Fritillaria eastwoodiae</i>	Butte County fritillary	None	None	-	
<i>Githopsis pulchella</i> ssp. <i>serpentinicola</i>	serpentine bluecup	None	None	-	
<i>Jensia yosemitana</i>	Yosemite tarplant	None	None	-	
<i>Juncus digitatus</i>	finger rush	None	None	-	1B.1
<i>Lathyrus sulphureus</i> var. <i>argillaceus</i>	dubious pea	None	None	-	
<i>Lewisia cantelovii</i>	Cantelow's lewisia	None	None	-	1B.2

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<i>Lilium humboldtii ssp. humboldtii</i>	Humboldt lily	None	None	-	
<i>Lycopodiella inundata</i>	inundated bog-clubmoss	None	None	-	2B.2
<i>Packera layneae</i>	Layne's ragwort	Threatened	Rare	-	1B.2
<i>Perideridia bacigalupii</i>	Bacigalupi's yampah	None	None	-	
<i>Phacelia stebbinsii</i>	Stebbins' phacelia	None	None	-	1B.2
<i>Poa sierrae</i>	Sierra blue grass	None	None	-	1B.3
<i>Rhynchospora capitellata</i>	brownish beaked-rush	None	None	-	2B.2
<i>Sagittaria sanfordii</i>	Sanford's arrowhead	None	None	-	1B.2
<i>Sidalcea gigantea</i>	giant checkerbloom	None	None	-	
<i>Sidalcea stipularis</i>	Scadden Flat checkerbloom	None	Endangered	-	1B.1
<i>Streptanthus longisiliquus</i>	long-fruit jewelflower	None	None	-	
<i>Viola tomentosa</i>	felt-leaved violet	None	None	-	