
# Eddleston Water Restoration Project
# Macroinvertebrate responses 2012-2019

## Tweed Forum

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## Revision and Amendment Register

| Version Number | Date | Sections | Pages | Summary of Changes | Approved by |
|---|---|---|---|---|---|
| 1.0 | 09/04/2020 | 1 | 25 | Interim report with summary of main findings | D. Bradley |
| 2.0 | 11/06/2020 | 4 | 28 | Draft final report | D. Bradley |
| 3.0 | 30/06/2020 | 4 | 32 | Final report addressing comments from J. Dodd. | D. Bradley |

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# Executive Summary


The Eddleston Water Project is a major national research project that aims to generate robust evidence of the impact, cost and benefits of working with natural processes to deliver Natural Flood Management (NFM) at multiple scales from the location of the individual measures, through to the cumulative effect at the catchment scale.

This report evaluates the impact of channel reconfiguration on the benthic macroinvertebrate community in Eddleston Water using data from a bespoke Before-After-Control-Impact (BACI) monitoring framework. Monitoring was conducted before (2012 to summer 2013), immediately following (autumn 2013 to 2015) and after (2016, 2017 and 2019) channel reconfiguration at two 'impact' sites (Lake Wood and Cringletie), and also at two 'control' sites: one (Signal Cottage) located upstream and one located (Rosetta) downstream of the impact sites. Macroinvertebrate community composition was measured at the mesohabitat-scale and reach-scale using a suite of ten biotic metrics (WHPT-ASPT; family- and species-level LIFE; family- and species-level PSI; taxon richness; total abundance; CCI; % of total abundance of Ephemeroptera, Plecoptera and Trichoptera (%EPT); and % of total abundance of oligochaetes and chironomids (%OligoChiro)). Changes in response to the channel reconfiguration work were interpreted in terms of changes in mesohabitat composition at the four sites.

The key results are as summarised below.

1. Prior to channel reconfiguration, the two impact sites – Lake Wood and Cringletie – had much less riffle/run and more glide habitat than the two control sites and had lower values than the two control sites for seven out of the eight biotic metrics (exception was %EPT).
2. Channel reconfiguration in 2013 initially increased the proportion of riffle and run habitat and increased overall habitat diversity, but subsequent geomorphological adjustment appears to have partially reversed these changes.
3. Against a background of rapidly increasing taxon richness at all sites, channel reconfiguration caused an abrupt shift in macroinvertebrate community composition at the impact sites from one dominated numerically by mayflies, stoneflies and caddisflies to one dominated by oligochaetes and chironomids.
4. Following the initial disturbance caused by the channel reconfiguration work, the impact and control sites have partially converged in macroinvertebrate composition but only total abundance and the %OligoChiro have increased significantly as a result of the intervention.
5. Six years after the channel reconfiguration work, five of the biotic indices (WHPT-ASPT, LIFE-species, PSI-family, PSI-species, and %EPT) remain significantly lower at the impact sites compared with the control sites.

In conclusion, the benthic macroinvertebrate community in Eddleston Water appears to be strongly influenced by mesohabitat composition. Channel reconfiguration has led to a partial improvement in macroinvertebrate community status (as measured by a variety of standard biotic indices) but full recovery from historical channel straightening is thought to have been constrained to date by the limited geomorphological changes at Lake Wood and Cringletie.

# 1. Introduction and Methods

## 1.1 The Eddleston Water Project

The Eddleston Water Project is a major national research project that aims to generate robust evidence of the impact, cost and benefits of working with natural processes to deliver Natural Flood Management (NFM) at multiple scales from the location of the individual measures, through to the cumulative effect at the catchment scale. Delivering NFM and environmental benefits from the restoration of natural habitats will expand the current knowledge base and aim to demonstrate the multiple benefits possible from NFM.

The three main aims of the Eddleston Water Project are:

1. to investigate the possibility of reducing the risk of flooding to the communities of Eddleston and Peebles by restoring some of the original natural features of the river, its flood plain and surrounding hill slopes;
2. to examine the potential for added benefits for wildlife and fisheries though improvements to river habitats; and
3. to work with landowners and communities in the Eddleston valley to maximise the benefits they would gain from such work, whilst maintaining the profitability of local farms.

In order to address the second aim, a monitoring strategy has been established to assess the effects of NFM measures on macroinvertebrates, macrophytes, fishes and geomorphology. Building on earlier studies (Veritas Ecology 2017; APEM 2018), this report evaluates the impact of channel reconfiguration on the benthic macroinvertebrate community in Eddleston Water using data from a bespoke Before-After-Control-Impact (BACI) monitoring framework (Feld et al. 2011). Mesohabitat- and reach-level macroinvertebrate sample data from control and impact sites were analysed to:

- describe the spatial and temporal patterns in macroinvertebrate composition;
- explore how these patterns are related to mesohabitat composition; and
- evaluate the local impact on macroinvertebrates of channel reconfiguration.

## 1.2 Experimental design

Eddleston Water is a tributary of the River Tweed. Monitoring was conducted before (2012 to summer 2013), immediately following (autumn 2013 to 2015) and after (2016, 2017 and 2019) channel reconfiguration at two 'impact' sites (Lake Wood and Cringletie), and also at two 'control' sites: one (Signal Cottage) located upstream and one located (Rosetta) downstream of the impact sites. Figure 1.1 shows the macroinvertebrate sampling locations.

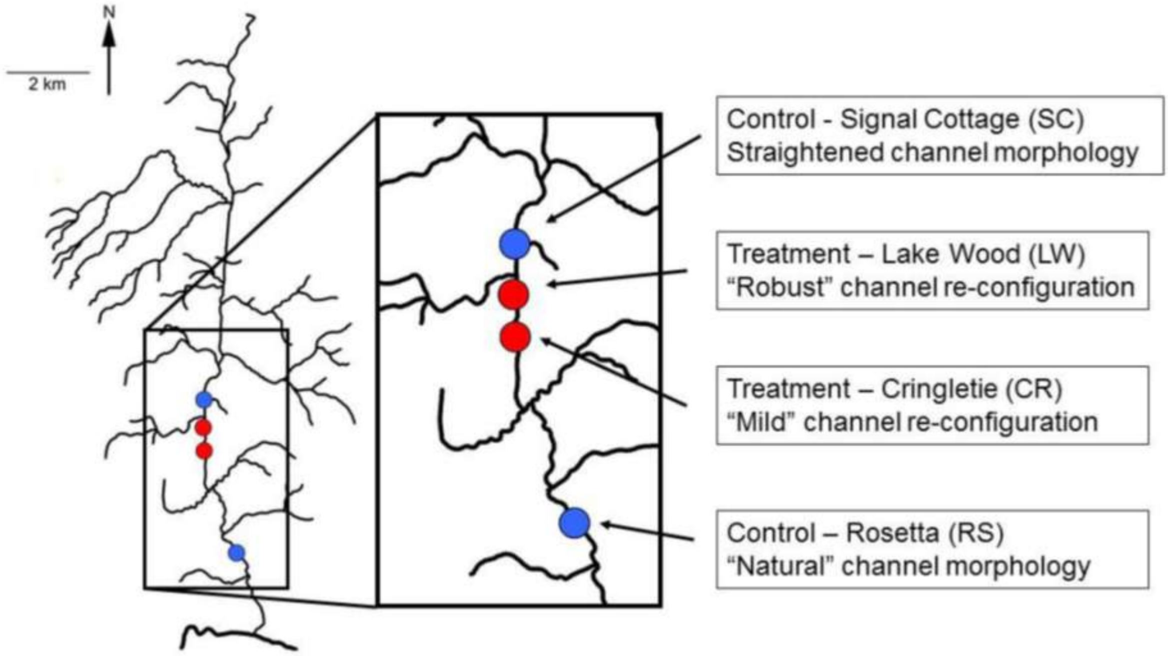


**Figure 1.1 Schematic diagram of the experimental design showing the treatment (red circles) and control (blue circles) sites where macroinvertebrate samples were collected**

At the impact sites, a new meandering channel was excavated, and the old channel was filled in. The details of the channel reconfiguration work differed slightly at the two sites.

1. The new channel at Lake Wood was much more sinuous than the new channel in Cringletie.
2. No substrate material was transferred from the old channel to the new at Lake Wood, as there was ample diversity of substrate encountered where the new channel was excavated. In contrast, at Cringletie, the material that was excavated to create the new channel was very soft and homogenous, and so material was taken from the old bed and laid in the new channel to create some harder patches of riffles.

Despite these differences, the two locations treated as replicate impact sites for evaluation purposes. The works were completed on 25/07/2013 at Cringletie and on 11/09/2013 at Lake Wood. Similarly, Signal Cottage and Rosetta were treated as replicate control sites despite having contrasting straightened and natural morphologies.

## 1.3 Field sampling

Macroinvertebrate samples were collected by SEPA in spring (all years), summer (2012-2014 only) autumn (all years except 2012). All samples were collected by the same operator for the duration of the project to minimise operator variability. Samples were collected using a modified version of the kick/sweep sampling method used by UK government agencies for monitoring under the EU Water Framework Directive (Environment Agency, 2017). A total of 20 kick samples were taken at each site, split proportionately between five mesohabitat types (riffle, run, glide, pool and slack). Three replicates were collected from each mesohabitat type on each sampling date. The exception was 2012, when a single threeminute kick/sweep sample was taken from each site on each sampling date. An overview of the sampling programme is provided in Appendix 1.

## 1.4 Laboratory sample analysis

Aquatic macroinvertebrate samples were analysed in accordance with the requirements outlined in SEPA's for mixed taxon level analysis (ES-Ecol-p-021). Samples were initially washed inside a fume cupboard using a 500µm sieve to remove fine silt and preservative. Samples were subsequently sorted to Mixed Taxon Level 5 (TL5) in accordance with SEPA Procedure ES-Ecol-G-007. Actual abundances were recorded rather than logarithmic abundances for counts up to 100. If abundances were greater than 100 then estimates of abundance will be calculated by multiplying the abundance within one quadrat by the number of quadrats within one sorting tray.

## 1.5 Data analysis

The 20 individual kick samples taken on each sampling occasion were aggregated to produce a single sample for each mesohabitat type ('habitat-scale' samples). These were then aggregated again to produce a single 'reach-scale' sample.

Macroinvertebrate community composition was measured at the mesohabitat-scale and reach-scale using a suite of eight biotic indices, detailed in Table 1.1.

**Table 1.1 Macroinvertebrate biotic indices analysed in this study**

| Index | Description |
|---|---|
| WHPT_ASPT | Whalley-Hawkes-Paisley-Trigg Average Score Per Taxon – an index of overall biological quality using macroinvertebrate families (Paisley, Whalley & Trigg, 2013). |
| LIFE_F | Lotic-invertebrate Index for Flow Evaluation – indexes the effect of flow variations on macroinvertebrate communities (Extence, Balbi & Chadd, 1999). Calculated at species level. |
| LIFE_S | Lotic-invertebrate Index for Flow Evaluation – indexes the effect of flow variations on macroinvertebrate communities (Extence, Balbi & Chadd, 1999). Calculated at species level. |
| PSI_F | Proportion of Sediment-sensitive Invertebrates – describes the degree to which river sites are impacted by fine sediment (Extence et al. 2011). Calculated at family level. |
| PSI_S | Proportion of Sediment-sensitive Invertebrates – describes the degree to which river sites are impacted by fine sediment (Extence et al. 2011). Calculated at species level. |
| Taxon richness | Count of the number of distinct taxa identified in the sample. |
| Total abundance | Estimated total number of macroinvertebrates in the sample. |
| CCI | Community Conservation Index – provides a standardised measure of the conservation value of macroinvertebrate communities at a site which can be compared across sites throughout Great Britain. CCI reflects both the rarity of the species found within each sample and the overall diversity of the sample. (Chadd & Extence, 2004). |
| %EPT | Ephemeroptera, Plecoptera and Trichoptera as a % of total abundance – |

| | |
|---|---|
| | indicates the relative abundance of three environmentally sensitive macroinvertebrate groups. |
| %OligoChiro | Oligochaeta and Chironomidae as a % of total abundance – indicates the relative abundance of two environmentally insensitive macroinvertebrate groups. |

The effect of the channel reconfiguration work on each biotic index at a reach scale was evaluated using a mixed-effects regression model to test for a statistically significant (α=0.05) interaction between treatment (Control or Impact) and time period (Before, Following and After channel reconfiguration). Time (year and month of sampling) and Site were included as crossed random effect to measure and account for the year-to-year and site-to-site variability. The structure of the model reflected the BACI sampling design and was designed to test the null hypothesis that the temporal patterns at the control and impact sites were the same; consequently, no model simplification was carried out. Diagnostic plots were examined to verify that the assumptions of homogeneous variance and independent, normally distributed errors.

The results were interpreted in terms of changes in mesohabitat composition at the four sites, and by comparing the habitat-level indices among sites.

All statistical analyses were performed using R v3.6.1 (R Core development Team 2020).

# 2. Results

## 2.1 How do the sites differ in mesohabitat composition, and how has this changed over time?

Figure 2.1 plots the proportion of riffle, run, glide, slack and pool at each of the four sites over the 2012-2019 study period. The two control sites – Signal Cottage and Rosetta – both had predominantly riffle and run habitat, despite having contrasting straightened and natural morphologies. Mesohabitat composition fluctuated slightly over time, with a slight trend towards more glide habitat at Signal Cottage.

By contrast, the two impact sites – Lake Wood and Cringletie – had a majority of glide and slack habitat prior to restoration. Immediately following channel reconfiguration, the proportion of riffle and run habitat at Lake Wood increased from 30% to 85% but then reduced to ca. 50% over the next two years. Similarly, channel reconfiguration initially increased the proportion of run habitat at Cringletie from 10% to 85% and created some new riffles (5%), but over the next two years the proportion of run and riffle reduced back to ca. 40%.


**Figure 2.1 Changes in proportional mesohabitat composition 2012-2019, based on the allocation of kicks to habitat units. Note: habitat re-configuration was completed on 25/07/2013 at Cringletie and on 11/09/2013 at Lake Wood.**

## 2.2 How do the sites differ in macroinvertebrate community composition, and how has this changed over time?

Figure 2.2 to Figure 2.11 illustrate the changes in macroinvertebrate community composition at the four sampling locations before, following and after channel reconfiguration. Detailed statistical comparison of sites and time periods is presented in Appendix 2.

With the exception of WHPT_ASPT, which was significantly higher in autumn and lower in summer, none of the metrics displayed clear seasonal differences.

In the Before period, prior to channel reconfiguration, nine of the ten biotic indices (the exception was %EPT) were lower at the Lake Wood and Cringletie impact sites than at the two control sites. However, the limited amount of baseline (pre-intervention) data limited statistical power to detect any impact of historical channel straightening, and only LIFE_F, LIFE_S and PSI_F showed a statistically significant difference between impact and control sites.

Over the entire (2012-2019) monitoring period, there was a strong and highly significant ($p < 0.001$) increase in **taxon richness** at all sites, from a mean of ca. 25 per site in 2012 to a mean of over 60 per site by 2019 (Figure 2.7). Mirroring this, there was also a less pronounced but statistically significant ($p = 0.001$) increase in **WHPT-ASPT** (Figure 2.2) and **CCI** (Figure 2.9). The reason for this underlying trend is not known; Eddleston Water has been consistently classed as High status for water quality and Good for macroinvertebrates under the Water Framework Directive (WFD), so there is no evidence that the river is recovering from historical water pollution. Nonetheless, there were no statistically significant differences between control and impact locations and all four sites exhibited similar trends, so there was no evidence that channel reconfiguration affected these three indices.

Prior to the channel reconfiguration work, mayflies, stoneflies and caddisflies (**%EPT**) accounted for ca. 50% of total abundance across all sites and there was no significant difference between the control and impact locations. Immediately following channel reconfiguration, %EPT at Lake Wood and Cringletie fell to 5% ($p <0.001$) but by autumn 2014 %EPT has increased again and was similar to pre-work levels (Figure 2.10). Between 2015 and 2019 there was a small (non-significant) increase in %EPT at the two control sites (relative to the before period) but this was not mirrored at the two impact sites. As a result, %EPT at the impact sites decreased relative to the control sites during the After period ($p <0.01$; Figure 2.10). Exactly the opposite pattern was observed for **%OligoChiro** (Figure 2.11). Thus, channel reconfiguration caused an abrupt shift in macroinvertebrate community composition from one dominated numerically by mayflies, stoneflies and caddisflies to one dominated by oligochaetes and chironomids, which are rapid colonisers of newly created or freshly disturbed substrates. As a consequence, **total abundance** at the two impact sites increased ($p < 0.001$) by 153% between the Before and Following periods (relative to the controls) and remained 50% higher in the After period (Figure 2.8).

Prior to channel reconfiguration, **LIFE_S** was on average 0.19 lower at the impact sites than at the control sites ($p = 0.004$), which is consistent with the lower proportion of riffle and run habitat at Lake Wood and Cringletie (Figure 2.3). Following channel reconfiguration, mean LIFE_S decreased sharply at the two control sites ($P < 0.001$). LIFE_S also decreased at the two impact sites, but by a smaller ($p = 0.04$) amount, suggesting that the intervention had the effect of holding up LIFE_S scores at Lake Wood and Cringletie. In the After period, LIFE_S at the two control sites recovered and in the most recent year of sampling (2019), LIFE_S was again 0.23 lower at the impact sites than at the control sites (Figure 2.3). A similar pattern was observed for **LIFE_F**. However, the reduction in LIFE_F was more prolonged at the control sites and minimal at the impact sites, and so the results had a higher level of statistical significance.

Finally, **PSI_S** was marginally lower (3 percentage points) at the impact sites than at the control sites during the Before period ($p = 0.07$). In the After period, PSI_S increased by 5.7 percentage points at the control sites ($p = 0.008$) but only by 2.0 percentage points at the impacts sites (Figure 2.5); the different responses at the control and impacts sites were marginally non-significant ($p = 0.06$). **PSI_F** was also lower (4 percentage points) at the impact sites than at the control sites during the Before period ($p = 0.01$), but there was no evidence that channel reconfiguration altered PSI_F at the impact sites.

In the After period (2016-2019), there was no significant difference between impact and control sites in taxon richness, total abundance, CCI or %OligoChiro, but WHPT-ASPT, LIFE_S, PSI_S and %EPT were all significantly lower at the impact sites than at the control sites.

As well as testing for an effect of channel reconfiguration, the models were also able to partition the unexplained variation in the data into component sources of error (see the 'Random effects' in the model outputs in Appendix 2). Without exception, the single largest source of unexplained variation in every model was **residual variation**; this comprises both measurement error (i.e. the random variability observed among replicate samples) *and* site-specific trends (i.e. temporal changes in mean metrics scores at individual sites that cannot be explained by season, time period, or year/month of sampling). The variance attributable to **time** (the variability in mean metric scores from sampling visit to another) was at least an order of magnitude lower than the residual variance for WHPT-ASPT, LIFE, PSI and CCI. For the other metrics, the time variance was 1.5 to 2 times smaller than the residual variance. Finally, the variance attributable to **site** (i.e. the variability in mean metric scores among replicate control and impact sites) was universally very small, and sometimes estimated to be 0. Thus, after accounting for the fixed effects in the model, there appears to be relatively little temporal variability that is consistent across all sites and little spatial variability that is consistent over time. Instead, each site exhibits its own idiosyncratic temporal behaviour, and measurement error is appreciable despite the same ecologist collecting all the samples (i.e. no inter-operator variability) and using a well-established sampling protocol.

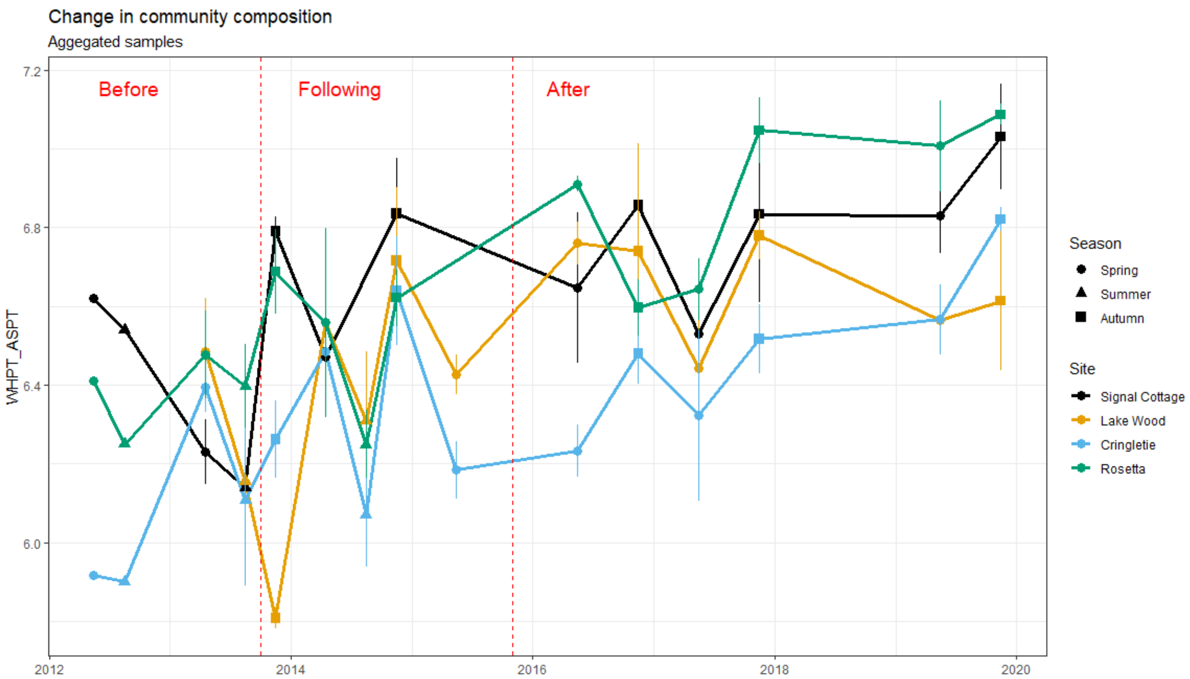


**Figure 2.2 Change in WHPT-ASPT score at the four sampling locations before, following and after channel reconfiguration**

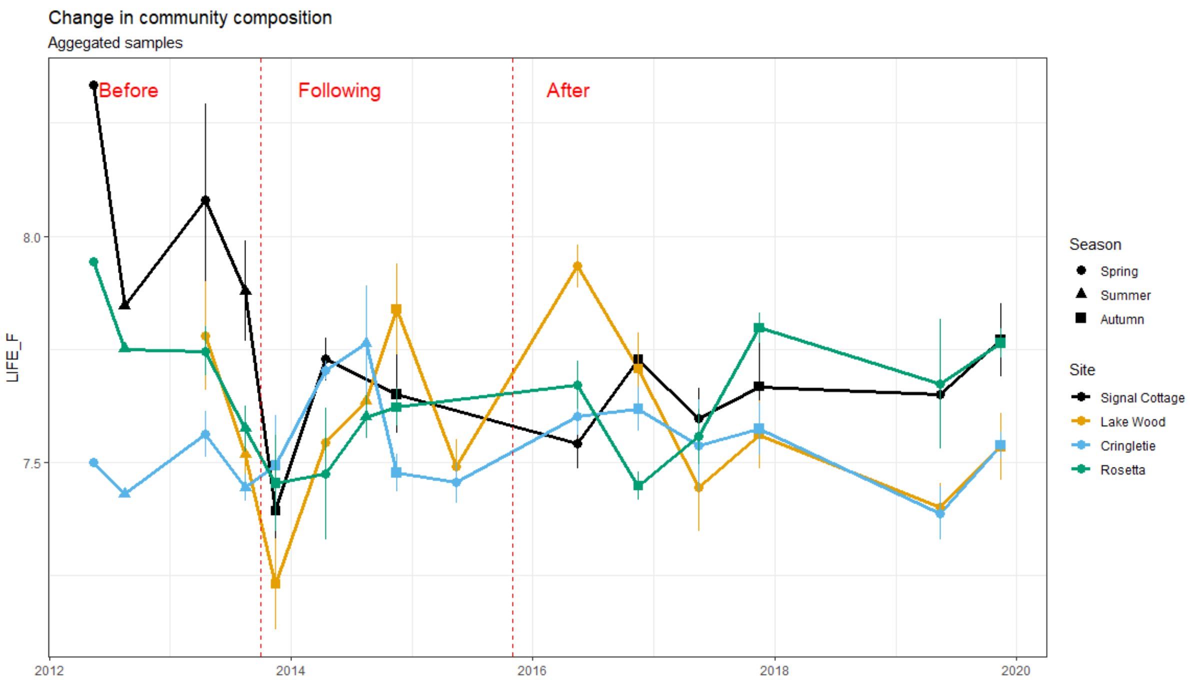


**Figure 2.3 Change in family-level LIFE score at the four sampling locations before, following and after channel reconfiguration**

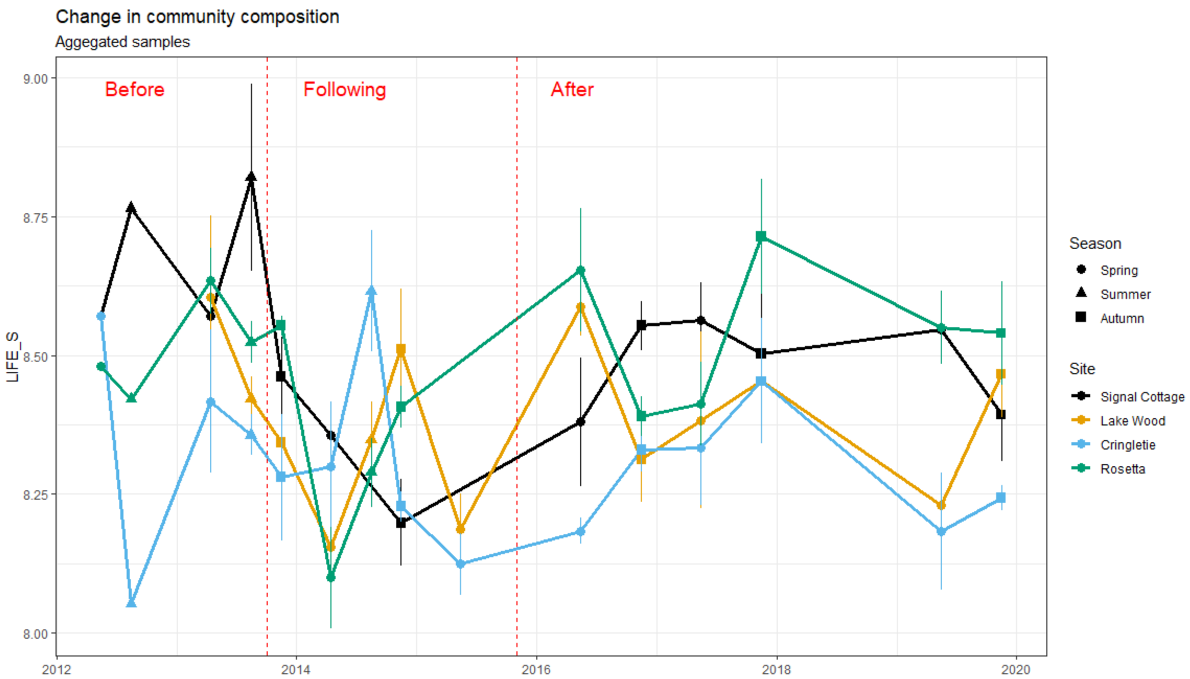


**Figure 2.4 Change in species-level LIFE score at the four sampling locations before, following and after channel reconfiguration**

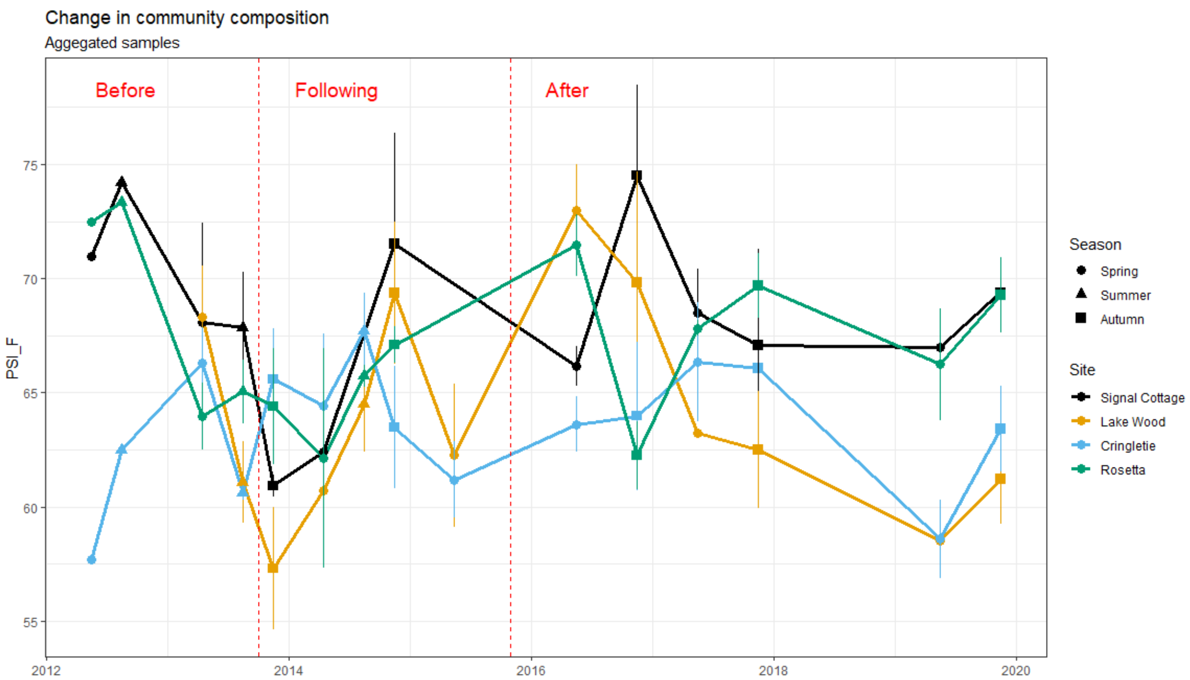


**Figure 2.5 Change in family-level PSI score at the four sampling locations before, following and after channel reconfiguration**

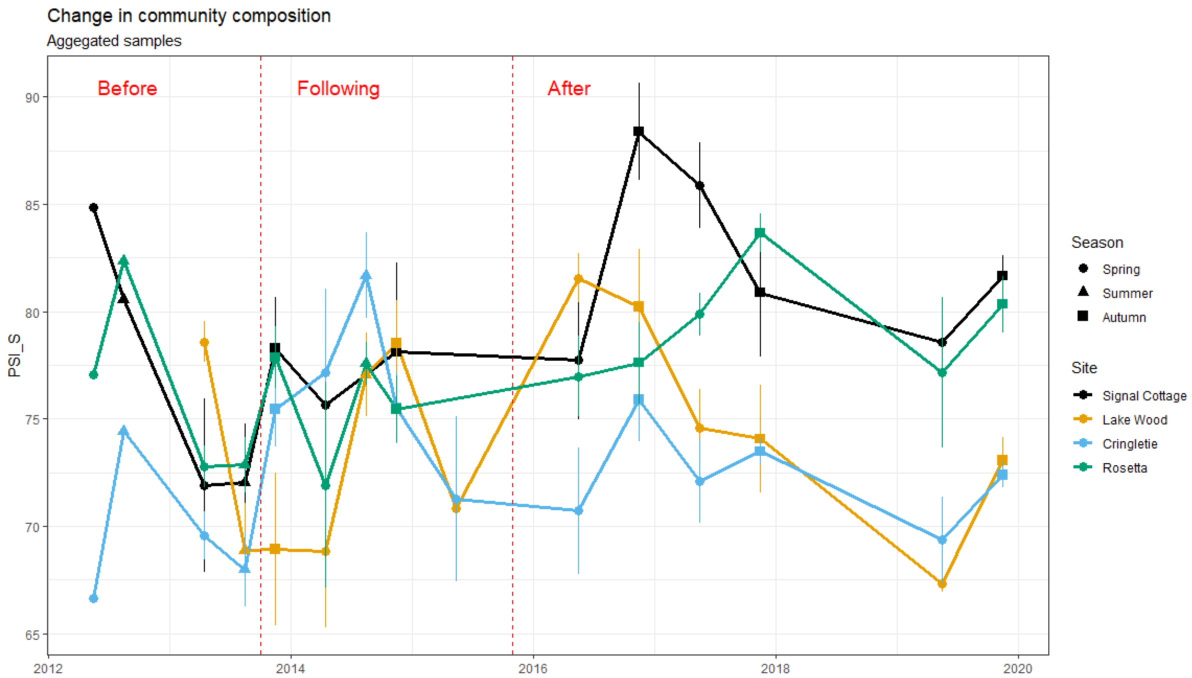


**Figure 2.6 Change in species-level PSI score at the four sampling locations before, following and after channel reconfiguration**

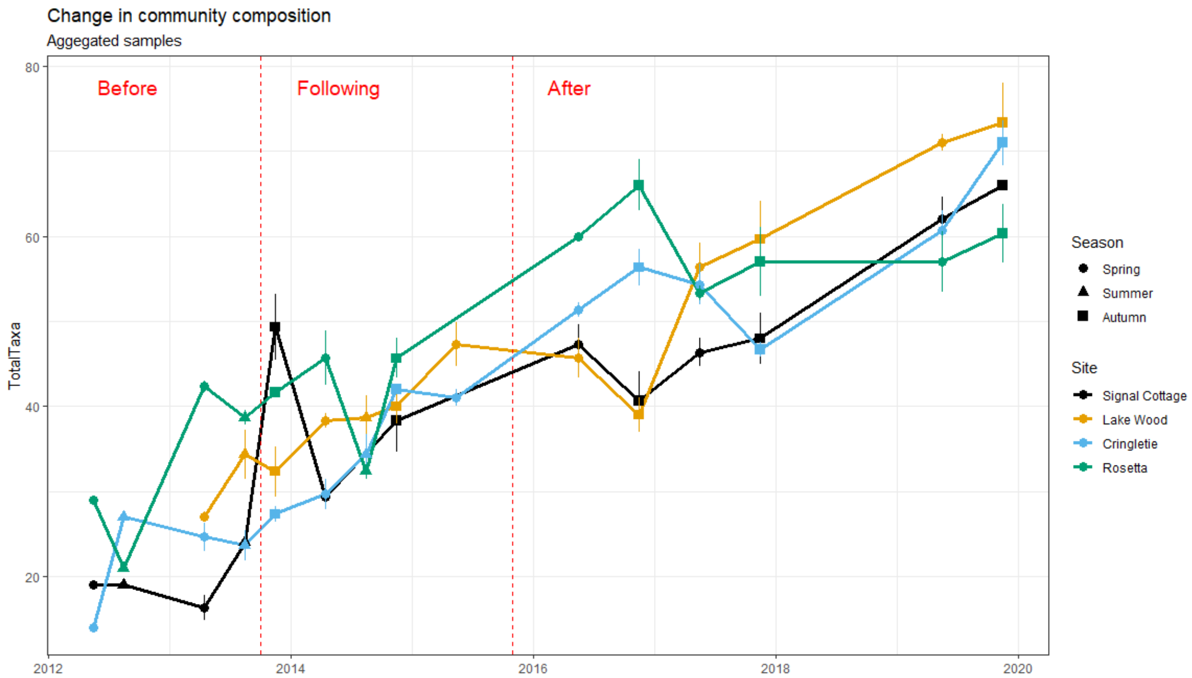


**Figure 2.7 Change in taxon richness at the four sampling locations before, following and after channel reconfiguration**

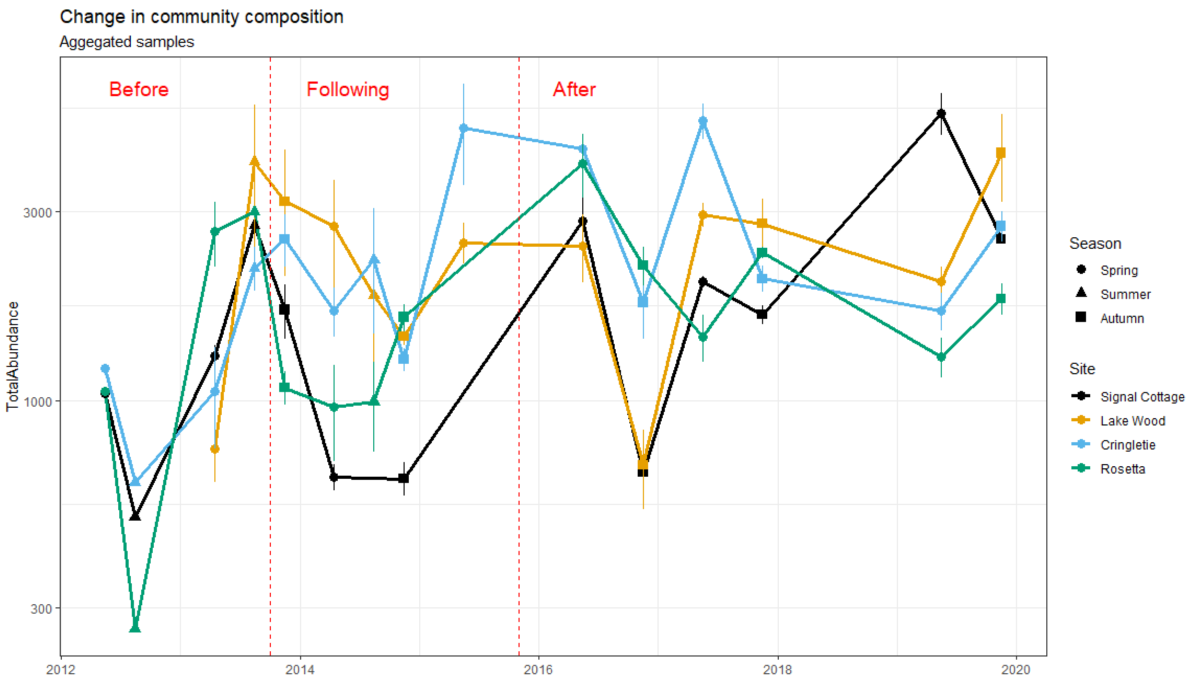


**Figure 2.8 Change in total abundance at the four sampling locations before, following and after channel reconfiguration**

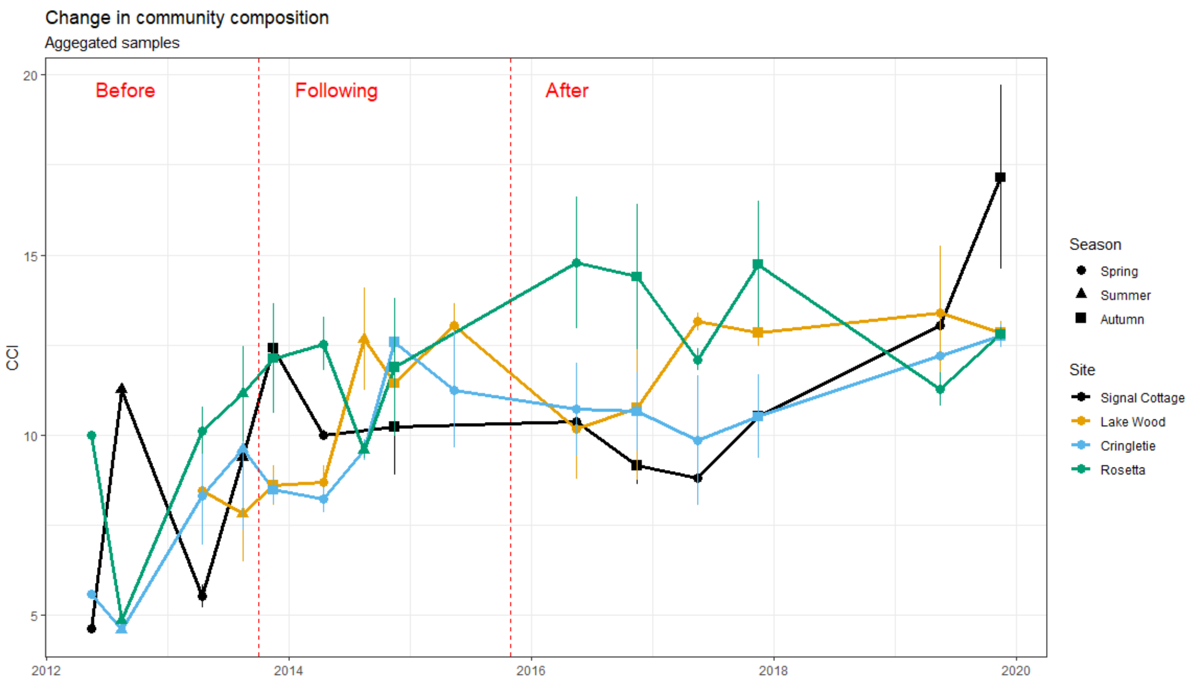


**Figure 2.9 Change in Community Conservation Index at the four sampling locations before, following and after channel reconfiguration**

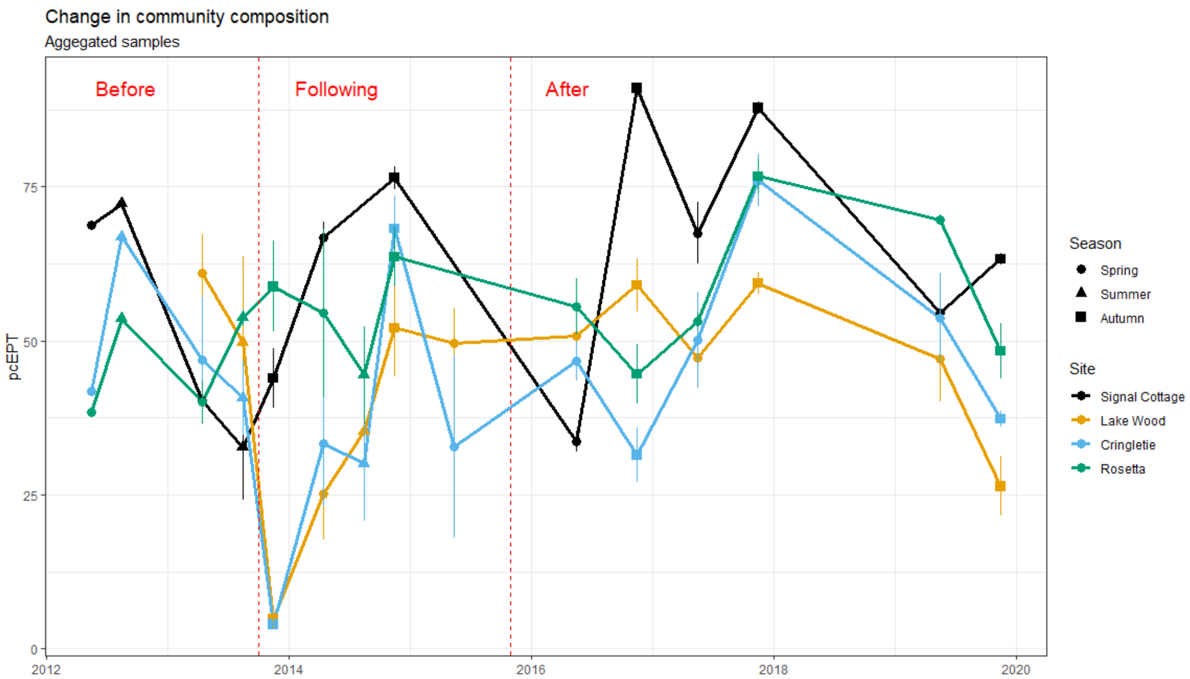


**Figure 2.10 Change in % Ephemeroptera, Plecoptera and Trichoptera at the four sampling locations before, following and after channel reconfiguration**

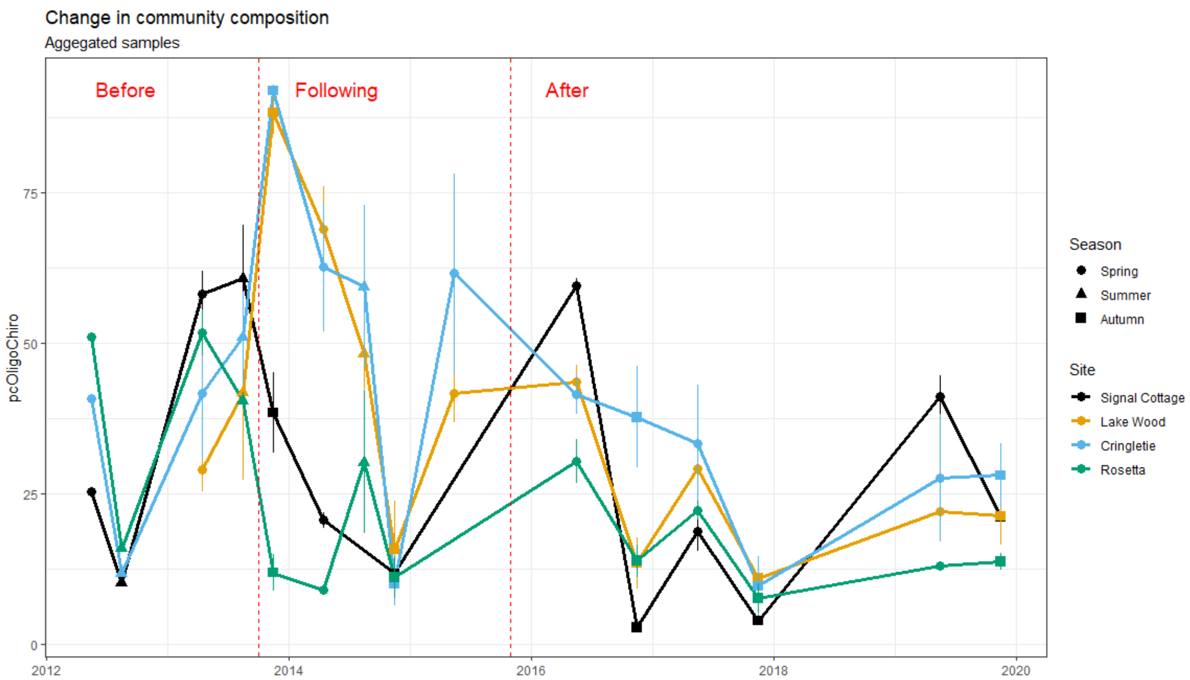


**Figure 2.11 Change in % Oligochaeta and Chironomidae at the four sampling locations before, following and after channel reconfiguration**

## 2.3 How does macroinvertebrate community composition vary by habitat and site?

Figure 2.12 to Figure 2.19 compare macroinvertebrate community composition at the four sites at the mesohabitat level. Samples collected before, following and after channel reconfiguration are plotted together.

All eight biotic indices showed large differences between habitat types. WHPT-ASPT, LIFE_S, PSI_S and %EPT were all highest in riffles and runs and lowest in slacks; the opposite pattern was true for %OligoChiro (i.e. lowest in riffles and runs and highest in slacks). Taxon richness and CCI were highest in runs and glides and lowest in pools and slacks. Finally, abundance was similar across all five habitat types after controlling for differences in sampling effort (i.e. macroinvertebrate density was similar).

Differences between the mesohabitat types were reasonably consistent across the four sites, but with a few exceptions. Notably, Signal Cottage had consistently higher WHPT-ASPT, PSI_S and %EPT and consistently lower %OligoChiro in slacks and pools than at the other three sites. Rosetta had consistently higher taxon richness and CCI in riffles and runs than at the other sites, but the lowest CCI in glides. It is likely that these differences reflect persistent local differences in morphology between the sites.

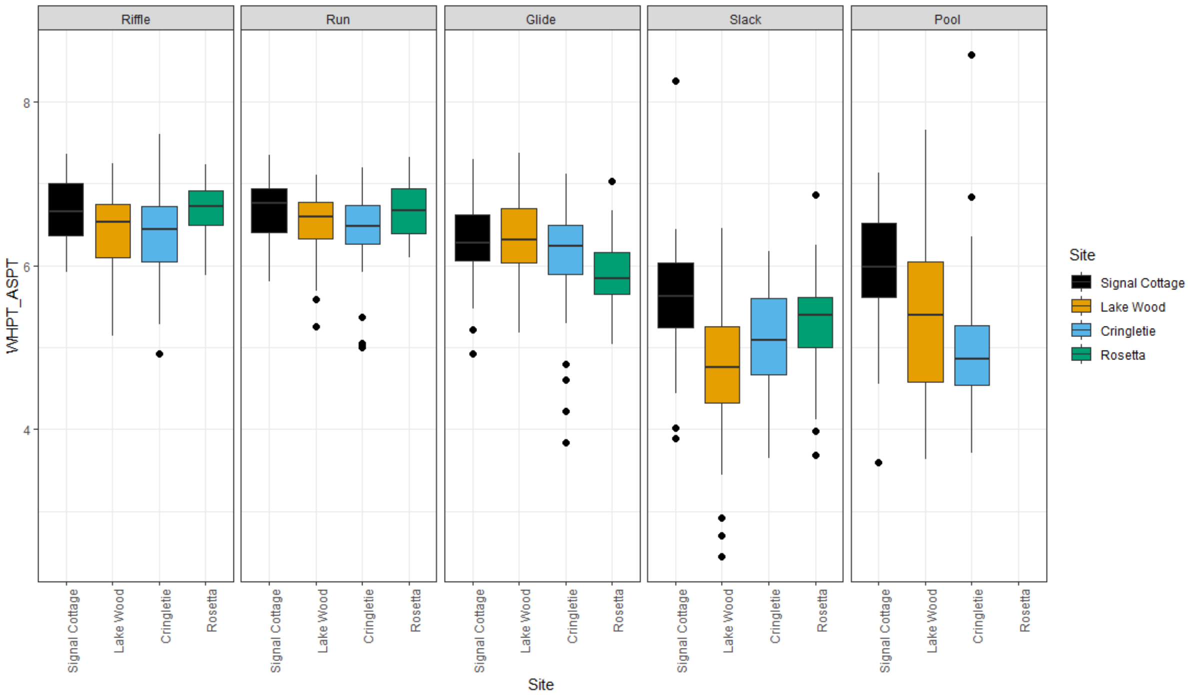


**Figure 2.12 Boxplot comparison of WHPT-ASPT by mesohabitat type and site**

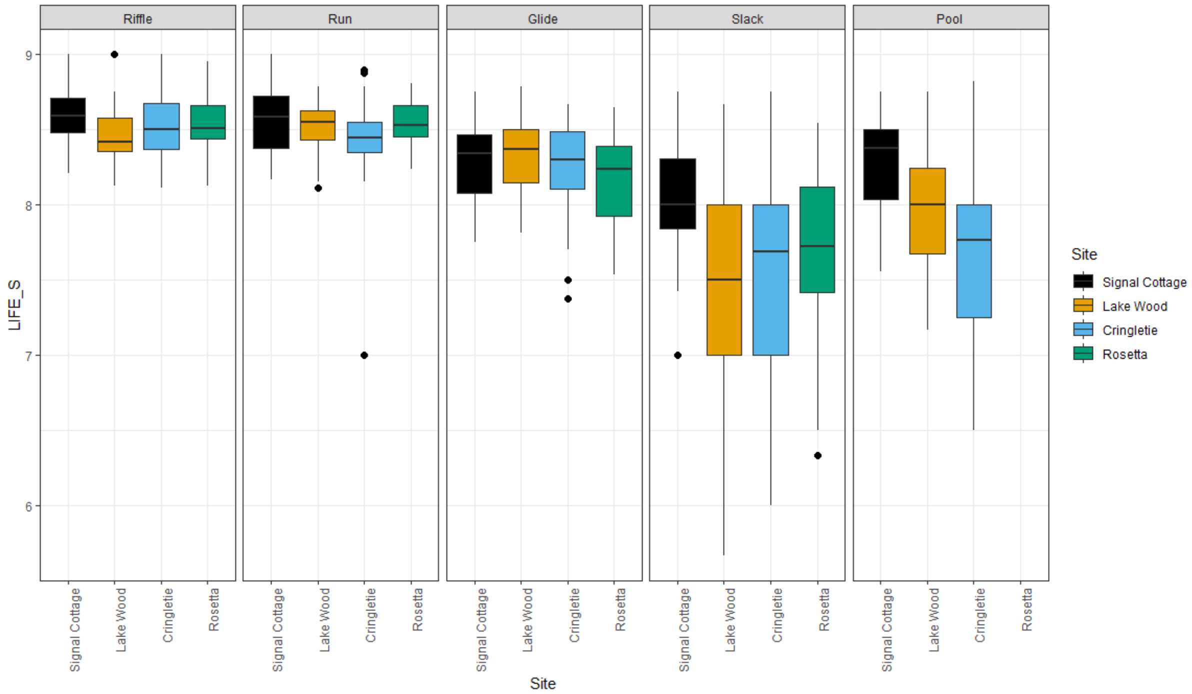


**Figure 2.13 Boxplot comparison of species-level LIFE by mesohabitat type and site**

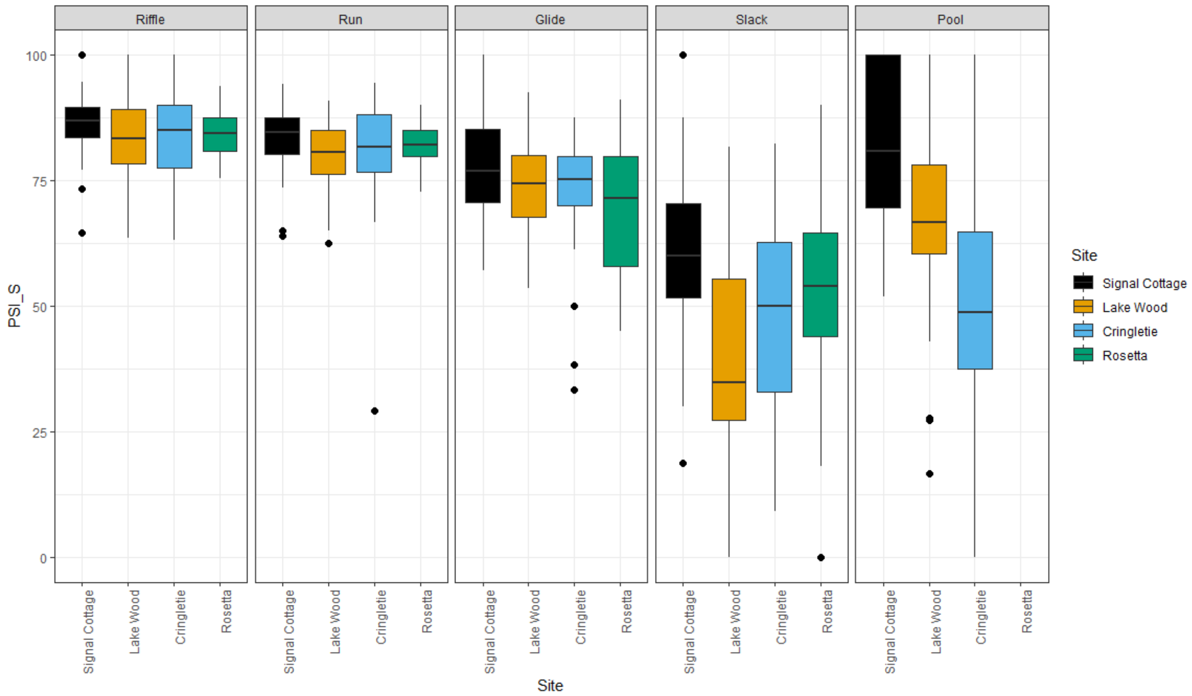


**Figure 2.14 Boxplot comparison of species-level PSI by mesohabitat type and site**

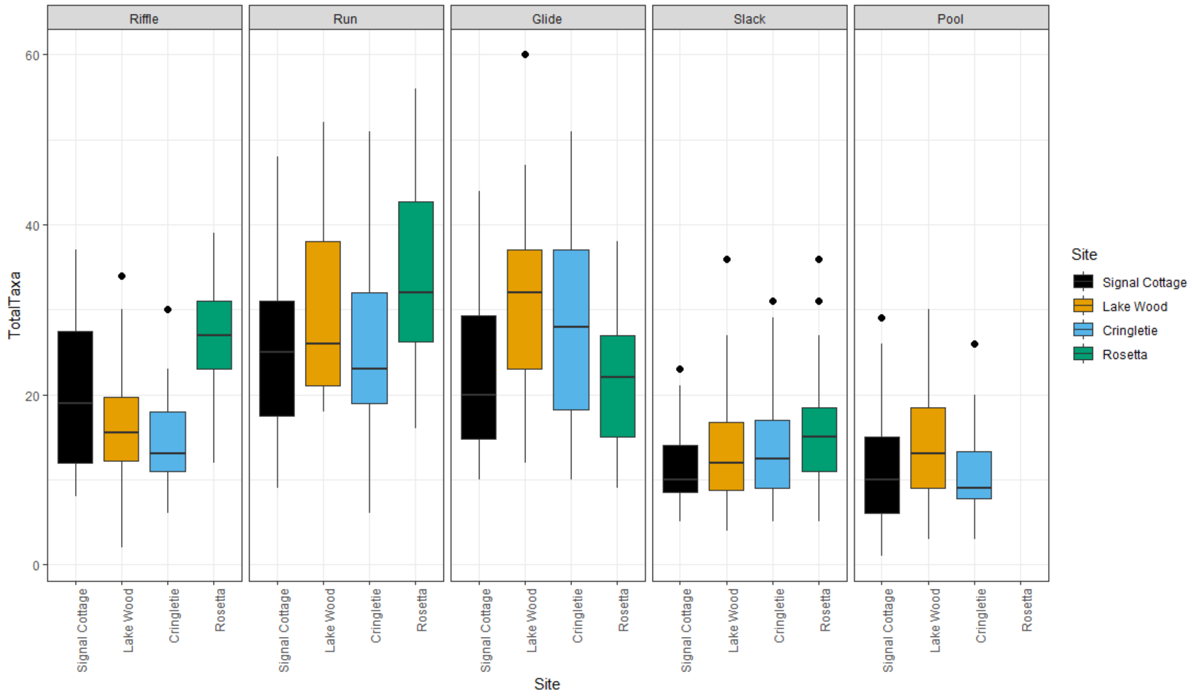


**Figure 2.15 Boxplot comparison of taxon richness by mesohabitat type and site**

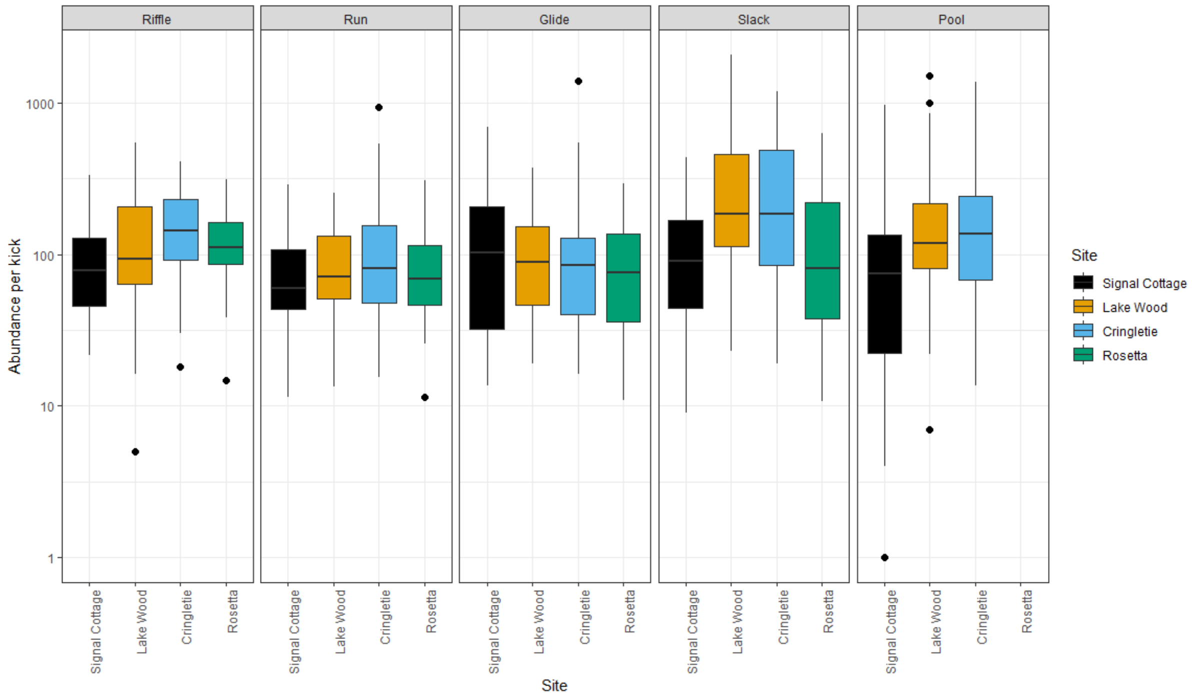


**Figure 2.16 Boxplot comparison of macroinvertebrate abundance by mesohabitat type and site. Note that abundance has been standardised by the number of kicks in each mesohabitat type to control for differences in sampling effort.**

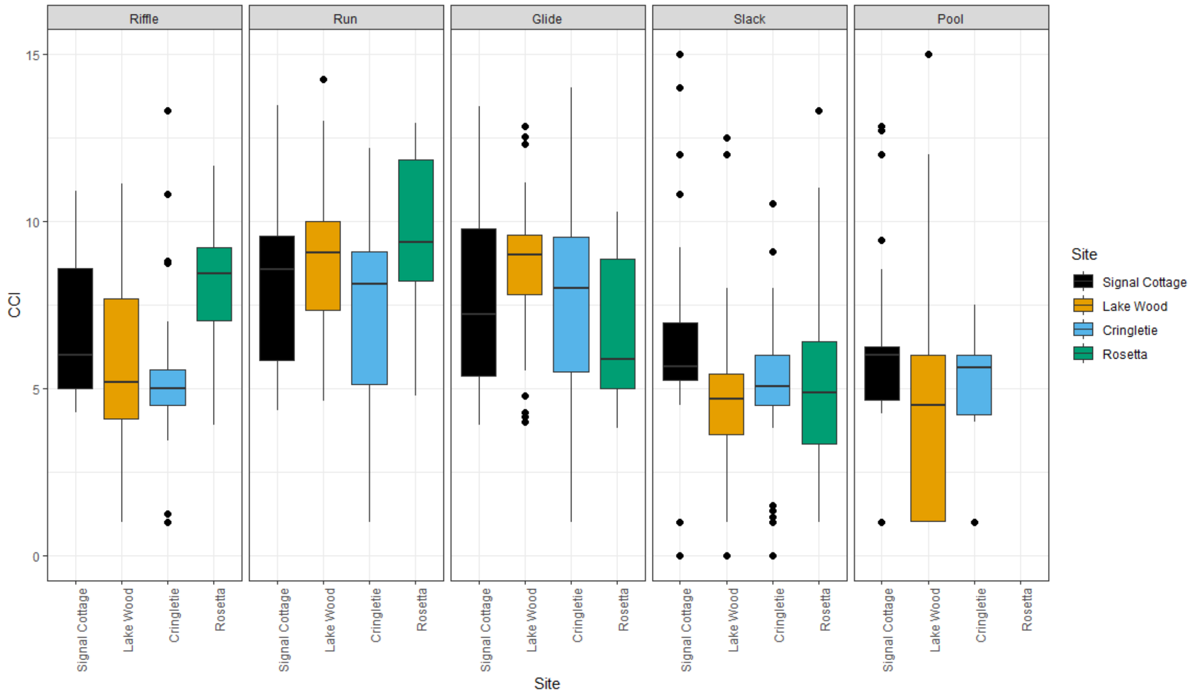


**Figure 2.17 Boxplot comparison of Community Conservation Index by mesohabitat type and site**

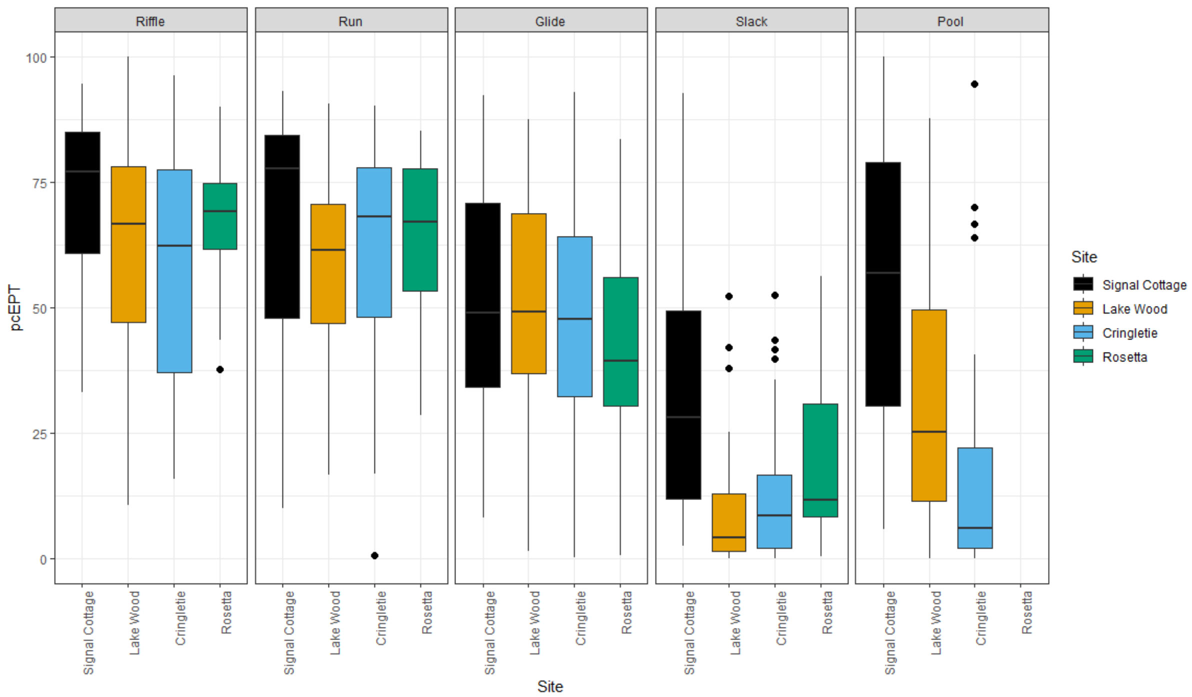


**Figure 2.18 Boxplot comparison of % Ephemeroptera, Plecoptera and Trichoptera by mesohabitat type and site**

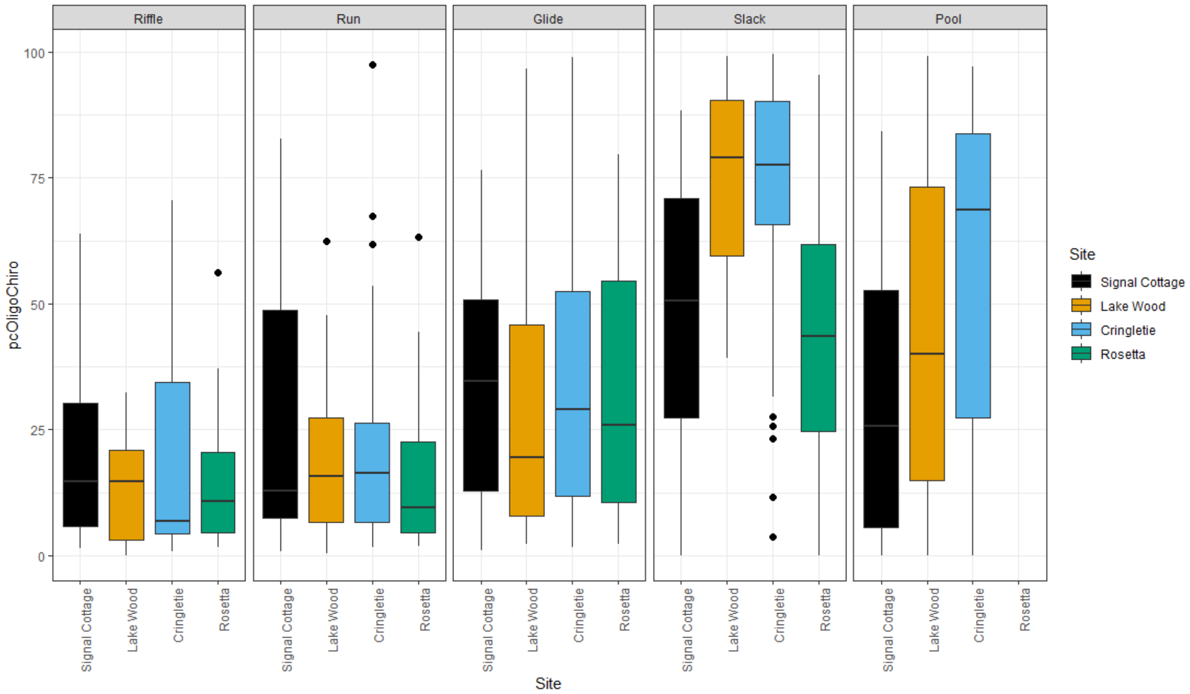


**Figure 2.19 Boxplot comparison of % Oligochaeta and Chironomidae by mesohabitat type and site**

# 3. Discussion

## 3.1 Conclusions

In summary, the application of bespoke Before-After-Control-Impact (BACI) monitoring framework has allowed the impact of channel reconfiguration on benthic macroinvertebrates to be evaluated at both reach and mesohabitat scales. The key results are as summarised below.

1. Prior to channel reconfiguration, the two impact sites – Lake Wood and Cringletie – had much less riffle/run and more glide habitat than the two control sites and, with the exception of %EPT, had lower scores for all biotic indices than the two control sites.
2. Channel reconfiguration in 2013 initially increased the proportion of riffle and run habitat and increased overall habitat diversity, but subsequent geomorphological adjustment appears to have partially reversed these changes.
3. Against a background of rapidly increasing taxon richness at all sites, channel reconfiguration caused an abrupt shift in macroinvertebrate community composition at the impact sites from one dominated numerically by mayflies, stoneflies and caddisflies to one dominated by oligochaetes and chironomids.
4. Following the initial disturbance caused by the channel reconfiguration work, the impact and control sites have partially converged in macroinvertebrate composition but only total abundance and %OligoChiro have increased significantly as a result of the intervention.

5. Six years after the channel reconfiguration work, WHPT-ASPT, LIFE_S, PSI_F, PSI_S and %EPT remain significantly lower at the impact sites compared with the control sites.

In conclusion, the benthic macroinvertebrate community in Eddleston Water appears to be strongly influenced by mesohabitat composition. Channel reconfiguration has led to a partial improvement in macroinvertebrate community status (as measured by a variety of standard biotic metrics) but full recovery from historical channel straightening is thought to have been constrained to date by the limited geomorphological changes at Lake Wood and Cringletie.

## 3.2 Lessons learnt

With the benefit of hindsight, it is possible to identify a number learning points that may be helpful when designing evaluation programmes for other river restoration projects in the future.

- Control sites are essential. Over the study period, there was a very strong and consistent increase in taxon richness at all four sites, which drove changes in some of the other biotic indices. If control sites had not been established, then the effect of channel reconfiguration would have been confounded by these background changes in macroinvertebrate community composition, and erroneous conclusions would have been drawn.
- In an ideal world, a longer period of baseline (pre-intervention) monitoring would have provided a more robust assessment of the impact of channel straightening at Lake Wood and Cringletie. With less than two complete years of sampling data available prior to the channel reconfiguration work, statistical power to detect differences was low.
- Geomorphological and biological responses to channel reconfiguration can take place over many years, and the extended period of post-intervention monitoring conducted at Eddleston Water has been valuable in revealing both short-term and longer-term effects of NFM measures.
- The use of upstream and downstream control sites helped to prevent confounding due to any longitudinal gradients in macroinvertebrate composition along the river, but there is a risk that the downstream site (Rosetta in this case) could be affected indirectly by the channel reconfiguration work (e.g. by mobilisation of fine sediment). Control sites should ideally be located on independent water courses that have similar characteristics, except for the effects of the intervention. In this case, however, there were no suitable independent controls available.
- The use of a dis-aggregated sampling method to gather data from individual mesohabitat types provided valuable insight into the importance of physical habitat in structuring the benthic macroinvertebrate community, yet still allowed responses to be assessed at a reach level.
- Macroinvertebrate metrics such as LIFE and PSI can show different patterns when calculated using family-level and species-level data. One reason might be that some families are more speciose than others. However, more granular species-level data does not necessarily reduce the level of residual (measurement) error in the data or produce clearer results when examining spatial differences and temporal trends.
- The use of a semi-quantitative (timed-effort) sampling method to collect macroinvertebrate samples resulted in an appreciable amount of measurement error (i.e. high variability among replicate samples), which limited the statistical power of the analysis to detect patterns in the data. Future studies may wish to consider the

benefits of collecting a greater number of replicate samples, or whether a fully-quantitative sampling approach might offer a more cost-effective solution.

## 3.3 Recommendations

This study has demonstrated a clear response of macroinvertebrates to channel reconfiguration. Habitat composition appears to have played a strong role in mediating these changes, but the rich combination of physical and biological monitoring data collected at Eddleston Water holds further potential to elucidate the mechanisms linking physical changes to biological responses. Specifically, we suggest that future analyses could:

- extend the BACI regression models to understand the influence of habitat composition, fine sediment, submergent vegetation and habitat diversity on macroinvertebrate composition and diversity;
- use multivariate ordination techniques to visualise spatial and temporal patterns in macroinvertebrate composition and identify sensitive taxonomic groups or species traits that could act as indicators of change;
- analyse changes in absolute abundance of key taxonomic groups; and
- examine mesohabitat-scale responses to channel reconfiguration, and how these influence responses at larger (reach) scales.

# 4. References

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# Appendix 1 Summary of sampling programme

| Period | Year | Season | Month | Cringletie | Lake Wood | Signal Cottage | Rosetta |
|---|---|---|---|---|---|---|---|
| Before | 2012 | Spring | May | 1 x3 min sample | | 1 x3 min sample | 1 x3 min sample |
| | | Summer | Aug | 1 x3 min sample | | 1 x3 min sample | 1 x3 min sample |
| | | Autumn | | | | | |
| | 2013 | Spring | May | | | | |
| | | Summer | Jun | | | | |
| Following | | Autumn | Nov | | | | |
| | 2014 | Spring | Apr | | | | |
| | | Spring | May* | Family level only | Family level only | Only 1 pool rep | |
| | | Summer | Aug | | | ** | |
| | | Autumn | Nov | | | | |
| After | 2015 | Spring | May | | | | |
| | | Summer | | | | | |
| | | Autumn | | | | | |
| | 2016 | Spring | May | | | | |
| | | Summer | | | | | |
| | | Autumn | Nov | | | | |
| | 2017 | Spring | May | | | | |
| | | Summer | | | | | |
| | | Autumn | Nov | | | | |
| | 2018 | Spring | | | | | |
| | | Summer | | | | | |
| | | Autumn | | | | | |
| | 2019 | Spring | May | | | | |
| | | Summer | | | | | |
| | | Autumn | Nov | | | | |

20 kicks x 3 reps at each site in each season, unless otherwise stated. Grey = no sampling.
* Excluded from analysis in preference to April 2014 samples, to match species-level identification used in other years.
** No sampling because site impacted by channel reconfiguration immediately upstream.

# Appendix 2 Results of statistical analyses comparing reach-level biotic indices among sites and time periods

## WHPT_ASPT

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: WHPT_ASPT ~ Season + Treatment * Period2 + (1 | YearMonth) +      (1 | Site)
   Data: agdata
     AIC      BIC   logLik deviance df.resid
    26.1     59.5     -2.1      4.1      142

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.63084 -0.59040  0.07547  0.64521  2.04260

Random effects:
 Groups    Name        Variance  Std.Dev.
 YearMonth (Intercept) 0.0042932 0.06552
 Site      (Intercept) 0.0006289 0.02508
 Residual              0.0564574 0.23761
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                  Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                        6.43567    0.08250  30.31523  78.008  < 2e-16 ***
SeasonSummer                      -0.18293    0.08227  19.22392  -2.223  0.03836 *
SeasonAutumn                       0.12894    0.06012  14.72932   2.145  0.04908 *
TreatmentImpact                   -0.11327    0.09073  48.59312  -1.248  0.21785
Period2Following                   0.11481    0.09944  41.91978   1.155  0.25482
Period2After                       0.33458    0.09589  32.20434   3.489  0.00143 **
TreatmentImpact:Period2Following  -0.10646    0.11139 142.78593  -0.956  0.34085
TreatmentImpact:Period2After      -0.15145    0.10363 138.16610  -1.461  0.14615
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Family level LIFE

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: LIFE_F ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 |      Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid 
   -77.2    -43.8     49.6    -99.2      142 

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-2.4447 -0.6355 -0.1171  0.5482  2.6214 

Random effects:
 Groups    Name        Variance  Std.Dev.
 YearMonth (Intercept) 0.0053241 0.07297 
 Site      (Intercept) 0.0006412 0.02532 
 Residual              0.0271893 0.16489 
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                   Estimate Std. Error         df t value Pr(>|t|)    
(Intercept)                        7.884039   0.069597  23.689154 113.282  < 2e-16 ***
SeasonSummer                      -0.040541   0.072647  16.554200  -0.558 0.584277    
SeasonAutumn                      -0.003769   0.054778  13.250180  -0.069 0.946172    
TreatmentImpact                   -0.292861   0.065717  32.296326  -4.456 9.41e-05 ***
Period2Following                  -0.316113   0.081748  29.168831  -3.867 0.000569 ***
Period2After                      -0.227432   0.080808  22.953097  -2.814 0.009849 ** 
TreatmentImpact:Period2Following   0.296934   0.077778 139.519036   3.818 0.000202 ***
TreatmentImpact:Period2After       0.207028   0.072028 135.564049   2.874 0.004703 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## Species level LIFE

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: LIFE_S ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 |      Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
   -84.6    -51.3     53.3   -106.6      142

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.2980 -0.7028 -0.1065  0.5715  2.9798

Random effects:
 Groups    Name        Variance  Std.Dev.
 YearMonth (Intercept) 0.0005686 0.02384
 Site      (Intercept) 0.0001030 0.01015
 Residual              0.0285487 0.16896
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                  Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                        8.58857    0.05104  27.44489 168.261  < 2e-16 ***
SeasonSummer                       0.05397    0.04878  14.94924   1.106  0.28609
SeasonAutumn                       0.06421    0.03467  10.94528   1.852  0.09113 .
TreatmentImpact                   -0.18741    0.06272  63.97427  -2.988  0.00398 **
Period2Following                  -0.29679    0.06315  41.82885  -4.699 2.83e-05 ***
Period2After                      -0.10400    0.05981  31.81767  -1.739  0.09171 .
TreatmentImpact:Period2Following   0.16848    0.07876 141.14350   2.139  0.03414 *
TreatmentImpact:Period2After       0.01741    0.07360 134.22498   0.237  0.81332
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## Family level PSI

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: PSI_F ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 |       Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
   927.4    960.8   -452.7    905.4      142

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.21202 -0.58163 -0.09944  0.57253  3.09646

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept)  2.204   1.485
 Site      (Intercept)  0.000   0.000
 Residual              20.259   4.501
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                  Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                       67.64876    1.61844  31.04305  41.799   <2e-16 ***
SeasonSummer                       0.87987    1.68665  18.06248   0.522   0.6082
SeasonAutumn                       1.10968    1.24669  14.05590   0.890   0.3884
TreatmentImpact                   -4.25808    1.65225 141.32068  -2.577   0.0110 *
Period2Following                  -3.54767    1.98575  36.67029  -1.787   0.0823 .
Period2After                       0.07783    1.93180  28.26389   0.040   0.9681
TreatmentImpact:Period2Following   3.19042    2.11357 144.94813   1.509   0.1333
TreatmentImpact:Period2After       0.16931    1.96352 140.75755   0.086   0.9314
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## Species level PSI

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: PSI_S ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 |      Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
   933.1    966.4   -455.5    911.1      142

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.5179 -0.6313  0.0135  0.5631  2.2510

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept)  2.3331  1.5275
 Site      (Intercept)  0.1506  0.3881
 Residual              20.8745  4.5689
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                 Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                       73.8856     1.6738  23.0889  44.141  < 2e-16 ***
SeasonSummer                       2.3576     1.7239  15.2872   1.368  0.19121
SeasonAutumn                       2.2436     1.2750  11.8383   1.760  0.10426
TreatmentImpact                   -3.2292     1.7220  50.3009  -1.875  0.06657 .
Period2Following                   0.8961     2.0257  31.6217   0.442  0.66123
Period2After                       5.7233     1.9714  24.1293   2.903  0.00778 **
TreatmentImpact:Period2Following   1.6069     2.1465 139.1003   0.749  0.45535
TreatmentImpact:Period2After      -3.7684     1.9936 133.6621  -1.890  0.06089 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## Taxon richness

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: TotalTaxa ~ Season + Treatment * Period2 + (1 | YearMonth) +      (1 | Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
  1077.0   1110.4   -527.5   1055.0      142

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.73796 -0.58596 -0.08071  0.71565  2.75104

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept) 22.637   4.758
 Site      (Intercept)  9.238   3.039
 Residual              46.565   6.824
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                 Estimate Std. Error      df t value Pr(>|t|)
(Intercept)                        27.560      4.230  19.690   6.516 2.56e-06 ***
SeasonSummer                       -1.168      4.132  16.173  -0.283  0.78107
SeasonAutumn                        1.176      3.215  13.836   0.366  0.72003
TreatmentImpact                    -2.172      3.946   8.392  -0.550  0.59642
Period2Following                   12.960      4.364  22.470   2.970  0.00696 **
Period2After                       27.185      4.434  19.050   6.131 6.73e-06 ***
TreatmentImpact:Period2Following   -1.486      3.238 138.276  -0.459  0.64706
TreatmentImpact:Period2After        3.949      2.986 136.109   1.323  0.18821
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## Total abundance

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: log10(TotalAbundance) ~ Season + Treatment * Period2 + (1 | YearMonth) +      (1 | Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
   -16.3     17.1     19.1    -38.3      142

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.1232 -0.6039 -0.1712  0.5063  2.6112

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept) 0.02631  0.1622
 Site      (Intercept) 0.00000  0.0000
 Residual              0.03732  0.1932
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                  Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                        3.15495    0.11790  17.81627  26.760 7.77e-16 ***
SeasonSummer                      -0.05007    0.13580  14.74019  -0.369   0.7176
SeasonAutumn                      -0.09841    0.10685  12.98017  -0.921   0.3738
TreatmentImpact                   -0.10804    0.07119 137.77875  -1.518   0.1314
Period2Following                  -0.07062    0.14045  18.95690  -0.503   0.6209
Period2After                       0.20168    0.14426  16.62306   1.398   0.1805
TreatmentImpact:Period2Following   0.40065    0.09166 139.26346   4.371 2.40e-05 ***
TreatmentImpact:Period2After       0.17682    0.08451 137.46408   2.092   0.0382 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## CCI

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: CCI ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 | Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
   725.3    758.6   -351.7    703.3      142

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.8537 -0.8007 -0.0011  0.5817  3.8248

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept) 0.2585   0.5084
 Site      (Intercept) 0.2650   0.5148
 Residual              5.4471   2.3339
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                 Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                        8.3487     0.8302  21.1111  10.056 1.66e-09 ***
SeasonSummer                       0.5242     0.7442  14.1405   0.704 0.492596
SeasonAutumn                       0.6046     0.5367  10.5309   1.126 0.284976
TreatmentImpact                   -0.6487     0.9990  21.9400  -0.649 0.522869
Period2Following                   2.5173     0.9269  35.3573   2.716 0.010159 *
Period2After                       3.7762     0.8855  26.5470   4.264 0.000226 ***
TreatmentImpact:Period2Following  -0.1103     1.0921 140.5996  -0.101 0.919675
TreatmentImpact:Period2After      -0.1291     1.0176 134.3415  -0.127 0.899220
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## % EPT

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: pcEPT ~ Season + Treatment * Period2 + (1 | YearMonth) + (1 |      Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
  1286.0   1319.4   -632.0   1264.0      142

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.18096 -0.69983 -0.03744  0.67837  2.10007

Random effects:
 Groups    Name        Variance  Std.Dev.
 YearMonth (Intercept) 8.836e+01 9.400e+00
 Site      (Intercept) 2.358e-08 1.536e-04
 Residual              1.922e+02 1.386e+01
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                 Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                       48.0423     7.2596  21.6955   6.618 1.27e-06 ***
SeasonSummer                      -0.2232     8.2124  16.8138  -0.027   0.9786
SeasonAutumn                       3.3761     6.3804  14.3479   0.529   0.6048
TreatmentImpact                    5.3601     5.1044 139.7895   1.050   0.2955
Period2Following                   9.8426     8.6964  23.6083   1.132   0.2691
Period2After                      12.4047     8.8294  19.9768   1.405   0.1754
TreatmentImpact:Period2Following -30.9949     6.5651 141.6222  -4.721 5.58e-06 ***
TreatmentImpact:Period2After     -18.7393     6.0605 139.4230  -3.092   0.0024 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

## % Oligochaetes and chironomids

```
Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: pcOligoChiro ~ Season + Treatment * Period2 + (1 | YearMonth) +      (1 | Site)
   Data: agdata

     AIC      BIC   logLik deviance df.resid
  1297.8   1331.2   -637.9   1275.8      142

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.11065 -0.62559 -0.04632  0.73558  2.36515

Random effects:
 Groups    Name        Variance Std.Dev.
 YearMonth (Intercept) 127.570  11.295
 Site      (Intercept)   9.898   3.146
 Residual              197.502  14.054
Number of obs: 153, groups:  YearMonth, 15; Site, 4

Fixed effects:
                                 Estimate Std. Error      df t value Pr(>|t|)
(Intercept)                        44.368      8.595  20.190   5.162 4.61e-05 ***
SeasonSummer                       -5.529      9.531  15.683  -0.580   0.5701
SeasonAutumn                      -11.669      7.480  13.716  -1.560   0.1415
TreatmentImpact                    -9.403      6.063  19.512  -1.551   0.1370
Period2Following                  -19.190      9.905  20.512  -1.937   0.0666 .
Period2After                      -17.886     10.146  17.839  -1.763   0.0950 .
TreatmentImpact:Period2Following   44.861      6.674 137.201   6.722 4.42e-10 ***
TreatmentImpact:Period2After       15.282      6.151 135.235   2.484   0.0142 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```