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# Bioassessment of Streams Within the Clay-Plains Region of Southwestern Ontario – Optimizing Sampling and Laboratory Assessment Methods

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## BIOASSESSMENT OF STREAMS WITHIN THE CLAY-PLAINS REGION OF SOUTHWESTERN ONTARIO – OPTIMIZING SAMPLING AND LABORATORY ASSESSMENT METHODS

by

Alyssa A. Frazao

A Thesis Submitted to the Faculty of Graduate Studies Through the Department of Biological Sciences In Partial Fulfilment of the Requirements for The Degree of Master of Science at the University of Windsor

Windsor, Ontario, Canada

2019

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# Bioassessment of Streams Within the Clay-Plains Region of Southwestern Ontario – Optimizing Sampling and Laboratory Assessment Methods

by

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December 18, 2019

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#### **Abstract**

Evaluating the ecological of condition streams can be accomplished by assessing the community composition of macroinvertebrates whose differential sensitivity to perturbations reflect the conditions of their habitat. Two sampling protocols used to assess Ontario streams (Canadian Aquatic Biomonitoring Information Network (CABIN) (employed across Canada), and the Ontario Benthic Biomonitoring Network (OBBN)) recommend using D-framed dip nets (Dnets) to effectively assess streams, most of which have rapid flow and either hard bottoms or coarse sediment. I assessed the relative effectiveness of D-nets and Petite Ponar grabs to sample macroinvertebrates during the summer in 19 southwestern Ontario clay-plain streams, which typically have fine sediments and slow or nondetectable velocity. The two methods identified similar community composition; but the D-net captured more aquatic invertebrates and greater family richness than the Petite Ponar grabs.

Although both protocols recommend processing and subsampling samples using a Marchant Box I found that sorting up to 300 animals per size fraction of a series of nested sieves took approximately half the time, yielded significantly greater richness estimates and reduced the marked overestimates of abundance sometimes observed when subsampling to fixed counts with the Marchant Box. Effective bioassessment of southwestern Ontario clay plain streams can be achieved by collecting 2-3 jab-and-sweep D-net samples from glide region in late April-early May and processing subsamples separated into size fractions using nested sieves. Most streams sampled were dominated by tolerant organisms producing HBI scores ranging from 7-8. Tolerance scores for streams in Essex County were significantly higher than scores for streams in the Lower Thames Valley conservation region.

*To my family and friends, for this journey would not be complete without you.*

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### **Chapter 1: General Introduction**

#### **Project Summary and Objectives**

Streams are an important component of the ecosystem surrounding the Great Lakes. They are the channels that not only transport water into the lakes but also collect and carry the nutrients, chemicals, and organisms contributed along their length from the surrounding land. Varying geographical features along the length of streams alter macroinvertebrate community composition and functions (Vannote et al. 1980; Lenat and Crawford 1994; Sciera et al. 2008). It is important to recognize the contributing factors that affect macroinvertebrate community composition and abundance and how this can impact the Great Lakes (Økland and Økland 1986).

One way to assess streams is by studying their macroinvertebrate fauna as an indicator of the system's ecological condition or 'health', as well as the degree of anthropogenic effects (Resh et al. 1998; Bailey et al. 2004; Hilsenhoff 1982). Stream organisms vary in their tolerances to habitat perturbations. Consequently, the presence of sensitive macroinvertebrates implies that a stream is relatively unaffected by anthropogenic stress, whereas disturbed streams are dominated by tolerant organisms (Hilsenhoff 1987; 1977).

In Canada, two protocols have been developed and recommended to assess aquatic invertebrate communities in Ontario streams. Environment Canada has developed and oversees the Canadian Aquatic Biomonitoring Information Network (CABIN; Environment and Climate Change Canada, 2019), which is employed across Canada. The CABIN program maintains a national database that permits comparisons of multiple stream ecosystems across the regions because they prescribe use of a standardized set of sampling protocols (Reynoldson et al. 1999;

ECCC 2018). This allows for the comparison of data and streams themselves since collection methods are the same.

The Ontario Benthic Biomonitoring Network (OBBN) is a protocol co-founded by the Ontario Ministry of the Environment (MOE) and Environment Canada (Ecological Monitoring and Assessment Network – EMAN; Jones et al., 2004). Because it was derived from CABIN, OBBN has similar goals, including recommending use the of standardized methods, as well as providing a database to allow the comparison of data and focusing on providing a rapid bioassessment of the streams using macroinvertebrates as an ecological measure (Boyle 2003; Jones et al. 2007). Like CABIN, the OBBN describes methods to assess lakes and wetlands in addition to wadeable streams.

Both programs use Rapid Bioassessment Protocols (RBP; Plafkin et al. 1989; Barbour et al. 1999) for field sampling, meaning that they promote an efficient, easy and cost-effective approach to stream assessment (Resh and Jackson 1993; Buss and Vitorino 2010). Both CABIN and OBBN field methods are designed to effectively assess the fauna of wadeable streams that have relatively rapid flow and coarse sediment by using a D-framed sweep net. Yet, much of the southwestern Ontario landscape sits on a glacial-remnant clay plain (Figure. 1.1). The parent materials of the St. Clair Clay Plains and other clay plains largely dictate the sediment texture. Stony streams (coarse substrate) provide habitat for benthic invertebrates that can be disturbed during sampling, resulting in the invertebrates being dislodged and swept into a downstream net by the current (Knight and Gaufin 1967; OBBN 2007). Because topographic relief is minimal in the St. Clair Clay Plain region, stream velocities are slow, and often negligible during low discharge periods. Consequently, riffles and pools can be difficult or impossible to locate.



Figure 1.1: The physiographic regions of Southwestern Ontario. (Map Series: Physiographical Series, Ontario Department of Mines and Northern Affairs, Ontario Research Foundation, Maps 2224-2227. Physiographic Series, Ministry of Natural Resources, Ontario Research Foundation, Map 2228.)

Streams that have clay-dominated sediment are considered to be soft-bottomed (Stark 2001), a substrate that is more typical of a wetland or pond than of a river (Faulkner and Richardson 1989). Thus, in some respects southwestern Ontario streams are more similar to wetlands than to riffle-and-pool streams. The lack of discernable current and soft mud or clay substrate may compromise the D-net's effectiveness due to back flow and a tendency for the fine particles to clog the net. Therefore, the methods used to sample benthos in wetlands and ponds may be more effective than dip net sampling in these slow-flowing, soft bottomed streams. One such possible alternative to the D-net is the Petite Ponar grab since it is best used in low-flow, muddy areas (Elliott and Drake 1981).

Both the CABIN and OBBN protocols recommend using the Marchant Box (Marchant 1989) in the laboratory when subsampling is necessary to reduce the time devoted to sample processing. The Marchant Box was designed to process a whole sample by distributing the sample evenly into 100 cells, a subset of which are randomly selected and individually sorted to enumerate the invertebrates. However, this method can be time consuming and, if biased, can ultimately alter assessment of ecological condition (Valois et al. 2016). When a sample is comprised of a large amount of organic material it can then be difficult to distribute the material evenly among the cells when flipping the box upright. Furthermore, the Marchant Box method is a fixed-count protocol that requires examining cells until at least 300 organisms have been retrieved. Although the protocol is intended to reduce sorting time, the fixed-count stopping rule can result in the omission of rare macroinvertebrates when only a small number of cells are examined. The exclusion of rate and sensitive taxa can bias metrics of richness and ultimately bias assessments of a site's ecological condition.

An alternative procedure is the Nested Sieve-Fractioning approach (Ciborowski 1991; Bourassa and Morin 1995; Vinson and Hawkins 1996) whereby a sample is subdivided by particle size using a series of sieves. Each subsample is sorted independently according to size-specific criteria, which improves sorting efficiency and the detection of large, rarer taxa (Ciborowski 1991). For each size fraction at least 300 organisms may be counted but typically as the size fraction gets smaller there are more invertebrates. For the finer sieves (i.e.  $0.05$  mm) a  $\frac{1}{4}$  of the size fraction can be counted. The detritus weight of what was unsorted can be compared to the sorted weight to estimate the individuals of the whole size fraction. This provides a better idea of what is in the entire sample rather than the sub-samples taken by the Marchant Box.

Around the world, agencies may use region-specific procedures to assess the streams within their jurisdictions. In the United States, the National Rivers and Streams Assessment (NRSA) collects information to describe the nation's stream and river ecological condition under the USEPA (Barbour et al. 1999). In Europe, multiple countries were involved in The Development and Testing of an Integrated Assessment System for the Ecological Quality of Streams and Rivers throughout Europe using Benthic Macroinvertebrates, (AQEM) project from 2000 to 2002 (AQEM 2002). These stream assessment procedures are now incorporated into the STAR (Standardization of River Classifications) project, which uses the rapid bioassessment protocol (Barbour et al. 1999). In 2002, the EU Water Framework Directive (WFD) was created to provide a collaborative effort amongst European countries to clean, protect and manage the waterbodies they share (EC 2000). In Canada, water quality guidelines were created to focus on the chemical, physical, and biological aspects of water quality, administered under the Canadian Water Quality Guidelines for the Protection of Aquatic Life (Canadian Council of Ministers of the Environment 2014; Reynoldson 2007).

For this study on the effectiveness of sample collection, I compared two alternative methods that accommodated the difficulties associated with sampling slow-flowing habitats that have soft substrates.

The objectives of my thesis were to

- a. propose field sampling protocols (timing, site selection, and intensity of sampling informed by OBBN and CABIN) suitable for conducting aquatic invertebrate bioassessments of lowgradient clay plain streams of southwestern Ontario;
- b. evaluate the effectiveness of two collection methods (D-frame kick net sampling and Petite Ponar grabs); and
- c. compare the efficiency of two laboratory subsampling and processing methods (Marchant Box vs. nested sieves) to determine which procedures can best characterize the streams' ecological condition.

I addressed these questions by using inventories of second to fifth-order streams for which the intensity of agricultural and rural/urban land use in contributing watersheds had been determined (Jones 2012) to stratified-randomly select a set of study streams representing the maximum range of potential disturbances to stream communities. Alterations in habitat, flow, and the materials transported in run-off due to human activity in watersheds can both directly and indirectly affect the invertebrate communities of receiving streams. Dance and Hynes (1980) found that two streams that were similar in community composition in 1840 had changed to having different communities due to changes in the surrounding agricultural land use. Similarly,

Stepenuck et al. (2002) found that the ecological condition of streams (measured in terms of the Hilsenhoff biotic index) became progressively poorer as urbanization increased.

With these guidelines, I sampled 19 streams in midsummer 2016 and 40 streams in April and May 2017. In 2017, I sampled within a seasonal timeframe based on long-term discharge/temperature records for the Thames River (see below) to ensure that discharge would be relatively high and that water temperatures below thresholds that might stimulate emergence of spring-developing aquatic insects.

The suitability of sampler type and intensity and habitat was assessed using the 2016 dataset. The efficiency of processing method was determined using samples from a subset of these streams by comparing sorting time, family richness and Hilsenhoff Biotic Index (HBI; Hilsenhoff 1987; Smith 2009) scores. Based on those findings, I subsequently processed triplicate D-net samples collected from the streams sampled in 2017 using the nested sieve protocol, and inferred stream condition from HBI scores for those samples (Appendix E).

This thesis is organized into 4 chapters. Chapter 1 introduces the research topic and describes my expectations. Chapter 2 compares the relative effectiveness of the CABIN and OBBN field protocols and the efficiency of two methods of sampling – a traveling sweep using a D-frame dip net, and Petite Ponar grabs. In Chapter 3, I assess the relative effectiveness of two methods of sample processing and subsampling – the Marchant Box method recommended by CABIN and OBBN, and the sieve fractionation method. In Chapter 4, I reiterate the strengths and weaknesses of the various protocols, recommend standard procedures for conducting macroinvertebrates rapid bioassessments, and identify future research needs. In Appendix B, I describe the general methods by which I selected sampling locations, determined the season during which samples should be collected, and the environmental and biological sampling conducted during field visits. The relative condition of southwestern Ontario clay plain streams as summarized by HBI scores calculated from samples collected and processed according to the recommended procedures is documented in Appendix C.

## **Chapter 2: Comparison of Benthic Macroinvertebrate Field Collection Methods: Assessing Abundance, Richness and Community Composition from D-frame Sweep Net and Petite Ponar Grab Samples.**

#### **Introduction**

The ecological status of streams and rivers is determined by its valley, including the surrounding land use and activities (Hynes 1975). Understanding the health of a region's watercourses is essential to conservation, preservation and restoration. The macroinvertebrate fauna is an especially good indicator of the system's ecological condition in relation to the degree of anthropogenic effects (Resh et al. 1998; Bailey et al. 2004; Hilsenhoff 1982). Benthic macroinvertebrates are indicative of stream water quality because they are small, which limits their mobility, and they are also a diverse group whose tolerances vary (Stewart and Loar 1994; Hynes 1960, 1970; Cummins 1979; Weber 1973; Platts et al. 1983; Patrick 1975). Consequently, the presence of pollution-sensitive macroinvertebrates at a site implies that a stream is relatively unaffected by anthropogenic stress, whereas disturbed streams are dominated by tolerant organisms (Hilsenhoff 1977; 1987).

Most methods recommended for assessing benthic macroinvertebrates are designed to sample relatively fast-flowing streams that have coarse substrate. However, these methods may not be equally effective for other stream types. Much of the southwestern Ontario landscape sits on a glacial-remnant alluvial clay plain. Consequently, streams are slow-flowing and have substrate composed largely of soft mud or clay, which in some respects are more similar to wetlands than to riffle-and-pool streams. The fauna of soft-bottomed streams tend to be dominated by invertebrates that are more tolerant of warm hypoxic conditions than the invertebrates of hardbottom streams, and are less affected by sedimentation (Stark and Maxted 2007). Thus, the fauna expected to be found in stony reference streams are not very suitable indicators of conditions expected in reference clay plain streams. In this study I compared two sampling protocols and equipment in streams in the Essex and Lower Thames Valley regions of southwestern Ontario, which flow through the St. Clair Clay Plain ecoregion (Baldwin et al. 2000; Richards et al. 1949). Because of the low relief of the region, the streams have little discharge and minimal velocity. Furthermore, many watercourses have been straightened to accommodate agricultural activity and resemble ditches rather than meandering natural streams, (Government of Canada: GeoGratis – Canada Base Map, 2010). Run-off from agricultural activity results in turbid water and significant sedimentation.

#### *Stream Sampling Equipment*

The guidelines and criteria by which to sample and assess macroinvertebrates vary among jurisdictions around the world (reviewed in detail in Chapter 1). Various samplers have been recommended for collecting invertebrates, yet these are typically used in fast flowing and rocky streams. They are less effective in atypical, slow flowing, and soft-substrate streams. I compared two samplers - D-frame sweep net and the Petite Ponar grab - as potential options to use in the clay-plain streams of southwestern Ontario.

In this study, I compared the D-framed sweep net using the jab and sweep method, and the Petite Ponar, since both instruments are used in still water, soft-bottom habitats (wetlands and lakes) similar to those of the Clay Plain streams and ditches of southwestern Ontario. The objective of this study was to contrast the sampling effectiveness of Petite Ponar grabs relative to D-frame net sampling in 19 southwestern Ontario streams. I predicted that:

- 1. The Petite Ponar grab would collect a representative benthic aquatic invertebrate sample in streams having soft sediment and little flow;
- 2. Invertebrate community composition would be better represented by ponar grab samples than by sweep net samples;
- 3. The relative effectiveness of sampler type (sweep net samples vs. Petite Ponar grabs) would depend on whether or not streams are stony (i.e., not within the clay plains) vs. silty or muddy (within the clay plain ecoregion). Sweep nets were expected to sample more effectively in streams outside of the clay plains, whereas the ponar was proposed to collect a more representative sample of the invertebrates in streams within the clay plains.

The findings of this study could result in a proposal to revise the methods for benthic macroinvertebrate sample collection be revised for slow-flowing, fine-sediment streams of the St. Clair Clay Plain region of southwestern Ontario.

#### **Methods**

#### *Study Sites*

For this part of the study, 19 streams were sampled in July and August 2016 in collaboration with the Essex Region Conservation Authority (ERCA) and the Lower Thames Valley Conservation Authority (LTVCA) to assess water quality and macroinvertebrate community composition in a cross-section of southwestern Ontario streams. Samples from a subset of these streams were chosen for the methods comparison study described herein.

Nineteen streams were visited -12 within the Lower Thames region, and 7 in the Essex County region of southwestern Ontario (Table 2.1; Fig. 1.1). As this was the first sampling season these sites were recommended by the Conservation Authorities administering each region.

#### *Habitat Assessment and Physicochemical Measurements*

On arrival, sites were inspected to confirm that they were accessible and wadeable. This was accomplished by either determining the water depth with a sweep net handle if there was a bridge or by entering the stream downstream of the sampling reach. Following inspection, stream habitat features were identified. A subjective visual assessment was made of the locations of riffles, runs and pools, meanders, location of the thalweg, and streambank/riparian features, as outlined in CABIN (Reynoldson et al. 2002) and OBBN (Jones 2015) guidelines. Where there was no evidence of rapidly flowing water at a site, the shallowest, most rapidly-flowing sections of the study area, containing the coarsest substrates were located and designated as riffles/glides (MPCA 2014). The areas immediately upstream and downstream of these locations were designated as pools - deeper, slower-flowing depositional zones that accumulate finer sediments (Hauer and Lamberti 2006). A sampling reach was on average 15 to 20 m in length for each site.

Environmental variables were sampled following protocols common to both CABIN and OBBN (Appendix A). Standard field-record sheets of both OBBN and CABIN (Appendix B) were used and completed on-site at the time of sampling. Measurements of stream temperature, dissolved oxygen concentration, electrical conductivity and pH were taken using a YSI Model 85 (Yellow Springs Instruments, Dayton, OH). All sections of the OBBN field sheets were completed; however, for CABIN field sheets, the sections labelled Slope, Velocity and Depth, and Substrate Data were excluded. Slope could not be determined because the landscape is so flat. Furthermore, the 100-pebble count (designed to estimate particle size-frequency distribution of coarse substrates) was not conducted because pebbles were either rare or absent at sites. Instead, sediment samples were taken in a riffle and pool using a 4.5-cm diameter coring tube and processed in the laboratory using sediment particle size analysis procedures (Appendix F).

Upon arrival, after safety checks and habitat location assessments had been completed water quality measurements were made using a YSI Model 85 meter before entering the stream. Five Petite Ponar samples were collected and 3 D-net traveling sweep samples were collected in the riffle and pool as described below. Point measurements of stream depth were taken with a meter stick within each habitat (two riffles/glides, one pool) at the deepest point. Habitat assessment attributes such as reach data (i.e. habitat types present, canopy coverage, riparian vegetation) were noted, along with stream width and bankfull width. Velocity measurements were not collected in2016.

#### *Macroinvertebrate Sampling*

A total of 8 samples were collected at each stream site, consisting of 3 D-frame sweep net samples and 5 Petite Ponar grab samples.

Petite Ponar grab Samples: The Petite Ponar grab collects a sample of substrate that is 15 cm x 15 cm in area and 15 cm deep (Mudroch and Azcue 1995). Samples were collected in a downstream-to-upstream order to minimize disturbance to the sediments prior to sampling. Grabs were collected from five locations in each stream; three in a pool, (one in the center and two along the edges of the stream) and two in a riffle/glide, (one-third of the distance from each streambank). This provided samples from across the range of habitat locations, ideally reflecting the diversity

of taxa present in the stream. Because all sites were wadeable, the sampler was placed on the stream bottom and manually pushed into the sediment rather than being dropped onto the substrate. The grab was then tripped by hand and manually closed. The sediment was then emptied into an enameled tray.

D-frame Sweep Net Samples: Sweep net samples were collected after Petite Ponar grab sampling had been completed, in two riffles/glides and one pool habitat. A 500-µm mesh net was used, performing the kick-and-sweep procedure whenever there was noticeable velocity and coarse sediment. Alternatively, the jab-and-sweep method was used when there was little or no detectable flow and where fine sediment occurred (Stark et al. 2001). For both methods, sweeping was conducted with the net held slightly downstream while moving backwards in a zig-zag pattern across the stream for 3 min (Jones et al. 2004, Reynoldson et al. 1999). Area sampled varied depending on each site but averaged 2.75 m x 30 cm (the width of the net).

Each Petite Ponar sample was emptied into an enameled pan. The pan was topped up with stream water, the contents were swirled to suspend organic debris, and the water and debris were carefully poured into a 250-µm mesh sieve bag. This 'gold-panning' procedure was repeated several times until only inorganic sediment remained in the pan. The sieve bag was repeatedly rinsed in the stream to remove fine sediments. Each D-net sample was rinsed in the stream while it was still in the D-net until most fine sediments passed. All sample contents were then placed individually in a labelled heavy-duty polyethylene soil bag, preserved with a formal-ethanol mixture (2.5:1 v/v 95% ethanol and 100% buffered formalin diluted 1:1 with stream water) (Pennak 1978; Edmunds et al. 1976; Wiggins 1927;1977; Krogmann and Holstein 2010) and the

bag was sealed with a twist-tie. Sample bags were returned to the laboratory where they were inventoried, heat-sealed to prevent leakage, and stored for later processing (Chapter 3).

### **Laboratory Procedures**

### *Preservation and Sorting*

In the laboratory, samples were processed and sorted in stratified-random order.

Samples were emptied into a 0.180-mm mesh 20-cm diameter brass soil test sieve to drain and were then rinsed under running tap water to remove residual preservative. They were then subsampled according the Nested Sieving procedures as outlined in Chapter 3. Invertebrates recovered from sample debris were identified to at least the family level and stored in scintillation vials containing 70% ethanol.



Table 2.1: Site names, coordinates and sampling date for 2016 benthic sampling year. Locations are illustrated in Fig. A.3.

\* Codes in brackets coincide with the Provincial (Stream) Water Quality Monitoring Network (PWQMN) for ERCA.

# **LTVCA**



#### **Statistical Analyses**

To assess the effectiveness of samplers, data from the 19 streams sampled in 2016 and sorted using Nested Sieves were analyzed. Analyses were conducted using STATISTICA 7.0 software, unless stated otherwise.

#### *Stream Specific Biodiversity*

The variability in family richness among streams was assessed from the 8 samples collected from the 19 streams (Appendix C). Family richness was calculated for each sample and collectively for each sampler (Petite Ponar vs. D-frame dip net). A two-way ANOVA was performed to estimate the among-stream variability and the effects of sampler type within streams on family richness. An Analysis of covariance (ANCOVA) was performed to compare family richness captured by each sampler type while accounting for differences in family richness among streams.

#### *Invertebrate Community Composition*

Both the abundance (numbers per sample) and relative abundance (Octaves – Log<sub>2</sub>(percentage of a sample comprised of a family)) of each taxon were tabulated. Non-metric Multidimensional Scaling (NMDS), with Bray-Curtis (Sorensen) distances, was used to portray similarity or dissimilarity between relative abundances of invertebrate collections for each sampler between different sites. Counts of all individuals belonging to a family that were collected by each sampler were pooled together for each site (i.e., specimens in the 5 Petite Ponar grabs from a stream were pooled, as were specimens from the 3 sweep samples). Relative abundances of families in each pooled sample were then calculated). Invertebrate families represented by fewer than 50 individuals per sampler and site, or that had a frequency of occurring in 5 or fewer samples were considered outliers and were removed from the analysis so as to not skew the outcome. This resulted in 39 families being included in the analysis and the exclusion of 30 families that did not meet the inclusion criteria. The relative abundance (octaves) of each common family then was calculated. The octaves were calculated according to the formula

$$
(4 + \text{Log}_2 (0.625 + \text{RA}))
$$
<sup>\*</sup> $(\text{RA} > 0)$ 

where RA is relative abundance (percent). The constant (4) at the beginning of the formula was added to prevent negative numbers from occurring when relative abundance values were less than 0.0625 (Log<sub>2</sub> (0.0625) = -4). The NMDS analysis was performed using PC-ORD Version 6 (McCune and Mefford 2011) and illustrated using the scatterplot feature of STATISTICA 7.

#### *Effectiveness of Sampler using Bioassessment Measures.*

A rarefaction curve was compiled to evaluate how many samples were necessary to reach the asymptotic family richness collected from a stream. The first point in each of the stream's rarefaction curve was the individual sample in each stream containing the highest richness. The second point was determined by identifying the sample from a stream yielding the greatest number of additional families and calculating the richness of the first and second samples combined. The third point in the cumulative richness curve consisted in the set of three samples yielding the greatest number of families per stream. The process was continued until all 8 samples, from both D-net and ponar samples from a stream had been incorporated into the cumulative curve. The progressive cumulative richness totals were then standardized by dividing the richness numbers by the overall family richness for a stream. Finally, the mean value and standard deviation were

calculated for each of the 8 cumulative values for the 19 streams sampled. A main-effects ANOVA between each of the samplers was calculated to determine their significance (Table 2.4 results).

An NMDS analysis with Bray-Curtis distances was performed to ordinate the community composition among all of the streams and to determine if there were differences in community composition collected by the two sampler types. Hilsenhoff Family Biotic Index tolerance scores were also calculated for each stream based on pooled samples collected using a D-net only, using ponars only, and using both samplers combined. Tolerance scores were based on the biotic tolerance values for New York State stream invertebrates (Smith et al. 2009), provided in the *Guide to Developing Conservation Authority Watershed Report Cards* provided by Katie Stammler (Essex Region Conservation Authority, pers. comm.). A scatterplot and regression of these tolerance scores was created to predict how well the actual tolerance score (based on D-net and ponar samples combined) was predicted by the samples collected using only one type of sampler. For each plot, the y-axis was the tolerance score based on all samples combined and the x-axis was the tolerance scores calculated for only one type of sampler. A scatterplot was created for each sampler individually.

#### **Results**

#### *Biodiversity and Community Composition among Streams*

Oligochaetes and chironomids were the most abundant taxa encountered (each totaling over 46,000 individuals), occurring at every site. The 5 most frequently encountered invertebrate families present among all the streams were Chironomidae, Oligochaeta (Naididae), Asellidae, Elmidae, and Sphaeriidae (last three all under 10,000 individuals). The overall number of taxa encountered in the study is summarized in Appendix C.

The streams within Essex and Lower Thames regions differed in that a larger proportion of LTVCA streams contained visible riffles (8/12) than did ERCA sites (1/7) (Appendix D). Streams in ERCA region had a mean±SD richness of 8.66±4.90 families (n=50) whereas LTVCA streams had 12.96±6.05 families (n=67; based on all 152 samples for each region).

Trends in biodiversity between ERCA and LTVCA streams (Appendix D) were similar, with some exceptions. McCarson Drain (LTVCA) was unique in supporting a variety of aquatic macrophytes. It was the only site at which emergent and rooted floating macrophytes were abundant. Sturgeon Creek had the lowest family richness (13), and McCarson Drain had the greatest number of families (43).

The invertebrates most frequently encountered in the streams regardless of abundance were Chironomidae, Oligochaeta, and Asellidae, each occurring in 19, 19, and 17 stream sites respectively. Chironomidae, Oligochaeta, Elmidae were the most abundant taxa in 17 streams. All the other macroinvertebrate families that we in the top 5 most frequently encountered were only captured in 6 or fewer streams (Table 2.3). Oligochaeta or Chironomidae were the most abundant taxa collected with the Petite Ponar grab; and were often more abundant than what the D-net collected. In contrast, the D-net samples typically had a larger variety of abundant taxa; Corixidae, Oligochaeta, Sphaeriidae, Chironomidae, Elmidae, Gammaridae. Most taxa were more abundant (total count) in the D-net samples than in Ponar grabs (Fig. 2.1) except for Chironomidae, Oligochaeta, and other invertebrates that are typically found within the substrate as opposed to being epibenthic.
### *Biodiversity differences due to Sampler Type*

Overall, mean±SD family richness estimated from D-net samples (22.9±8.1; n=19) was greater than richness estimated from Petite Ponar grabs (20.4±7.3; Fig.2.1). Mean richness estimated from the 3 D-net samples exceeded richness estimated by the 5 Petite Ponar grabs in 16 of the 19 streams sampled (Fig. 2.1). Overall the difference in richness was statistically significantly different between sampler type when accounting for among stream variation (main effects ANOVA, F=2.78, *p>*0.05; Table 2.2). However, when among-stream variation in overall family richness was incorporated as a covariate, there was a significant effect of sampler type on richness (ANOVA, F=4.135,  $p<0.04$ ; Table 2.3; Fig. 2.3). The slopes of the two regression equations were not significantly different (D-net:  $y = -1.7475 + 0.8467*x$ , and ponar:  $y = -2.3343$  $+ 0.78*$ x). but the intercepts were significantly different (F= 4.136;  $p = 0.048$ ; Table 2.3). Thus, across all the levels of among-stream richness 3 D-net samples collected a significantly larger proportion of the families present in a stream (85%) than the 8 Petite Ponar grabs (78%). A categorized scatterplot of family richness in individual samples illustrated the consistency of the differences (Fig. 2.3). The estimated percentage of the families collected by a single D-net (58%) and by a single ponar grab (44%) shows the D-net is closer to what is available in the entire stream (Figure 2.4).



Invertebrate Abundance Collected with D-net and Petite Ponar.

Figure 2.1 Bar graph of the mean abundance of invertebrates (the sum of all individuals collected by each sampler) arithmetically averaged across all streams) collected using either the D-net (black) or the ponar (grey). Note the octave (Log<sub>2</sub>) scale.



Figure 2.2: Arithmetic mean ± SE invertebrate family richness of D-net and Ponar samplers. There is a significant difference between sampling devices (ANOVA, F=4.14, p=0.050).

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Effect	ЭF	SS	MS	н				
Stream		1627.07	1627.07	110.98	$0.001**$			
Sampler		60.63	60.63	4.14	$0.050*$			
Discrepance		513.15	14.66					
Total		2200.85						

Table 2.2: Main effects ANOVA table illustrating effects of sampler types and streams on family richness; samples pooled together based on sampler type.



Figure 2.3: Number of families collected from D-net (red diamonds, n=3) and Petite Ponar grabs (blue triangles, n=5) as a function of stream-specific family richness. Dotted line represents equal richness. D-net:  $R^2 = 0.75$ ; SE= 7.89; y = -1.7475 + 0.8467\*x. Petite Ponar:  $R^2 = 0.78$ ; SE=10.07;  $y = -2.3343 + 0.78*x$ . Each point represents one of the 19 streams sampled in 2016 (Table 2.1).



Figure 2.4 Number of families collected from D-net (red diamonds, n=3) and Petite Ponar grabs (blue triangles, n=5). Dotted line represents equal richness. D-net:  $R^2$ =0.4883; SE=18.28; y  $= -2.6852 + 0.5751$ \*x. Petite Ponar: R<sup>2</sup>=0.5202; SE=20.33; y = -2.9754+ 0.4389\*x. Each point represents one sample collected in each stream of the 19 streams sampled in 2016.

Overall, the D-net collected more families in 13 streams and in only 5 streams did the ponar collect the most (mean $\pm$ SD= 5.5 $\pm$ 3.7; ANOVA, F=2.782). The largest difference in family richness between D-net and Petite Ponar samplers was observed where the Petite Ponar collected 13 more families than the D-net. The next greatest difference was where the D-net collected 12 more families than the Petite Ponar.

The 5 most common animals collected using the D-net were Chironomidae (22,546 individuals), Oligochaeta (18,798), Asellidae (6,597), Gammaridae (4,894), and Elmidae (2,765). The five most common for ponars were Oligochaeta (27,598), Chironomidae (25,343), Asellidae (3,516), Elmidae (1,276), and Caenidae (762). (Table 2.3).

According to the rarefaction curve (Figure 2.5) each of the three of the D-net samples provides the largest increase in the mean number of macroinvertebrate families, indicating that they would provide more information (invertebrates) than if the ponar samples were included next. The mean $\pm$ SD proportion of the richness collected by D-net 1 (riffle habitat) was, 0.47 $\pm$ 0.13; when combined with another sample (D-net 3 (riffle)) the mean $\pm$ SD rose to 0.70 $\pm$ 0.16, and if a third sample was combined (D-net 2 (pool)) the mean $\pm$ SD was 0.77 $\pm$ 0.17. D-net 1 is significantly different from any other sample, and D-net 3 is significantly different from all but D-net 2. A plateau is reached at Ponar 4, which was also in a riffle, and is not significantly different than the previous sample (D-net 2) as shown in Table 2.4. There was no significant difference among the cumulative values for any of the ponar samples.

Table 2.3: The 5 most abundant taxa collected by each sampler in each stream. Abundances are based on values extrapolated from the mass of sorted detritus relative to the unsorted biomass in the 4.0, 1.0, and 0.5 mm sieve size fractions.



ERCA



## LTVCA









Figure 2.5 Rarefaction curve of the number of samples that should be collected in the field. Mean±SD values of richness based on 19 sites from 2016 sampling year. Letters represent a significant difference for that sample. Samples with the same letter indicates no significant difference between them. Calculations illustrated in Table 2.4.

	D-net 1	D-net 3	D-net 2	Ponar <sub>4</sub>	Ponar <sub>3</sub>	Ponar <sub>2</sub>	Ponar 1	Ponar 5
D-net 1		0.00003	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
D-net 3			0.22392	0.01557	0.00835	0.00029	0.00012	0.00002
D-net 2				0.18192	0.12191	0.01721	0.00951	0.00239
Ponar <sub>4</sub>					0.85336	0.45094	0.35700	0.18330
Ponar 3						0.58129	0.47233	0.25546
Ponar <sub>2</sub>							0.84139	0.45006
Ponar 1								0.56218
Ponar 5								

Table 2.4: Table of significance values between difference samples using a t-test. Bolded numbers indicate statistical significance.  $(\alpha=0.05)$ 

An NMDS ordination was performed to illustrate the relationship between the ponar and D-net invertebrate collections (Figure 2.6; stress=11.25). An NMDS represents the distribution of communities in relation to one another in a multidimensional space. It incorporates multiple variables in reduced dimensionality that is more easily interpreted. The dimensions then are a reflection of the variables that were more or less related with each invertebrate spreading them across the dimension. What is plotted are the streams associated with the invertebrates along that dimension. A cloud of points representing the different streams can be compared to each other.

The taxa whose relative abundances were most highly correlated with the two dimensions were Elmidae, Hydropsychidae, Baetidae, Empididae, Tipulidae, Simuliidae, Hydroptilidae, (positively associated with scores of Dimension one; Appendix B) and Branchiobdellida, and Oligochaeta (negatively correlated with scores of dimension one). Acari, Elmidae and Heptageniidae were most highly positively correlated with Dimension two scores, and Glossiphoniidae, Planorbidae, Ceratopogonidae, Asellidae, Physidae, Sphaeriidae, Erpobdellidae, Nematoda, Mesoveliidae, and Lymnaeidae were negatively correlate with scores of dimensions two . The vectors created by connecting the D-net sample point with its Petite Ponar counterpart for each stream tended to be oriented in a bottom left to top right direction, indicating that Elmidae, Hydropsychidae, Baetidae, Empididae, Tipulidae, Simuliidae, Hydroptilidae, Acari, and Heptageniidae were relatively more abundant in D-frame dip net samples than in Ponar grabs, whereas the Ponar grab samples had greater relative abundances of Branchiobdellida, Oligochaeta, Glossiphoniidae, Planorbidae, Ceratopogonidae, Asellidae, Physidae, Sphaeriidae, Erpobdellidae, Nematoda, Mesoveliidae, and Lymnaeidae.

The vectors for three pairs of streams cross each other (Sharon and 16 Mile Creek, West Branch and South Dales Creek, and Talbot Creek and Belle River), indicating that interpretation

12

of the community compositional similarities between these pairs would depend on the method by which they had been sampled. Otherwise, the ordination indicates that each stream was distinctive enough that Ponar Grab sampling collects community composition similar to D-net sampling. The fauna are similar in McCarson Drain and Turkey Creek between each sampler since their points are close together.

Three axes captured most of the variation in the macroinvertebrate communities in streams sampled in 2016 (n=19) across southwestern Ontario. Higher dimensions did not further reduce the stress to improve the model. The final instability for a 3-dimensional solution is 0.00000 and the number of iterations was 64.

An NMDS ordination plot was created for all of the samples showing the relationship between D-net for both the D-net and ponar combined (Figure 2.7). Only 1 pair of streams cross in this ordination (Sharon Creek and McCarson Drain), illustrating that the information provided by including Petite Ponar grab samples did not alter the pattern of community composition derived from D-net sampling alone. The final stress was = 12.42, for a 3-dimensional solution. South Dales Creek and Muddy Creek are the two streams that illustrate similarities in fauna collected since their points on the plot are close together.



Figure 2.6: NMDS ordination plot showing the relationship between D-net and ponar collections for each stream based on invertebrate community compositions. Stress  $= 11.25$ , dim=3. Lines connect the D-net and Ponar grab samples from each stream. Sampler type influences interpretation of stream community composition only for pairs of streams whose lines cross.



Figure 2.7: NMDS ordination plot showing the relationship between D-net and all samples collected (both D-net and ponar combined) for each stream based on invertebrate community compositions. Stress = 12.42, dim=3.

### *Sampler Effectiveness with Biotic Indices.*

Table 2.5 shows the Hilsenhoff Biotic Index (HBI) scores calculated for the taxa found in each sampler separately and when they are combined. A scatterplot and regression based on these scores was performed for the D-net samples and the Petite Ponar grab samples individually compared to the scores found when all samples are combined (Figure 2.8 (D-net), Figure 2.9 (Ponar)). A paired comparison test showed there was a significant difference between the HBI scores of the D-net and the Petite Ponar samples  $(p<0.012$ , Table 2.6).

A one-way ANOVA comparing HBI scores was performed for all the samples combined and it was found that there was a significant difference between streams located in the Essex region when compared to the streams found in the Lower Thames region (ANOVA, p<0.05, Table 2.7, Figure 2.10).

Table 2.5: Hilsenhoff Biotic Index scores calculated from D-net, Ponar grab and combined samples for 2016 streams.





### LTVCA





Figure 2.8: Scatterplot and regression of the Hilsenhoff scores for samples from 19 streams (ERCA: solid black circle; LTVCA: open black circles) collected using only the D-net compared to scores calculated for all samples from a stream combined (D-net and ponar samples combined).  $Y = 1.929 + 0.7809x$ .  $R^2 = 0.8848$ ,  $R = 0.9406$ ,  $p = 0.001$  The dashed line represents expected perfect correspondence.  $R^2 = 0.8923$ ,  $r = 0.9446$ ,  $p=0.0000000001$ ,  $y=1.4108 + 0.8429x$ .



Figure 2.9: Scatterplot and regression of the Hilsenhoff scores for samples collected using only the ponar compared to scores for all samples combined (D-net and ponar samples combined). ERCA: solid black circles, LTVCA: open blue circles.  $y=1.5605+0.7017*x$ .  $R^2 = 0.4453$ ,  $R =$  $0.6673$ ,  $p = 0.0018$ \*\*\*

Table 2.6: Paired comparison test of difference between HBI calculated from D-Net samples vs. Petite Ponar grab samples. The mean  $(\pm SE)$  difference was -0.50  $\pm$ 0.18 (n=19), which was significantly different from zero  $t = 2.8$ ,  $p < 0.012$ .

Mean Diff.				t-value	
$-0.501053$	0.778288	0.178552	18 -2.80621		0.011680

Table 2.7. One-way ANOVA comparing Hilsenhoff Biotic Index scores for Essex Region Conservation Area streams (n=7) with Lower Thames Valley Conservation Area streams (n=12)

	D.F.		MS		
<b>ERCA vs. LTVCA</b>		7.195	7.195	5.028	0.039
Error		24.328	1.431		
Total		31.523			



Figure 2.10: The mean  $\pm$  SE of the Hilsenhoff Biotic Index Scores (HBI) between the Essex County and Lower Thames Regions (ERCA and LTVCA respectively). There is a significant difference between these regions (ANOVA, F=5.028, p=0.039).

### **Discussion**

Streams in the southwestern Ontario region are unique in that traditional samplers like the D-net may be difficult to use. Since streams in the study region do not follow the stereotypical rocky-substrate and instead have fine-grained, muddy substrates, it was thought that a Petite Ponar grab may be more effective than a D-frame net at collecting a representative sample of the macroinvertebrate community. There were highly significant differences in family richness which reflects inherent differences among streams, in that no two streams are exactly alike. Certainly, overall abundance of invertebrates varied greatly among streams (Table 2.3), and so D-net samples were found to collected significantly higher richness of invertebrates than the Petite Ponar grabs (ANOVA Table 2.2). It is noteworthy that even though more Ponar grab samples than D-net samples were collected, the D-net collected a greater number of invertebrate families per stream. Across all 19 streams the invertebrates that were collected using the D-net but not the Petite Ponar were Calopterygidae, Polycentropodidae, Notonectidae, Dixidae, Athericidae, Carabidae, Belostomatidae, Dryopidae, and Stenasellidae. The only family of invertebrates that was collected by the Petite Ponar but not the D-net was Crangonyctidae. (Figure 2.1). This may be because the D-nets sampled a variety of the microhabitats present across the entire width of the stream (on average 2.75 meters sampling track) and amongst the water column, whereas the Ponar grabs collected only a smaller portion of the stream's habitat diversity (collected  $15x15x15$  cm<sup>3</sup> volume within the sediment, not along the water column and not along the entire width of the stream). Carter and Resh (2006) described larger samples as beneficial when collecting from microhabitat patches, allowing widespread degradation across the stream to be detected, which can be more informative than interpreting one sample representing an entire stream. Stark et al. (2001) also concluded that in soft-bottomed streams multiple habitats should be sampled using semiquantitative methods (i.e. kick-net) in an area of  $3 \text{ m}^2$  since it may provide important information on environmental condition and no one area can represent the other microhabitats in that stream.

The rarefaction curve (Figure 2.5) illustrated that the D-net samples contributed the most to the biodiversity and richness estimates. A single D-net sample collected ~45% of the mean richness, 2 D-net samples collected an average of 70%, and 3 samples acquired just under 80%. Collecting until at least 70% of the total number of invertebrate taxa are detected is a common cut off point that allows a practical coverage of present taxa and minimizes the time spent going through samples (Mackey 2006). Furse (1981) found that within the first three samples, 62, 78, and 87% of families were collected, and Morgan and Egglishaw (1965) found that 51-87% of the total number of species were found within the first two kick-samples and an additional 9-36% were found in the next two samples. Thus, I recommend collecting 3 D-net samples from a stream -two in riffles and one in a pool because this strategy provides the greatest cumulative richness before reaching a plateau (approximately 90% of the total) and ensures that a representative sample of the invertebrate community is collected. Merritt and Cummins (1996) suggest that the numbers of samples depend on the site and the type of study, but generally with samples that have a low invertebrate density more samples are needed. Since the cumulative richness added by Petite ponar sample #4 was not significantly greater than from D-net sample #2 nor from any of the other Petite ponar samples (Table 2.4), I conclude that 3 samples per stream are sufficient for general bioassessment.

It also appears that samples taken in riffle/glide habitats have a higher mean richness than those taken in pool habitats. Even though riffles and pools were difficult to identify, they still seem to play a role in richness. Carter and Resh (2006) found that most sampling protocols (63.4%) only involved sampling from one habitat type (riffles: 25.6% and riffle and run: 24.4%) since these are also considered the areas where there is high species richness. This is evident in Figure 2.5. However, since these are soft-bottomed streams, multiple microhabitats should be sampled as well (Carter and Resh 2006; Stark et al. 2001; Poulton et al. 2003).

Poulton et al. (2003) compared how well a rock basket artificial substrate, a kicknet, and a Petite Ponar performed - the former two methods in rocky habitats and the latter behind wing dikes. They found that kicknets collected a larger mean number of taxa that were in the community (88.4%) and that community composition was similar in rock baskets and kicknet methods, where 75.3% of the taxa were the same. The rock baskets and Ponar were similar in 73.1% of the taxa the yet was speculated that invertebrates captured with the Ponar grab in the slower flowing waters had been transported there due to drift (Poulton et al. 2003). Overall kicknets collected a higher richness in less-tolerant organisms, whereas the Ponar collected a higher-tolerant organisms, however the ponar collected the most unique taxa (Poulton et al. 2003). In contrast, I collected only one (relatively uncommon) family exclusively with Petite ponar sampling. In conclusion, the qualitative method of the D-net is more effective and provides a greater estimate of taxa richness than using the Petite Ponar grab. For the clay plains of Essex and Lower Thames, 3 samples should be collected, 2 in riffle habitats and one in a pool to generate a sufficiently representative collection of the macroinvertebrates present.

Examination of the most common taxa found among streams by each sampler indicated that more families were collected by the D-net than by the ponar. This was especially evident when only looking at the single most abundant family for each of the streams (Table 2.4, see also Figure 2.1, illustrating that chironomids and oligochaetes are the most abundant invertebrates). This may be because the Ponar collects quantitative samples and was consistently deployed in the same habitat among streams (within the sediment). Chironomidae can be abundant and species-rich,

especially in pool habitats (Ferrington et al. 1995), and in detritus and sand (Mackay 1969). They are also used as bioindicators of water quality due to their sensitivity (Richardson 1928), and the ratio of oligochaetes to chironomids is useful to locating areas of pollution (Saether 1979).

The NMDS analysis (Figure 2.6) illustrated the distinction between the D-net and the ponar grab. Since only a few site vectors crossed, it suggests the community composition identified by the two types of samplers are not distinct relative to among stream variation in community composition. The same pattern was evident when comparing all samples to the D-net (Figure 2.7). This finding is consistent with those of Poulton et al. (2003) since ponar and D-net richness, number of taxa and mean number of taxa were not statistically significant. These results suggest that since the samplers are similar in community composition that they collect, ponar grabs need not be included in sampling procedures. The paired-comparison analysis (Table 2.8) also suggests there is a significant difference in HBI tolerance scores between the two sampling methods. It suggests the score calculated from D-net samples is 0.5 units less (less tolerant overall score) than the score calculated from Petite Ponar grab samples from the same stream. This may be a result of the collection of invertebrates that have a higher tolerance in the Petite Ponar than in the D-net. For instance, Oligochaeta has a higher tolerance score (8) and was found more frequently in the Petite Ponar.

### **Conclusion**

When comparing the effectiveness of the D-net and the Petite Ponar, results of the analyses indicate that the D-net is more suitable for rapid bioassessment since it collects a more representative sample of the stream community (greater proportion of the families present) than the ponar. Three D-net samples should be collected. Additional Petite Ponar grab samples need not be taken because they do not add family richness that the D-net samples don't already collect.

# **Chapter 3: Efficiency of Laboratory Macroinvertebrate Sample Processing; A Comparison of the Marchant Box and Nested Sieves Methods.**

### **Introduction**

When stream or wetland benthic materials are collected, the benthic macroinvertebrates are typically either hand-picked from the detritus in the field, while they are living, or the entire sample is preserved, and individuals are sorted from the sample in the laboratory. Field sorting is much more time-effective than lab processing. However, field-picked samples may not be representative of macroinvertebrate community composition. Large or active organisms are more likely to be seen and selected than smaller, inactive, or cryptic individuals (Payne 2017). Labsorted samples are less subject to these potential biases because sorting is normally done with the aid of a dissecting microscope. Different methods have been suggested or compared (Brinkman and Duffy 1996; Fairchild et al. 1987), with aims to reduce sample sorting time by using subsampling methods or devices, (Ciborowski 1991; Marchant 1989; Wrona et al. 1982; Hickley 1975), or fixed number counts (Barbour and Gerritsen 1996; Somers et al. 1998). Finding ways to reduce processing time allows more samples to potentially be included in study designs and/or reduces research costs (Brinkman and Duffy 1996).

Various subsampling methods have been proposed to reduce the amount of time required to sort a sample. Wrona et al. (1982) proposed using an Imhoff cone with an air supply at the tip of the cone to mix the invertebrates without damaging them. Although the subsampler is easy to build, this method requires a count of 100 individuals taken from at least 5 subsamples, which is a disadvantage because the combined subsamples will often yield a count of more than 100 individuals.

Hickley (1975) proposed placing the sample on a sieve resting on top of a subsampling chamber that would randomly split the sample. A lid with a hole in it allows water to be added, which will begin to bubble and gently separate the sample once compressed air is turned on. This allows invertebrates to be subsampled and avoids them becoming damaged during washing. Even though this method allows for the division of the sample, this apparatus is expensive to build.

In Ontario, two subsampling/sorting methods are commonly used - the Marchant Box (Marchant 1989) and a stack of nested sieves (e.g., Ciborowski 1991). The former is a plexiglass box that is subdivided internally into 100 cells in which components of a sample become evenly distributed and which can then be randomly selected for sorting. A count of 300 individuals must be collected and if this is reached before the contents of the 50<sup>th</sup> cell have been enumerated the sorting may stop; otherwise, the sorter must sort the materials within the entire box (CABIN 2011; Jones 2007). The advantage is that of only a subset of the sample needs to be sorted; yet, it is timeconsuming to initially spread the sample evenly across the box, and subsequently to remove subsamples from the randomly selected cells. If a cell contains few invertebrates, then time that could otherwise be spent sorting is needed to remove the many individual subsamples from the box. The Marchant Box is also heavy and difficult to manipulate if one is to comply with the recommended methods of mixing the sample by repeatedly inverting the container. Furthermore, rare organisms (those that may be present in only a few cells) may not be encountered during the subsampling process and thus are not incorporated into the analyses. Depending on the metric used, this could affect the assessment of ecological condition.

An alternative approach is the Nested Sieve-Fractioning Method. This method involves devoting differential effort to sample fractions differing in particle size. The sample is elutriated in a pan and slowly poured into the topmost of a nested stack of sieves with mesh sizes of 4.00,

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1.00, 0.50, and 0.25 mm. This not only prevents the sample's denser inorganic material (which remains in the pan for separate inspection) from being incorporated into the sample, but it also facilitates sorting because the materials in a single sieve are similar in size. This, in turn, should speed the inspection process, thus reducing processing time, allowing more samples to be sorted and hence increasing the precision of information about the stream (Vinson and Hawkins 1996; Colwell and Coddington 1995; Allanson and Kerrich 1961).

The frequency with which these two methods are used varies geographically and by jurisdiction, reflecting both the sampling environment (e.g. stream size and substrate characteristics) and the history of regional sampling programs.

### *Great Lakes Region*

Sorting protocols used by agencies adjacent to southwestern Ontario were reviewed because the streams in these jurisdictions are likely to be similar to my study area. The Michigan Department of Environment, Great Lakes, and Energy may either hand pick invertebrates from samples in the field, or use the bucket-and-swirl method in the lab, whereby a sample is placed in a bucket and stirred, which suspends lighter, fine material and leaves coarse, inorganic materials on the bucket bottom (Michigan Department of Environment, 2008). Subsamples are taken from the bucket using a small, 1-mm mesh net and sorted for approximately 20 min until a total count of 300±60 organisms are acquired (without the aid of a microscope). This procedure was derived from the United States Environmental Protection Agency (USEPA) Rapid Biological Assessment Protocols (Barbour et al. 1999), Ohio Environmental Protection Agency protocols (Ohio Environmental Protection Agency 1987a, 1987b, and 1987c), Illinois biological procedures, and tested by the Michigan Department of Environmental Quality (MDEQ). The protocols are

inexpensive, and flotation and elutriation methods such as this work well for highly inorganic samples (Rosenberg et al. 1998). However, these procedures are less effective for samples collected from areas where substrates are fine-grained (mud or clay). Instead, such samples may be field-rinsed through a sieve to eliminate inorganic materials, which can make up 50% of sample volume (Rossillon 1987; CABIN Field Manual 2009).

The Ohio EPA recommends sorting samples using a Caton tray (Caton 1991), sampling at least 10% of the tray, counting to at least 500 individuals, and using a microscope at 6X to 10X magnification. This is based on the RBPs of the US EPA (Barbour et al. 1999). The Caton tray is similar to the Marchant Box in that the sample is spread evenly over a grid within a container. In this case, a tray, where any overhanging material or material that crosses the grid can be cut, and a scoop is used to remove the contents from the randomly selected grids. Material is sorted under a dissection microscope (Barbour et al. 1999). Although this method counts to a larger number of individuals providing potentially greater richness, it is still time-consuming because only small sections of the Caton tray are sampled at a time. Another limitation is that multiple-sized organic particles are present, which makes it difficult for the sorter to inspect.

Texas is another jurisdiction in which stream substrates mostly comprise clay (Miller and White 1998). The Texas Commission on Environmental Quality (TCEQ) created the Surface Water Quality Monitoring Procedures, Volume 2 (2007). This protocol involves rinsing samples through a  $\leq$ 595 $\mu$ m mesh, or a No. 30 sieve, or sieve bucket ( $\leq$ 595 $\mu$ m) to remove preservative and fine sediments. The material is then distributed evenly over the bottom of a white pan. Subsequently, a cookie cutter or Mason jar lid is used to isolate and allow removal of 4 subsamples, which are sorted beneath a stereo dissecting microscope to a count of 140 individuals (Surface Water Quality Monitoring Procedures, Volume 2, 2007). This approach is similar to the Caton tray and the Marchant box in that subsamples (albeit large ones) are taken and examined. Although this method might be time-efficient, the 140-specimen count criterion might not represent the full diversity of the stream community composition. This is especially true when large, rare organisms, such as crayfishes, are present.

Several national programs have developed protocols that regions can employ, using various approaches. For example, Moulton et al. (2000) compared quantitative and qualitative sample sorting methods by the U.S. Geological Surveys National Water Quality Laboratory Biological Group. The qualitative method focuses on estimating the abundance of each taxon by sorting a sample for approximately 2 h, collecting only undamaged invertebrates. The sample is elutriated in a bucket, poured over 4.75-mm aperture sieve, and the coarse material retained is examined for 15 min. The remaining (finer) material is examined for 105 min. The quantitative method consists of collecting either 100 or 300 individuals from an elutriated sample placed on a gridded subsampling frame. However, because 3 subsampling frames and 2 estimation trays can be used, this leads to increasing variation amongst sorters. Moulton et al. (2000) even state that the number of possible combinations of frames and trays is too large, may have influence the analyses, and that a more standard approach is preferred.

#### *International: Europe, New Zealand*

Hasse et al. (2004) compared the *River InVertebrate Prediction And Classification System* (RIVPACS) (Wright 2000) and *The Development and Testing of an Integrated Assessment System for the Ecological Quality of Streams and Rivers throughout Europe using Benthic Macroinvertebrates/ STAndardisation of River Classifications* (AQEM/STAR) protocols (Furse et al. 2006; STAR consortium 2003). RIVPACS is a model that uses environmental data to predict the macroinvertebrate assemblage expected in a location in the absence of anthropogenic environmental stress, which is a tool to assess the quality of rivers (Wright 2000). To sort samples, the investigator hand-picks invertebrates in the lab from a fraction (i.e.,  $\frac{1}{2}$ , or  $\frac{1}{4}$ ) of a sample without magnification, and looks through the unsorted fraction for taxa that were not found in the sorted fraction (Haase et al. 2004). AQEM/STAR aims to standardize macroinvertebrate sampling protocol and assessments. In the sorting protocol, at least 700 individuals comprising at least  $1/6<sup>th</sup>$ of the sample are identified without magnification (Haase et al. 2004). Estimates made using the RIVPACS were highly variable in terms of the fraction that had to be sorted; and the AQEM/STAR approach was very time-consuming. Haase et al. (2004) proposed an alternative modified AQEM/STAR method (MAS method), which consisted of using a 2-mm aperture sieve. This reduced sorting time and associated costs compared to RIVPACS and AQEM/STAR. This procedure is similar to using nested sieves in that similarly sized objects remain together, which eases processing.

New Zealand recognized the challenges and created a protocol to accommodate sampling soft-bottomed streams within their National River Water Quality Network (NRWQN). Maxted et al. (2003) observed a difference in abundance of invertebrates between soft-bottomed and hard bottomed streams, and consequently recommended that soft-bottomed samples should be entirely processed to increase information obtained. Stark et al. (2001) contrasted the three major methods of processing macroinvertebrates used by New Zealand biologists - full counts, fixed counts, and coded abundance (semi-quantitative assessments of samples from hard-bottomed streams). Stark et al. (2001) prepared a manual for the Ministry for the Environment of New Zealand and elaborated on all three methods; but only the first two will be summarized. The fixed count protocol consisted of counting up to 200 individuals and then scanning for rare taxa first by

washing the sample on a 0.5-mm aperture sieve (and 4.0 mm if desired), and distributing the retained material evenly in a white, gridded sorting tray (6 cm by 6 cm). Grids are randomly selected for examination (without a microscope) until 200 individuals are reached. The entire tray is subsequently examined for rare taxa. The second method is full count enumeration with a subsampling option. Stark et al. (2001) describe the latter as time-consuming and expensive but having the benefit of allowing for a direct measure of abundance and percent composition. Thus, it can be used for comparisons of abundance or calculation of metrics.

The full count protocol consists of pouring the sample through a stack of sieves (4.0, 2.0, 1.0, 0.5 mm) and inspecting the fractions to make sure materials are separated by size appropriately. The 4.0- and 2.0-mm size fractions are examined first, without the aid of a microscope. Subsampling is an option for reducing sorting time if more than 500 individuals are present (Stark et al. 2001). Thus, using sieves reduces sample sorting time and they have been recommended for samples from both coarse, and fine-grained substrates.

As reviewed above, although sample sorting protocols vary among programs, sieves are commonly used to speed the sorting process. Ciborowski (1991) found that for samples from two stony-bottomed streams, the processing time for samples that have abundant invertebrates can be greatly reduced by subsampling or simply using a smaller sampler. Allanson and Kerrich (1961) also recommended using sieves to reduce sorting time for samples collected from streams with sandy, muddy or stony substrates.

This study investigated which of two widely used laboratory processing protocols (Marchant box and nested sieve-fractioning) was better suited to sorting the invertebrates from clay plain stream samples. The efficiency (total processing time), effectiveness (number of individuals and family richness) and accuracy (nearness of an estimate extrapolated from a subsample to the actual number) of the two subsampling techniques were compared.

The objectives were to:

- 1. Compare sample total processing times of each procedure. I predicted the Sieve-Fractioning Method to require less sorting time than the Marchant Box;
- 2. Compare the estimated family richness of samples processed by each method. I predicted the Sieve-Fractioning Method to have a larger family richness than the Marchant Box;
- 3. Assess the similarity in community composition estimated from samples processed by each method.
- 4. Determine the relative precision and accuracy of extrapolated counts estimated from subsamples using each procedure

### **Methods**

Method comparisons were conducted on 40 samples (3 D-frame sweep and 5 Petite Ponar grab samples collected from each of 5 streams in 2016 - Big Creek, Little River, Sharon Creek, Sixteen Mile Creek, and White Ash Creek; Table 2.1 in Chapter 2). Samples were examined in stratified-random order. Each sample was first processed using the Marchant Box method (recommended by OBBN and CABIN). Subsequently, all invertebrates and detritus were recombined and processed according to the sieve-fractioning and subsampling method of Ciborowski (1991).

### *Marchant Box Method*

A sample was washed through a 0.50-mm aperture soil test sieve stacked on top of a 0.25 mm sieve using a gentle stream of water from a faucet equipped with an aerator. Particles retained on the 0.25-mm sieve were archived due to time constraints but may be used for other future projects. Materials in the 0.50-mm sieve were rinsed into a Marchant box (Marchant 1989), which was then completely filled with water. The box lid was secured, and the entire box inverted to distribute the debris in the sample evenly in the water. The box was quickly returned to its upright position, allowing the sample contents to randomly settle into the 100 cells. A photo was taken after each inversion to illustrate how the sample may be distributed, and the number of inversions was recorded. The material from a randomly selected cell was removed with a pipette, transferred into a Petri plate, and all invertebrates were removed and identified at 10X magnification beneath a dissecting microscope. The procedure was repeated by sampling randomly selected cells (using numbers obtained from a random number generator) until the required number of animals was recovered. Wash time and sorting time were recorded to the nearest minute.

Sorting stopped once a total of 300 animals had been found, but only if this total was achieved by examining between 5 and 50 cells. The material from the cell in which the  $300<sup>th</sup>$ organism was found was sorted entirely. If 300 individuals were found before the 5th cell, sorting continued until the biota in at least 5 cells had been enumerated. This did not occur in my study. If more than 50 cells had to be examined, detritus from the full complement of 100 cells was sorted. The sample (detritus + invertebrates from all cells) was then recombined and subsequently sorted using the Sieve-Fractioning Method.
#### *Nested Sieve Fractioning Method*

The sample was emptied from its storage bag into a white enameled tray containing 5 cm depth of tap water, and clumps of debris were gently teased apart with a pair of forceps. A nested stack of standard soil test sieves was placed in a sink and was used to split the sample into fractions sorted according to particle size. The stack was composed of a 4.00-mm, 1.00-mm, 0.50-mm and 0.25-mm US standard brass sieves. The 0.25-mm sieve was included to incorporate materials that did not pass through the D-net or the sieve bag while sampling. The tray contents were slowly poured through the top sieve. Additional water was repeatedly added to the tray to resuspend debris that remained on the bottom of the tray, and that water (and suspended debris) was also poured into the top sieve. Once all organic material from sample had been poured onto the top sieve, a gentle stream of running water was used to wash smaller particles through the largest-aperture sieve. Materials retained on the top sieve were then rinsed back into the pan, and the process was repeated to ensure that all fine material had passed through the coarsest sieve. Subsequently, the material remaining on the 4-mm sieve was rinsed into the enameled tray, the contents poured onto a 0.18-mm sieve (to drain off the water), and the material in that sieve was emptied into a Petri dish for later inspection under the microscope. The same steps were repeated for the 1.00-mm, 0.50-mm, and 0.25-mm size fractions. Depending on the volume of the entire sample, sieves could become clogged, causing them to begin to fill with water. In such cases, I carefully lifted and separated one sieve from another and allowed the water to drain into the sieve below.

Once the size fractions had been placed in individual Petri dishes, the materials were examined under the microscope. For this study, the 0.25-mm size fraction was archived (placed into a scintillation vial with ethanol for other potential projects).

For most samples, the entire subsample was sorted, but where there was a lot of detritus and more than 300 organisms were suspected to be in a size fraction, that size fraction was quartersampled using a right-angled plastic wedge that would isolate  $\frac{1}{4}$  of the dish contents from the remainder. Typically, the 4-mm and 1-mm size fractions were completely sorted, and the 0.5-mm size fraction was quarter-sampled. All detritus aliquots (sorted or unsorted) were kept separate and placed in an oven at 70°C and dried to constant mass (at least 24 h). The masses of both the sorted and (if applicable) unsorted sample fractions were recorded. These proportions of detritus were then used to estimate the total number of invertebrates present in a size fraction by extrapolating the number of invertebrates in the sorted fraction of detritus to the total mass of detritus in the sample.

The total processing time needed to prepare and sort each sample (sum of washing time + handling time + sorting time to achieve the appropriate criterion) by each subsampling method was recorded to the nearest minute.

#### *Invertebrate Identification*

Invertebrates were identified to the family level of taxonomic resolution using keys of Merritt et al. (2008), typically as the sample was sorted. The identification times for each sample were recorded separately from the sorting time by using a stopwatch and recording the length of time it took for each. Invertebrates were stored in shell vials separated by fraction size and placed into scintillation vials for later verification. The time needed to identify taxa to the appropriate level of resolution is assumed to be independent of the processing method and thus was recorded, but not included in the comparison of lab techniques.

# **Statistical Analysis**

Various measures of sample-processing efficiency were assessed. An effective process provides a precise and accurate estimate of the true number and kinds of organisms present, requiring the shortest possible period of time to sort organisms from detritus. Unfortunately, washing and sorting times were lost due to misplacing the written data for 14 of the 40 samples and a regression analysis was conducted to estimate these missing times. For each sample, I determined the following aspects of processing, identification and sample composition (Table 3.1):

Table 3.1. Summary of variables determined for assessment of processing efficiency of Marchant Box vs. Nested Sieve procedures.

Independent variables (units)	Dependent Variables (units)		
Stream name	Sample preparation time (min)		
Sampler type (D-frame net; Petite Ponar)	Sample sorting time (min)		
Processing method (Marchant box; nested sieves)	Estimated invertebrate abundance (number of invertebrates in sample, extrapolated from subsamples where appropriate)		
Detrital mass (g dry mass) [Actual] abundance (total number of invertebrates in a sample)	Estimated sample family richness (based on 300-animal count; families per sample)		
[Actual] sample richness (total number of families observed in a sample)	Estimated streamwide family richness (based on processing method; families per stream)		
	NMDS axes of community composition (dimension score; sampler & process type specific)		

## *Subsampler Efficiency – Processing Time*

The relationship between the length of time taken to process each sample using the Marchant Box vs. sieve-fractionation method was assessed by regression. To account for variation in human factors, samples were sorted in a randomized order. A distance-weighted least squares line was fitted through the data to summarize the trend. Main effects (unreplicated; processing type x sample number) ANOVA was performed to compare the mean processing time of each procedure accounting for inter-sample variation. Because both processing times and the size of samples varied greatly, multiple regression analysis was performed to determine the degree to which other covariates influenced processing time (washing time  $+$  sorting time). The independent variables included both dummy variables (sorting method (Marchant Box vs. Sieves), sampling method (Dnet vs. Petite Ponar), habitat type (riffle vs. pool)), stream sampled (4 variables to summarize the 5 streams) and quantitative variables (total detrital mass). In addition, variables representing several interactions (sorting method x detritus mass, sampler type x detritus) were included. Relationships were assessed by both forward and reverse stepwise regression. Because the same results were achieved by both methods, forward stepwise results are reported here.

## *Estimated Richness and Abundance*

Abundance was expressed as the total number of invertebrates estimated to be present in a sample collected from a stream by one of the subsampling methods. Taxa were identified to family unless otherwise noted (depicted in Appendix C). Richness was variously expressed as the number of families present in a sample (sample richness; families per sample), the mean number of families collected by a particular sampler type in a particular stream (sampler richness; D-frame net vs. Petite Ponar grab), the cumulative number of families encountered in a particular stream (stream richness; families per stream) or processing-specific richness (mean number of families observed per sample using the Marchant box procedure vs. nested sieve procedure). Regression analysis was used to estimate the relationship between estimated (extrapolated) abundance determined from the Marchant box procedure vs. the estimated (extrapolated) abundance determined from nested sieve procedure.

The relationship between best estimate of stream richness (based on the combination of subsamplers) compared to what is indicated by each subsampler individually was also considered. The absolute difference in abundance between the sieves and the Marchant Box relative to the estimated abundance from the sieves as a percent of the Marchant Box was also evaluated.

## *Community Composition*

Community composition data were analyzed using the abundance and relative abundance using Octaves –  $Log_2$  (percentage of a sample comprising of a family) (as in Chapter 2). Nonmetric multidimensional scaling (NMDS) with Bray-Curtis distances was performed to express community composition along a reduced number of biological axes and graphically illustrating the within vs. among sample differences of each subsampling procedure. The NMDS analysis was performed using PC-ORD Version 6 (McCune and Mefford 2011), and the scatterplot using STATISTICA 7.

## **Results**

## *Subsampler Efficiency – Processing Time*

The time in minutes was recorded for 40 samples collected with either a D-frame net or a Petite Ponar grab from among 5 streams for each processing method. Processing times that were not recorded for 12 out of 40 samples were interpolated using regression analysis to estimate what the time may have been to be included in the analysis. The equation used was The sievefractionation method was most efficient when samples required less than about 230 min of sorting time ((Sorting time =229 + 0.1189 x mg detritus; Figure 3.1). A main effects ANOVA showed a significant difference between sorting times of the two subsampling methods (Figure 3.2 and Table 3.2: ANOVA,  $F(1,31) = 9.15$ ,  $p=0.005$ ).

Multiple regression was performed to determine whether sorting time was significantly influenced by subsampling method (Marchant Box vs. Sieves), field method (D-net vs. Petite Ponar), habitat type (riffle and pool), and detritus mass in a sample. Sorting time was independent of all variables except for detritus mass (Table 3.3). A simple regression with detritus mass (mg dry mass) was significant ( $p=0.0095$ ) and the equation of the line is Sorting time (min) =160.1841+4.6673xDetrital mass (mg). Thus, at an increase in one gram of detritus will increase the total time to go through a sample by 5 minutes. Because detritus was significant at the  $\alpha$ =0.05 level, a standard stepwise regression analysis was conducted with interactions between sorting, sampling, and habitat with detritus. There was a significant effect of sorting method on sorting time, but it depended on the amount of detritus present in the sample (Table 3.4).



Processing Time vs. Detritus Mass for 2 Subsampling Methods

Figure 3.1: Scatterplot of the time taken to process one sample using nested sieves (squares and dotted line) and the Marchant box (triangles and solid line). The lines represent distance-weighted least squares fits through the data points (stiffness =  $0.5$ ).



Figure 3.2: Mean ±SE; n=31 processing time for samples using the Marchant Box and sieving subsampling methods (note the Log scale). There is a significant difference between sorting methods (ANOVA, F(1,31) = 9.14.589, p=0.005).

Effect	D.E.	SS	MS	F	
Subsampler		0.9541	0.9541		9.139 0.005087
Sample	30	3.6086	0.1203		1.152 0.350312
Discrepance	30	3.1321	0.1044		
Total		7.6947			

Table 3.2. Main Effects (unreplicated) ANOVA of effects of sampler type on Log<sub>10</sub> transformed combined processing time.

Table 3.3 Results of multiple regression analysis of the effects of subsampling method (Marchant Box = 1; Sieves = 0), sampling method (D-net =1; Petite Ponar = 0), habitat type (riffle = 1; pool =0) and detritus mass (grams) on Log-transformed total time required to process a sample (minutes; n=36 samples;  $R^2 = 0.256$ )



 $n=36$ 

$n=35$					
Variable	All variables				
	Reg. Coeff.	S.E.	p	$R^2$	
Intercept	169.139	18.71	0.000		
<b>SortingxDetritus</b>	8.870	4.272	0.047		
SamplingxDetritus	$-4.675$	9.109	0.612		
HabitatxDetritus	$-1.769$	8.569	0.838		

Table 3.4 Results of standard stepwise multiple regression analysis of the effects of the interaction between detritus mass (grams) with subsampling method (Marchant Box = 1; Sieves = 0), sampling method (D-net =1; Petite Ponar = 0), and habitat type (riffle = 1; pool =0) on total time required to process a sample (minutes;  $n=36$  samples).  $R2 = 0.141$ 

## *Richness and Abundance*

The actual abundance of invertebrates in samples (those that were entirely sorted by at least one processing method) was compared to the estimated abundance extrapolated from the subsample of the other sorting method (Figure 3.3). The equation of the line for the Marchant box was y = -102.6804+3.2853\*x and for the sieves was y = -46.268+1.164\*x. The Marchant box method sometimes greatly overestimated the abundance of invertebrates in a sample, whereas the nested sieve procedure slightly overestimated true abundance when over 300 individuals were in subsamples. The slopes of the two lines were highly significantly different from each other (Marchant Box:  $R^2 = 0.22$ ,  $p = 0.09$ ; Sieves:  $R^2 = 0.89$ ,  $p < 0.001$ ). The regression line for the sieve method was relatively unbiased (similar to the dashed line in Figure 3.3, which represents perfect prediction of invertebrate abundance in the whole sample extrapolated from the partial subsample).

A comparison of the richness estimated by the two sorting methods revealed that D-net samples processed by the sieving method collected more families than samples processed by the Marchant box in only 2 streams and equal in richness to the Marchant Box in one stream. Petite Ponar samples processed by the sieving method contained more families than when processed by the Marchant Box in 3 streams and an equal number in 1 stream (Table 3.5). There was a significant difference in richness between each sorting method (Main Effects ANOVA,  $F_{(1,19)} = 5.959$ , p<0.05; Figure 3.4, Table 3.6).

The sieving method detected, on average, 94% of the families estimated to be present in a stream (estimated by regression;  $y = -0.8341 + 0.9421 \times x$ ,  $SE = 0.139$ ,  $R^2 = 0.9380$ ,  $p=0.0067$ ; Figure. 3.5). In contrast, the Marchant Box only detected about 83% of the families ( $y = 0.0835$ )  $+$  0.827<sup>\*</sup>x, SE = 0.118, R<sup>2</sup>= 0.9709, p=0.0059). Neither equation differed significantly from a slope of 1.0.



Invertebrate Abundance from Samples Sorted as a Whole Compared to the Estimated Abundance.

Figure 3.3: Estimated invertebrate abundance extrapolated from subsamples versus true abundance. Each point represents one sample  $(n=27)$ . The solid blue line represents the projected estimates of the Marchant Box (Estimated abundance  $= -102.6804 + 3.2853$ \*true abunance), and the solid red line represents that of the sieve method (estimated abundance=46.0799+0.784\*true abundance). The dotted line indicates the expected extrapolated abundance in a sample if the subsampling method is unbiased (Extrapolated abundance = actual abundance).







Figure 3.4. The mean(±SE) family richness found using the Marchant Box and nested sieves fractionation method. (n=40).

Effect	df	<b>SS</b>	MS	F	n
Sample	9	1079.050 119.894			19.601 0.000070
<b>Process</b>	1	36.450	36.450	5.959	0.037295
Discrepance	9	55.050	6.117		
Total	19	1170.550			

Table 3.6. Main Effects (unreplicated) ANOVA of effects of processing type on number of families recovered from sweep and Petite Ponar samples collected from 5 streams.

 $\overline{\phantom{0}}$ 



Family Richness for Whole Stream Compared to Richness Found Using Subsamplers.

sieve fractionation processing methods vs. total number of families observed in source stream. The x-axis is a combination of both samplers. Each point represents the mean richness for 8 samples per stream using the respective subsampler. The dotted line represents equal richness for both axes. The Sieve standard error is 0.139 and for the Marchant Box it is 0.118. The slope of the equation for both sorting methods is not significantly different from a slope of 1.0. (Marchant Box: t=1.47, p>0.05, Sieves: t=0.41, p>0.05)



The Absolute Difference in Estimated Abundance Between Two Sorting Methods Compared to Sieves as an Estimated Percentage of the Marchant Box.

Figure 3.6 Scatterplot and regression with polynomial fit of the absolute difference between the Marchant Box and Sieves, to the Sieves as a percentage of the Marchant Box. Each point represents one sample.  $R2 = 0.2981$ , p=0.0015, y=208.9075+0.1009\*x.

## *Community Composition*

Non-metric multidimensional scaling (NMDS) ordination of the invertebrate families collected in the D-net samples from the 5 streams represented community composition in 2 dimensions (stress=12.22). The similarity in community composition of Marchant Box vs. sieve subsampling was represented by connecting the two estimates from each sample with a line (Figure 3.7). Ellipses were drawn by eye to enclose the sample estimates from each of the 5 streams.

The NMDS indicated that community composition of each stream was relatively distinct from the others. There was little or no overlap among the ellipses for Little River and Sixteen Mile Creek, indicating that the fauna within these streams are different in composition from the communities of the other streams. White Ash Creek and Big Creek overlap, suggesting these two streams have similar community composition. Big Creek and Sharon Creek also overlap. The invertebrates whose relative abundances are positively associated with scores of Dimension 1 are Chironomidae and the dragonfly family Gomphidae, whereas many other families' relative abundances were negatively correlated with scores of Dimension 1 (Appendix B). The invertebrates whose relative abundances were positively correlated with scores of Dimension 2 were Corixidae, Elmidae, Heptageniidae, Hydropsychidae, Hydroptilidae, Simuliidae, and Tipulidae. Relative abundances of Oligochaeta were negatively correlated with scores of Dimension 2. Accordingly, one can infer that Sixteen Mile Creek is predominately influenced by oligochaetes, chironomids and Gomphidae. Little River is influenced by many invertebrates in the negative direction of Dimension 1, but minimally influenced by those associated with Dimension 2 (Appendix B). Sharon Creek is not dominated by any particular taxon. White Ash Creek and Big Creek are similar in composition, so their fauna are composed predominately of Corixidae, Elmidae, Heptageniidae, Hydropsychidae, Hydroptilidae, Simuliidae, and Tipulidae. Overall,

sorting method did not produce large differences in community composition except for samples from Big Creek (D-net sample 2 taken in pool habitat) and White Ash Creek (D-net sample 3 taken in a riffle).

## **Discussion**

Minimizing sample sorting effort is one of the objectives of a rapid bioassessment protocol, (Resh et al. 1995; Barbour et al. 1999), because sample processing can be much more timeconsuming than field collection. Several investigations have suggested that using sieves will reduce sorting time, (Ciborowski 1991; Vlek, Šporka, and Krno 2006; Barba et al. 2010). The goal of this chapter was to determine whether sieving procedures are more effective in sample processing than the recommended Marchant Box method (Marchant 1989; CABIN 2011; Jones et al. 2004, (OBBN)).

Comparisons of sorting times using the two subsampling methods indicate the sieve subsampling protocol is indeed more time-efficient than the Marchant Box. When using the sieves, a sample was completed in about 1 to 2 h, whereas the Marchant box typically took 4 h or more (Figure 3.1). The length of time taken to sort through a sample increased as a function of the amount of detritus in the sample until about 6 g of detritus. When more than 6 g of detritus occurred in a sample, the Marchant Box sorting time increased slightly, whereas sorting time required using the sieves method actually decreased, presumably because the finer sieve fractions could be subsampled. There was great variability in the time required to go through a sample.

I had hypothesized that invertebrate abundance may have been a contributing factor to overall processing time, as reported by Ciborowski (1991). However, multiple regression analysis indicated that this factor was not significant ( $p=0.177$ ). This may be because the Marchant box

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Figure 3.7: NMDS ordination of invertebrate community composition estimated from D-net samples collected from 5 streams, illustrating compositional differences inferred by subsampling methods. The red dots represent samples sorted using Sieve fractionation and the black dots connected to each red dotrepresents the same sample sorted using the Marchant box procedure. Ellipses enclose the replicate samples collected from each stream. ( $BC = Big Creek$ ;  $LR = Little$ ) River;  $SC =$  Sharon Creek;  $SM =$  Sixteen Mile Creek;  $WA =$  White Ash Creek;  $#S =$  rep number of sample sorted by Sieves;  $#M = rep$  number of sample sorted by Marchant Box).

method uses a fixed count approach (300 individuals), whereas the sieve fractionation protocol is a fixed fraction subsampling method, so sieving only partially relies on the number of individuals present in the sample. Carter et al. (2006) found that fixed-count subsampling (typically 100 or 300 individuals but ranging up to 550) is the most common approach in Canada and the US. Carter, (2006) reported that almost 70% of studies reviewed reported using sieves to remove the large, rare organisms before going through the sample.

An important determinant of the length of time spent using the Marchant box method is the handling time spent removing materials from each cell. If few animals are present in a sample, then a considerable time is spent removing the cell contents and less time is devoted to searching for animals. The size fractionation achieved by the nested sieve method allows time to be spent primarily in sorting a single aliquot rather than having to handle many small subsamples, as is required using the Marchant box.

The amount of detritus in a sample was an important determinant of the time needed to sort samples, as has been frequently reported (Culp et al. 1983; Reice 1980). Each additional gram of detritus in a sample increased the sorting time by about 5 min using the sieve fractionation protocol (Table 3.3). In contrast, the Marchant box protocol required 8.87 minutes longer per gram of detritus to complete a sample (Table 3.4). This difference is especially noticeable for clay plain stream samples because the fine sediments or large quantities of debris can sometimes make it difficult to wash samples thoroughly. Overall, it takes significantly more time to extract materials from the Marchant box cells than it does to sort the contents of a sieve fraction in one go on a petri plate. Clearly, thorough field-washing of samples is an important aspect of removing as much fine sediment and detritus as possible. But when residual materials remain in samples, the sieve fractionation method is particularly more efficient than the Marchant Box.

A comparison of the estimated numbers of invertebrates in samples revealed that the Marchant Box sometimes markedly overestimated abundance compared to the sieving method (Figure 3.3). This was a function of the degree and method of subsampling. On average, sieves slightly overestimated the true abundance (by a factor of about 1.16 times;  $(R^2 = 0.94)$ , whereas the Marchant box overestimated abundance on average by a factor of 3.29 ( $R^2 = 0.22$ ). This may be due to too few cells in the Marchant Box being sorted, producing an overestimate of the abundance since there is increased variability. For example, if 10 cells are sorted and 300 animals are found, the resulting estimated abundance is 3000, but if sorting continued it could be found that when the  $50<sup>th</sup>$  cell is reached there are only 1000 individuals, which changes the estimated abundance from 3000 to 2000 organisms. The estimated abundance accuracy would increase if more cells were sorted since the values are closer to the true abundance. Courtemanch (1996) identified this limitation of the fixed count method with respect to invertebrate richness. He commented that a fixed number of organisms is not consistent because two communities cannot be assumed to be similar, and that when only collecting to a certain number the proportion of the total community that has been found is unknown; therefore, rare organisms may be missed, thus altering the estimate of biological integrity. Courtemanch (1996) discussed 3 options to resolve the short-coming - whole sample processing, two-phase processing, and serial processing. Of all of these, the sieving method is consistent with both the first and second approaches. When using the sieve fractionation approach, a larger proportion of the sample is processed. Furthermore, large organisms (in the coarsest size fraction) are collected first, and then the remainder of the sample is subsampled. The abundance of invertebrates in several samples was strongly overestimated by the Marchant box procedure (Figure 3.3), likely due to the very small proportion of cells that were examined by the time a stopping point (300 organisms) had been reached.

The result of the ordination analysis suggests that the community composition of Little River and Sixteen Mile Creek differed from the other streams, whereas White Ash Creek, and Big Creek were very similar in composition. The Sharon Creek ellipse slightly overlapped with that of Big Creek, so their community compositions are also similar. The dominant invertebrates in Sixteen Mile Creek were Chironomidae, Gomphidae, and Oligochaeta, suggesting that this stream is more degraded than the others. This is because these are deemed to be tolerant taxa, which can withstand degraded conditions, compared to the fauna that dominated the other streams which are not as tolerant. Although the family richness varied greatly among streams, the tolerance scores of the communities were relatively similar.

When looking at each of the streams individually there are a few distinct patterns that suggest the Marchant Box is different than sieves in Dimension 1 because the orientation between each of the connected points in Figure 3.7 tend to be separated in a left to right pattern. Distinct differences in sorting methods were seen in Big Creek sample 2 (D-net in pool habitat) and White Ash Creek sample 3 (D-net in riffle habitat)). In conjunction with the richness of each of the sorting methods, this coincides with the significant difference between what each collected (Table 3.6).

## **Recommendations**

Several lines of evidence indicate that the sieve fractionation method is more effective than the Marchant box for processing samples collected from clay plain streams of southwestern Ontario. Although both subsampling techniques yield comparable overall community composition, the sieve method requires less washing and sorting time, recovers more specimens (leading to more precise abundance estimates) and greater family richness, and does not overestimate abundance of invertebrates. The efficiency of the sieve fractionation method can be

increased by ensuring that samples are thoroughly field-washed before preservation to ensure that fine materials are rinsed through the D-net and that large twigs and coarse detritus are removed from the sample. This also reduces the amount of preservative needed. Although both the Marchant box and sieve fractionation procedures characterize community composition similarly, the sieve methodology is preferable because it provides a more precise estimated abundance and is more time-efficient than the Marchant Box protocol.

## **Chapter 4: General Discussion**

## **Project Overview**

The objective of this study was to review, assess, and recommend sampling and sorting methods to optimize stream sample collections that would reflect the zoobenthic community composition of the streams in southwestern Ontario. Because streams in this region are slow flowing and have soft, largely clay-dominated sediments, currently used provincial and national protocols, which are designed for assessing faster-flowing, hard-bottomed streams, may not be appropriate or effective for the low gradient, fine-substrate systems of the St. Clair Clay Plain region. I compared two methods of sample collection from 19 streams, and two macroinvertebrate subsampling methods of processing the collections.

I found that using a D-framed sweep net as recommended by the Canadian Aquatic Biomonitoring Information Network (CABIN) and Ontario Benthic Biomonitoring Network (OBBN) protocols was as or more effective than using a Petite Ponar grab, even in locations that had deep water, muddy substrate and negligible flow. In the laboratory, the use of nested sieves was more time efficient and better represented the family richness of streams than the Marchant Box method recommended by CABIN and OBBN. Three D-frame sweep net samples per stream (two from riffles and one from a pool) each collected more invertebrates and a larger number of families than five Petite Ponar grabs. The samples from the 19 sites surveyed in 2016 were collected in July and August. During this season many other headwater streams that were visited had dried up, and this was a significant limitation to sampling during the summer. Consequently, I examined a 10-y temperature and discharge record for the Thames River to determine the duration and timing of spring melt conditions. On that basis, I determined the period of time during which discharge was likely to be low enough to permit safe access and yet cool enough (<20

degrees C) that eurythermic overwintering taxa were unlikely to have emerged. The recommended interval is between April 1st and May 7th. In 2017, samples were collected between April 18<sup>th</sup> and June 10<sup>th.</sup> Water temperatures were 20 degrees C or less in most of the streams at the time of sampling.

Of the two sample processing methods, the Marchant Box procedure took on average about 160 min longer per sample (62.5 percent longer) to process than the sieve fractionation protocol. The amount of detritus was a significant determinant of the variation in the time needed to go through a sample. There was a significant difference in the number of families recovered per sample by each method and the sieve fractionation procedure detected a higher proportion of the taxa found per stream (92%) than the Marchant Box method (82%), especially when macroinvertebrate densities were high. Although, an ordination of the two subsampling procedures found no evidence of bias in community composition, the sieve subsampling procedure produced consistently accurate estimates of actual macroinvertebrate density, whereas the Marchant Box procedure often greatly overestimated the number of animals in a sample. The differences in precision were associated with the proportion of a total sample that was sorted.

In conclusion, the D-framed sweep net and the nested sieves are the methods that should be used in the field and laboratory processing, respectively. These methods collect representative samples from the stream, allow efficient processing and provide a more accurate assessment of the streams than the complementary methods.

OBBN is the provincial protocol for benthic assessment and is the condensed version of CABIN, which is the national protocol. Because both approaches are available to use in the region, the question arises as to which protocol is best suited and most feasible for use in terms of efficiency and data collection. The stream habitat assessment features that OBBN does not require include slope, velocity and pebble count (which are part of the CABIN protocol field data sheets) because these data are used in assigning test sites to the most appropriate suites of reference sites under the reference condition approach (Jones et al. 2007, Reynoldson 2002). Many streams in the Essex and Lower Thames region have minimal slope and negligible velocity (even during spring) due to the flatness of the local topography (Appendix B). Consequently, stream slope is likely best determined using map-based estimates of changes in elevation; and velocity records of <5 cm/s (the lowest effective reading of many current meters) will have to be used to estimate discharge of the sites that are sampled across the region. OBBN does, however, include elevation on the field data sheets. Because the streams are within the clay plains, it is impractical to conduct the pebble count protocol stipulated by CABIN. However, the sandy or muddy substrates can be sampled with sediment cores (which was done for 2017 field sampling), and particle size can be reported using the Wentworth scale after conducting appropriate particle size frequency analysis in the laboratory (Wentworth 1922). This was completed for 2017 samples, but due to time constraints, it has not been analyzed in conjunction with other factors that were presented in this thesis. Overall, there really is no true basis for comparison between CABIN and OBBN because there is no benthic information on reference streams in the clay plains regions. Yet, I recommend using the OBBN protocol to assess southwestern Ontario streams because it is a condensed rapid approach and does not include the sections of CABIN that would be difficult to assess.

#### **Major Findings and Recommendations for Regional Conservation Authorities**

The D-frame sweep net collected a higher abundance of invertebrates and greater family richness than the Petite Ponar grab samples. Although sweep-netting is a more qualitative method than fixed-area sampling with a Petite Ponar grab, the sweep net procedure collected macroinvertebrates across the entire width of the stream and thus the fauna encountered were more representative of the range of microhabitats. Samples taken from both riffle (or glide) and pool areas are needed to represent the biodiversity that is present. Of the two types of sampling used to estimate community condition as represented by the Hilsenhoff Biotic Index, the D-net-derived estimates produced values closest to those determined from both D-net and Ponar grabs combined. However, NMDS ordination indicated that the type of sampler used had little influence on the interpretation of overall community composition among streams.

Of the two laboratory processing and subsampling methods, the Marchant box took about 160 minutes longer to complete a sample than the sieve fractionation method. The quantity of detritus significantly affected the time needed to complete a sample, even though both protocols entail subsampling of large samples. Ponar grabs required less time to sort, especially when processed using the sieve fractionation technique, because sieving removes residual clay in the samples during the washing process. Samples processed using the sieving procedure had significantly higher family richness, presumably because all large, rare individuals (those in the coarse size fraction) were found and identified. However, there was no significant difference in community composition between processes detected by the NMDS ordination relative to amongstream variation. Overall, the weight of evidence indicates that sieve fractionation is the more effective method, and it is highly recommended over the Marchant box for the Clay Plain streams assessed in this study.

#### **Limitations**

Limitations to this work include the relatively small number of samples for which data were available to compare the subsampling methods. Although 40 samples from 5 streams were used in the analysis, the loss of the written records of detritus biomass data compromised the power of the analysis to identify the covariates that contributed most to variation in sorting time. Nevertheless, the data were sufficient to show that sieving is a more effective protocol than using the Marchant Box. However, to increase the power of the study more samples should be sorted through comparing both methods.

Another limitation is in my reporting identity of macroinvertebrates only to the family level of taxonomic resolution. I identified invertebrates to genus or species where possible, but very immature animals lack certain features needed for identification to the genus level. The family level of resolution is recommended for many studies because it reduces the time needed for identification providing more time in a limited budget for additional samples to be processed. The family level of resolution is reported to be sufficient for conducting multivariate analyses (Bowman and Bailey 1997) and for calculating tolerance indices (Hilsenhoff 2017), but researchers often advocate genus- or species-level identification for biomonitoring studies (Bailey et al. 2006). According to Milošević (2014) for any study the taxonomic resolution depends on where the threshold of information loss is acceptable. It should be at a level where the community can still be detected to have changes in response to differences in the environmental conditions it's subject to (Milošević et al. 2014).

#### **Future Studies and Implications**

Further research on factors influencing invertebrate community composition could include observing the effects of alterations to the stream- comparing the effects of excavation or maintenance of streams used as agricultural drains to streams that are left unaltered. Most streams in southwestern Ontario serve as agricultural drainage systems, and some are physically

manipulated. Ward-Campbell et al. (2017) studied the effects of excavation to fish communities in 8 southwestern Ontario streams. They found there was no significant difference in abundance or composition in fish communities (Ward-Campbell et al. 2017), possibly because fishes are able to travel larger distances than invertebrates. It would be interesting to assess the alterations in invertebrate community composition since it may be difficult for the slow-moving invertebrates (in comparison to faster moving fish) to repopulate the affected area.

Further research could also include developing a better understanding the relationship between macroinvertebrate community composition and the sediment type together with the role of sediment in determining the benthic community of clay plain streams, independent of anthropogenic activities. It would also be beneficial to understand the potential differences in the benthic community with respect to changes in season (Furse et al. 1984; Humphrey et al. 2000; Buss et al. 2015). Because streams of the clay plain are maintained largely by surface water rather than groundwater (due to clay's impermeability), these streams likely exhibit much greater seasonal variation in discharge and temperature than predominantly groundwater fed streams.

For this project, the 0.25-mm sieve size fraction was archived. Although this fraction contains many immature organisms (often dominated by small chironomids and oligochaetes) few programs report densities of such small individuals because sampling is conducted with 0.5-mm or coarser nets. However, examination of this size-fraction could provide complementary information about the zooplankton and benthic microcrustaceans.

This study provides important baseline information and an objective assessment of sampling methodology of special value to the Conservation Authorities of southwestern Ontario. Implementation of the recommended protocols will generate data that are representative of local streams and do so efficiently. The survey data collected by my study is of value in informing regional authorities and the community at large about the ecological condition of southwestern Ontario's river systems, which have a role in and flow into larger systems, i.e. the Great Lakes. Although this study is a synopsis of only summer and spring conditions during 2016 and 2017, it provides an important baseline of the local fauna and a frame of reference against which to compare clay plain streams with other rivers of Ontario.

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#### **Appendices**

**Appendix A:** General methods of field and laboratory sampling for 2016 and 2017. *Environmental Surveys:*

During field trips, I measured and recorded data using standard field procedures and record sheets prescribed by both OBBN and CABIN. Field observations were completed and transcribed on-site at the time of sampling. Several procedures of the CABIN field surveys were omitted. In particular, slope could not be determined in the field because the landscape was essentially flat. The 100-pebble count (designed to estimate particle size-frequency distribution of coarse substrates) was not undertaken because pebbles were either rare or absent at sites. Instead, sediment cores were collected and used for laboratory sediment particle size analysis (see Appendix F).

Several stream habitat features are particularly important predictors of aquatic invertebrate community compostion, including indices such as 'residual depths' (to determine the depth of pools; Lisle, 1987) or Froude number velocity/depth ratio as suggested by Jowett (1993). Although riffles and pools can easily be located in stony streams, Essex and Lower Thames Valley streams are often so slow-flowing and turbid that these features may be difficult to locate. As an alternative, stream width and depth were measured at several transects. Because riffles were typically absent, I located and sampled glides (MPCA, 2014), characterized as the shallowest, most rapidly flowing sections of a study area that contain the coarsest substrates.

### *Site Selection:*

Streams were sampled within the St. Clair Clay Plain region of Essex County and the Lower Thames River valley. In 2016, 19 streams were sampled based on recommendations from the Conservation Authority representatives for each region. The candidate stream sites for 2017 were selected from an inventory of 808 locations for Essex County and 716 locations for Lower Thames, compiled as part of the Ontario Benthic Biomonitoring Network (OBBN) program by Jones (2015). This extensive list consisted of second to fifth order streams in 31 physiographic regions in Southwestern Ontario. The sites had been selected based on accessibility and uniform spatial distribution across each region. Jones (2015) also calculated various catchment- scale attributes representing anthropogenic stresses, of which I used areal percentage of the drainage basin devoted to crop row agriculture (PCTCR) and areal percentage of the drainage basin used for municipal development (PCTDEV). Values for each site were determined using ArcMap 9.3.1 (ArcInfo) and the SOLRIS v.1.2 land inventory. I created a bivariate scatterplot of the two values for all streams in the inventory that occurred within the Essex region (Figure 1.2) and Lower Thames region (Figure 1.3).

In Essex County region (Figure 1.2), the overall level of land use for either municipal development or agriculture tended to be high, in that as the percentage of agriculture land use (crop row) increases, the percentage of development decreases. The percentage of land in row crops ranged from zero to 100%, and the proportion of land that was rural or municipal ranged from zero to over 80%. A similar trend is evident in the Lower Thames region. However, in this region all sites (except for one) had over 40% of the landscape devoted to row crops and (with one exception) less than 25% of the watershed area was developed for rural or urban use (Figure 1.3). Clearly, all of the sites identified in Essex (Figure 1.2) and Lower Thames Valley (Figure 1.3) are subject to some degree of disturbance as a consequence of agriculture and development. Nevertheless, I wished to sample streams that represented the broadest possible range of disturbances to ensure that my methodological comparisons pertained throughout the clay plain region. Accordingly, for

each of the stream locations illustrated in Figures 1.2 and 1.3, I calculated the Euclidean distance of the candidate sample sites from the graph's origin (the square root of the sum of the squares of the values of the two stress scores; "AgDev composite stress score"; Host et al. 2019) and arranged the sites in order of increasing stress for each region.

The list of sites within each region was then ordinated by composite stress score and the cumulative distribution was divided into deciles (10 sections). Two sites were then randomly selected from each decile using a random number generator to provide 20 candidate sampling sites per region. Therefore, in spring 2017, I sampled 20 sites in each region (Table 1.1), resulting in a total of 40 sites visited in 2017. Combined with 19 sites that were visited in the summer of 2016 for the pilot study, a total of 59 streams were sampled for this project (Figure 1.5, 1.6). Sites that were situated within 3 km of another site were replaced with other sites randomly selected from the same decile to ensure that coverage across each region as a whole was spatially relatively uniform.



Figure A.2: Scatterplot of land use (areal percentage of land in row crops (X-axis; areal percentage of developed land) in the contributing watershed upstream of 809 stream sites within the Essex County region of Southwestern Ontario, and associated site numbers.



Figure A.3: Scatterplot of land use (areal percentage of land in row crops (X-axis; areal percentage of developed land) in the contributing watershed upstream of 717 sites within the Lower Thames Valley region of Southwestern Ontario and associated site numbers.

Sampling Period

Although CABIN recommends that sampling typically be conducted in the late summer or fall (when discharges typically become more stable and lower than earlier in the season), sampling in other seasons is permitted, as long as the timing of sampling is consistent from year to year. In contrast, OBBN allows sampling to be completed at any season and even lists costs and benefits for sampling in each season. OBBN also acknowledged that seasonal differences in abundance and the taxa captured can be expected due to variation in macroinvertebrate life histories. Most sediments of the Clay Plain region of southwestern Ontario are impermeable. Thus, streams are primarily surface-water fed. This makes them susceptible to very low summer discharges and high water temperatures. I wished to identify a sampling period that would ensure temperatures were low enough and discharges were high enough to support invertebrate fauna typical of perennial streams. To determine seasonal criteria for sampling streams I used a 10-y water temperature record provided by LTVCA for the Thames River. Data from 2007 to 2016 were plotted to illustrate variation in temperature by calendar date (Figure 1.4). To determine the time frame during which streams should be visited, the Thames River water temperature record (Figure 1.4) was analysed and compared to the temperatures at which many overwintering macroinvertebrate taxa emerge.

Most overwintering or early-spring developing taxa emerge when the water temperature reaches 12-24°C (Corbet, 1957; Trottier, 1973; Singh, 2008; Cushing, 2006; Becker, 2005; Milošević, 2013). Typically, the mean stream water temperature common macroinvertebrates of the region emerge is between 12°C and 20°C. As shown in Figure 1.4, that period in which sampling was therefore suggested to occur was from April to the beginning of May. Using the Thames River 10-year data I was able to determine which calendar dates would



Figure A.4: Water temperature readings for the Thames River in Southwestern Ontario from 2007 to 2016. Black horizontal lines represent temperatures at 12°C and 20°C. Black vertical lines depict the sampling window.

best delineate the beginning and end of the sampling season. This was done by determining the date on which the water temperature first reached 12°C each year, and the last date in spring on which it reached 20°C for each year of the 10-y record. I then selected the first date on which the 12°C and 20°C temperatures were observed. On this basis I determined that the annual sampling period should begin in April and end at the end of the first week of May. The dataset on which this determination was based was interpreted in fall 2016 after the season's sampling had been concluded Samples in 2016 were collected between July 4 and August 30 (Figure 1.4).

### *Macroinvertebrate Sampling*

At each study site, macroinvertebrates were collected using two sampling instruments. Three samples were taken using a 30-cm wide, 0.50-mm mesh D-frame sweep net, and 5 Petite Ponar grab samples were collected (Chapter 2). Each sample was emptied into a 0.25-mm mesh sieve bag, which was repeatedly rinsed in the stream to remove fine sediments. All samples were placed in a labelled heavy-duty polyethylene soil bag, to which formalin-ethanol solution (2.5:1 v/v 95% ethanol and 100% buffered formalin diluted 1:1 with stream water) was added (Wiggins, 1977). Samples were returned to the laboratory where they were inventoried, heat-sealed to prevent leakage, and stored for later processing.



Figure A.5. Map of the Essex County and Lower Thames Valley region of Southwestern Ontario showing stream sites sampled in 2016 with the associated stream names. (n=19)



Figure A.6. Map of the Essex County and Lower Thames Valley region of Southwestern Ontario showing stream sites sampled in 2016 and 2017 with the associated stream names.

Table A.1. Sampling site, GPS coordinates, and sampling year.





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## Table A.1 (Cont'd). Sampling site, GPS coordinates, and sampling year



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# LTVCA Sampling Sites

### **Appendix B: Summary Tables of NMDS Analyses**

Table B1: Summary of Pearson correlations between relative abundances of families collected in D-net and Petite Ponar samples and their scores along NMDS axes as described in detail in Chapter 2 (ordination stress = 11.25). Bold-faced correlations are statistically significant ( $p$  < 0.05; uncorrected for multiple tests). Taxa names are sorted in decreasing order of their strength of correlation with then NMDS axis with which they are most highly associated.





Table B2: Summary of Pearson correlations between relative abundances of families identified using the Marchant Box and Nested Sieves protocols and their scores along NMDS axes as described in detail in Chapter 3 (ordination stress = 12.22). Bold-faced correlations are statistically significant (p< 0.05; uncorrected for multiple tests). Taxa names are sorted in decreasing order of their strength of correlation with then NMDS axis with which they are most highly associated.





**Appendix C:** List of taxa observed in at least one sample (3-D-net and 5 Petite Ponar grabs) in 19 streams sampled in 2016


































# **Appendix D – 2016 Field Data.**

Field measurements recorded at the 19 streams sampled in 2016. \*\*NR: no data were recorded during sampling.































#### **Appendix E: Invertebrate Species List (2017)**

List of taxa observed in at least one sample (3-D-nets) in 40 streams sampled in 2017.





















#### **Appendix E: Invertebrate Species List (201 7 ) continued**




















## **Appendix E: Invertebrate Species List (201 7 ) continued**





















## **Appendix E: Invertebrate Species List (201 7 ) continued**





















## **Appendix F: 2017 Field Data:**

Field measurements were collected in the field during the 2017 sampling season of 40 sites across southwestern Ontario. \*NR indicates there was no record taken in the field










































































### **Appendix G: Sediment Analysis Data (2017 Sampling Year):**

Two sediment samples taken at each site (riffle and pool) for the locations listed that were sampled in 2017. LOI is the total loss of ignition and the incremental measurements represent the different sizes of sieves that were used to separate the sediment particles.





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