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Classification and prediction of macroinvertebrate assemblages from running waters in Victoria, Australia

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Abstract. We constructed predictive models using 2 macroinvertebrate data sets (for both species and family) from bankside habitats at 49 undisturbed reference sites from 6 Victorian river basins; data were accumulated over 4 to 6 sampling occasions. Classification (by unweighted pair-group arithmetic averaging with the Bray-Curtis association measure) showed 3 site groups were evident at the species level and 4 at the family level. A subset of 5 of 22 environmental variables provided maximum discrimination (using stepwise discriminant analysis) between the 3 species site groups; these variables were: conductivity, altitude, substrate heterogeneity, distance of a site from source, and longitude. Four variables discriminated between the 4 family site groups: conductivity, catchment area upstream of site, mean annual discharge, and latitude. From the discriminant analysis, it was possible to predict the group into which an unknown site (specified only by measurements on the 4 or 5 variables just noted) would be placed and thus the probabilities of occurrence of taxa at this site. To test predictive ability, 4 sites were removed at random from the 2 data sets and the classification and discriminant models were recalculated. This process was repeated 5 times. The identity and number of taxa observed at each of these sites were compared with those predicted with a probability of occurrence >50% and the results expressed as a ratio of numbers observed to numbers expected (O/E). This ratio varied from 0.75 to 1.05 at the species level and from 0.83 to 1.12 at the family level, indicating that the fauna conformed with expectation (O/E near 1.0). To test such predictive models on independent data, O/E ratios were also calculated for family data collected in spring at 18 sites from a basin not used in the original models. Two new discriminant models based on single sets of samples from the reference sites taken in spring were constructed for this purpose. O/E ratios varied from 0.09 to 1.01 for the 18 sites and were inversely correlated ($r = -0.4$ to -0.8) with a range of water quality variables, the values of which increased as water quality deteriorated. The O/E ratio could thus be considered a sensitive measure of disturbance.

Key words: prediction of benthic communities, classification, lotic macroinvertebrates, discriminant analysis, observed/expected number of taxa, Victoria (Australia).

A previous multivariate classification of the macroinvertebrate assemblages of undisturbed sites on a number of Victorian rivers (Marchant et al. 1994) demonstrated that changes in faunal composition are distinct and well correlated with changes in several environmental variables, e.g., water temperature, conductivity, nature of the substratum. By extending such analyses to a wider range of undisturbed sites, it should be possible to predict community composition at unsampled sites from knowledge of those environmental characteristics that are best correlated with the classification patterns. The sites from which predictions like this are made are known as reference sites and represent community composition under natural conditions or at least in the absence of obvious disturbance.

The prediction of the composition of the macroinvertebrate fauna of rivers using data from reference sites has mostly been used in the UK (Moss et al. 1987, Wright et al. 1993a). There, a system known as RIVPACS (River Invertebrate Prediction and Classification System) has been developed over the last 20 y. A similar approach has been used in Canada to predict the benthic invertebrate fauna of near-shore sediments in the Great Lakes (Reynoldson et al. 1995), and in the Australian Capital Territory to predict the macroinvertebrate fauna (at the family level) of local rivers (Parsons and Norris 1996). In all

these cases a fairly small number of environmental variables were shown to be closely associated with the classification patterns of the faunal data.

At present in Australia a RIVPACS-like approach has been adopted for monitoring the biological condition of rivers in each state and territory (Monitoring River Health Initiative [MRHI], Anonymous 1994, Parsons and Norris 1996). In most states identifications are being taken only to the family level because taxonomic information in many regions is limited. In Victoria, however, identifications can be taken to the genus or species level for many of the taxa. Currently data are available for 55 reference sites from 6 AWRC (Australian Water Resources Council) drainage basins out of 30 present in Victoria (Rural Water Commission of Victoria [RWC] 1990). Our purpose here is to construct predictive models using the available Victorian data at both the species and family level and to evaluate the predictive capabilities of these models. Successful predictions will provide confidence in using the predictive approach at the national level as our data sets are small compared with those (200+ sites) being compiled in each state or territory for the MRHI. It is not the purpose of this paper to provide a detailed account of the background to this type of predictive modelling. This has already been done (Wright et al. 1993a).

Methods

Reference sites

The macroinvertebrate data were collected between March 1990 and May 1993 on behalf of the Environment Protection Authority (EPA) of Victoria (Butcher 1991). A total of 55 sites were selected, from 6 AWRC basins: Snowy (10 sites), Ovens (10 sites), Campaspe (9 sites), Barwon (8 sites), Otway (10 sites), and South Gippsland (8 sites) (Fig. 1, Appendix 1). Reference sites were selected to represent the main types of river in a basin and exemplified the least disturbed conditions likely to be found. Sites were either surrounded by native vegetation or located in cleared areas where agricultural activities or low density housing were the main land uses. Further examination deemed that 6 of the 55 were unsuitable as reference sites because they either had low numbers of species (<22) compared with the remaining sites (26–74 species out of a total of 110—see below) or were disturbed by upstream discharges. These 6 are referred to below as disturbed sites. A total of 49 reference sites remained on both upland and lowland reaches.

Sites were sampled on 4 occasions over 2 years (or on 6 occasions over 3 years in the Barwon and Campaspe basins) in spring and autumn to allow for any seasonal variation in community structure. Each site was subdivided into 3 habitats: bankside (and other low-velocity areas), main-channel, and submerged wood. Sampling consisted of a collection over a 10-m transect for each habitat using a triangular hand net (250–μm mesh), followed by 30 min picking of live specimens. The resulting samples were taken in 5% formalin to the laboratory, where they were identified to species or genus; specimens of Oligochaeta, Hydracarina, Nematoda, and Turbellaria were not identified further. Additional information on the sites and sampling protocol is given by Butcher (1991).

Data on 22 environmental variables were also recorded at each site (Table 1). Meter readings as well as measurements of width, depth, substratum, and vegetation were taken in the field, while information on location, hydrology, and topography were obtained later from maps and discharge records. Only the mean values (calculated over the 2 or 3 y of sampling) for each variable were used in subsequent analyses.

Data

Data for the bankside habitat were available for all 49 reference sites and are the only data analysed in this paper (data for the other habitats were less complete). Two data sets were compiled: one with taxa identified to species or genus (with some exceptions given above), henceforth called the species data set; and one with taxa identified to family except for Chironomidae, which were identified to subfamily or tribe, called the family data set. Numerical data from all samples at a site were combined and transformed to records of presence or absence because live-picking did not give reliable estimates of relative abundance. Each of the data sets was further reduced by removing taxa that occurred at 10 sites or fewer in the species data or those that occurred at 2 sites or fewer in the family data. These operations reduced the spe-

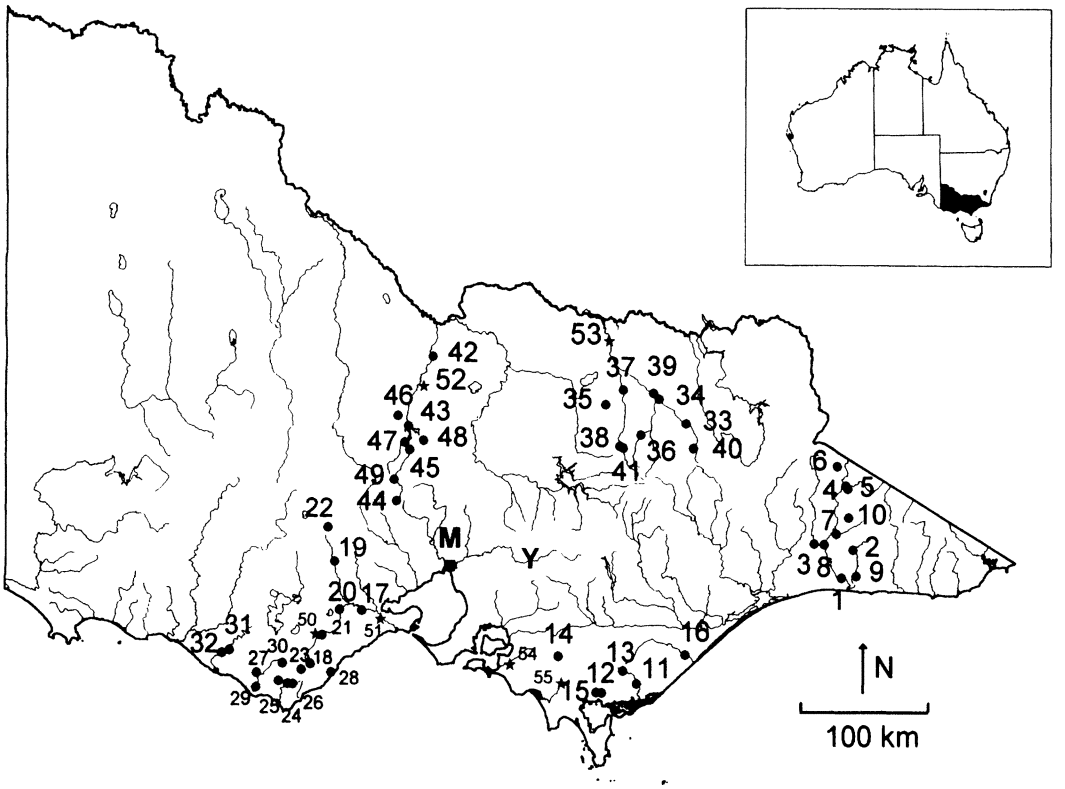

FIG. 1. Location of the 49 reference sites and 6 disturbed sites (nos 50–55, shown by stars) in Victoria. M indicates the city of Melbourne; Y, the Yarra River. See Appendix 1 for the identity of the site numbers. The inset shows the location of Victoria in Australia.

cies data set to 110 taxa (from 700+ taxa), and the family data set to 93 taxa (from 123 taxa). Lists of these taxa appear in Appendix 2. These reductions were justified by the fact that rare taxa contribute little to multivariate analyses (Gauch 1982), particularly those used in this study (see below), and by the fact that predictions are based on small sets of commonly occurring taxa.

Multivariate analyses

Community patterns among the reference sites were described using classification techniques in PATN (version 3.5, CSIRO, Canberra, Belbin 1993). The reference sites were classified into groups using the Bray-Curtis association measure and a clustering technique known as unweighted pair-group arithmetic averaging (UPGMA, $\beta = -0.1$). Group selection was confirmed by examining the positions of the groups in ordination space using detrended correspondence analysis (DCA).

Multiple discriminant analysis (MDA) was used to discriminate the site groups on the basis of environmental characteristics. All environmental variables were checked for normality using the PPLOT routine in SYSTAT (version 6.0, SPSS Inc., Evanston, Illinois), and where necessary were transformed (log or arcsine transformation). The number of variables required to discriminate the groups was determined using a stepwise procedure (PROC STEPDISC) in SAS (version 6, SAS Institute Inc., Cary, North Carolina). Variables were entered until no variables remained which significantly separated the groups at $p < 0.05$. The set of variables selected could then be used to predict into which site group a new site, i.e., a site not used in the original MDA, would fall. A new site may have a probability of belonging to more than one group; this is taken into account when calculat-

TABLE 1. Environmental variables measured at the reference sites, their abbreviations, and details on collection and measurement. Suffix denotes log transformation (L) or arcsine transformation (A).

Variable (unit of measurement)	Abbreviation
Distance of site from source (km)[a]	DIST-L
Slope of site (m/km)[a]	SLOPE-L
Altitude of site (m)[a]	ALT
Latitude (decimal degrees)[b]	LAT
Longitude (decimal degrees)[b]	LONG
Catchment area upstream of site (km^2)[c]	CA-L
Mean width (m)[d]	WIDTH
Mean depth sample area (cm)[d]	DEPTH
Mean particle size of substratum (phi)[e]	SUBSI
Substrate heterogeneity (7 categories)[f]	SUBHET
Vegetation (4 categories)[g]	VEG
Mean macrophyte cover (%)[h]	MAC-A
Mean annual temperature (°C)[i]	MAT
Range of mean annual temperature (°C)[j]	RMAT
Coefficient of variation in annual discharge (%)[k]	CV
Mean annual discharge (ML)[k]	MAD-L
Water temperature (°C)[l]	TEMP
Dissolved oxygen (mg/L)[l]	DO
Conductivity (μS/cm)[l]	COND-L
pH[l]	pH
Water velocity (m/s)[l]	VEL
Turbidity (NTU)[l]	TUR-L

[a] Obtained from 1:100,000 maps

[b] Degrees/minutes/seconds converted to decimal degrees

[c] Obtained from RWC (1990) discharge data, or area calculated from 1:100,000 maps

[d] Mean width and depth taken as the median of the range, measured over all sampling occasions

[e] Mean phi values calculated using percentage of sample area covered by 7 particle types, estimated by eye: boulders (−9); cobbles (−6.5); pebbles (−4.5); gravel (−2); sand (2.0); silt (6.5); clay (9.5)

[f] Number of particle types with percentage cover >10% of sample area

[g] Assessed from riparian vegetation and adjacent land use; categories: 1 = Agriculture, urban development, grass, no native vegetation; 2 = Agriculture, native vegetation, introduced plant species, no urban development; 3 = Native vegetation, introduced plant species, no agriculture or urban development; 4 = Native vegetation, no introduced plant species, agriculture or urban development

[h] Mean percentage of sample area covered by macrophytes, calculated from all sampling occasions

[i] Mean annual temperature at a site calculated from all years on record, using mean daily maxima and mean daily minima; all data from the Bureau of Meteorology

ing the probability of occurrence of an individual taxon (see below).

Validation of predictive models

To test the predictive capacity of the discriminant models for the species and family data sets, 4 calibration sites, each from a different basin, were randomly selected and removed from the reference data set. The remaining sites (45) were reclassified using UPGMA and discriminant models were recalculated, using the subset of environmental variables chosen previously. (In each case the groups of sites were the same as or very similar to those derived from the 49 site data sets; the previously chosen environmental variables were used as their selection was based on the maximum amount of data available.) These models were then used to predict the group membership of the 4 calibration sites. This process was repeated 5 times. As the number of basins exceeded the number of sites selected, the basins chosen in each run were varied. Predictions were also made during each of the 5 runs for the 6 disturbed sites earlier excluded from consideration as reference sites.

The success of a prediction was measured by comparing the predicted invertebrate assemblage, i.e., the list of taxa that were characteristic of a group of sites, with that recorded at a site. The ratio of the number of taxa observed at a site to those expected (from the predicted list) was calculated for each site following Moss et al. (1987). A summary of this procedure is given below: 1) the probabilities of a new site belonging to each of the reference site groups were calculated from the discriminant model; 2) the probability of occurrence of a given taxon (species or family) at this site was calculated by multiplying the outcomes of step 1 by the percentage frequency with which the taxon occurred in

←

[j] Range calculated by subtracting the mean daily temperature for the hottest month (usually February) from the mean daily temperature for the coldest month (usually July), for all years on record

[k] Mean and standard deviation of annual discharge calculated over all years on record from RWC discharge records

[l] Mean of meter readings taken on each sampling occasion

each site group; 3) the probabilities for a given taxon were summed for all groups to give an overall (or weighted average) probability of occurrence; 4) only taxa with overall probabilities of occurrence of 50% or higher were considered further—these were the predicted taxa; (50% is an arbitrary cut-off level, but is based on the experience of Moss et al. 1987); 5) the number of expected taxa at a site equalled the sum of the individual probabilities of occurrence of all of the predicted taxa (the number of expected taxa was always less than the number of predicted taxa); 6) the number of observed taxa represented the number of those taxa predicted to occur which actually occurred at this site; 7) the number of observed taxa was divided by the number of expected taxa to give an O/E ratio; the closer this ratio is to 1.0 the closer the observed community conforms with expectation. A program was written in SAS using the procedures contained therein to perform these steps.

The Yarra River study

A more thorough demonstration of the predictive capacity of the discriminant models was gained by applying them to a set of test sites from a basin not used in the initial modelling. Sites sampled by the Victorian EPA in the partly urbanised Yarra catchment (which includes much of the city of Melbourne; see Fig. 1 and Appendix 3) were considered ideal for this purpose because they were subject to a range of human disturbances.

The Yarra data comprised a single set of bankside samples from 18 sites, collected in spring 1994, from which the taxa had been identified to family only. We considered it inappropiate to use our family discriminant model (see above) to make predictions because it was based on a greater sampling effort (4–6 sampling visits) than had been applied at the Yarra sites and thus might overestimate the expected number of taxa (see Discussion). As a consequence, 2 new discriminant models were constructed based on single sets of samples collected at reference sites in spring 1990 (49 sites × 84 families) and 1991 (48 sites × 91 families). Chironomidae had not been identified to subfamily or tribe in the Yarra data; so these subfamilies were amalgamated for the construction of the 2 models. As data for only 14 of the 22 environmental variables used in earlier analyses could be obtained for the Yarra sites, a revised list of variables was used during the stepwise MDA procedure. This list included: ALT, LAT, LONG, CA-L, COND-L, DIST-L, SLOPE-L, TUR-L, DO, SUBSI, pH, SUBHET, TEMP and WIDTH (see Table 1 for definitions). O/E ratios for families were calculated for each of the Yarra sites, using both the spring 1990 and 1991 discriminant models.

Trends in the predictions were examined by correlating the O/E ratios for each of the sites with a range of water quality variables. Eight variables were selected from a study of water quality in the Yarra (Anonymous 1992). The variables included: suspended solids, biological oxygen demand (BOD), total organic carbon (TOC), ammonia, total phosphorus, faecal coliforms, total copper, and total zinc. Measurements had been made weekly over 14 wk between January and April 1992. The means for each variable were correlated with the O/E ratios using both Pearson and Spearman rank correlation coefficients; higher Pearson correlation coefficients were obtained after natural log transformation of the variables. A principal components analysis (PCA) of the 8 variables was also carried out (in SYSTAT) and the scores on the first 2 axes correlated with the O/E ratios.

Results

Species and family groups

The species level UPGMA classification (Fig. 2A) indicated 3 groups of sites were present. Group 1 comprised all the sites from the Campaspe and Barwon basins except a small upland site (18) from the Barwon basin which was located within Group 2. Group 3 consisted almost entirely of sites from the Snowy and Ovens basins, with the exception of 1 site from the South Gippsland basin (site 12). Group 2 contained most of the Otway basin sites, but also included smaller, upland sites from other basins such as site 10 from the Snowy basin and site 40 from the Ovens basin as well as sites from the South Gippsland basin.

At the family level (Fig. 2B) 4 groups were evident, although there were obvious similarities in composition between these groups and those identified at the species level. Group 3

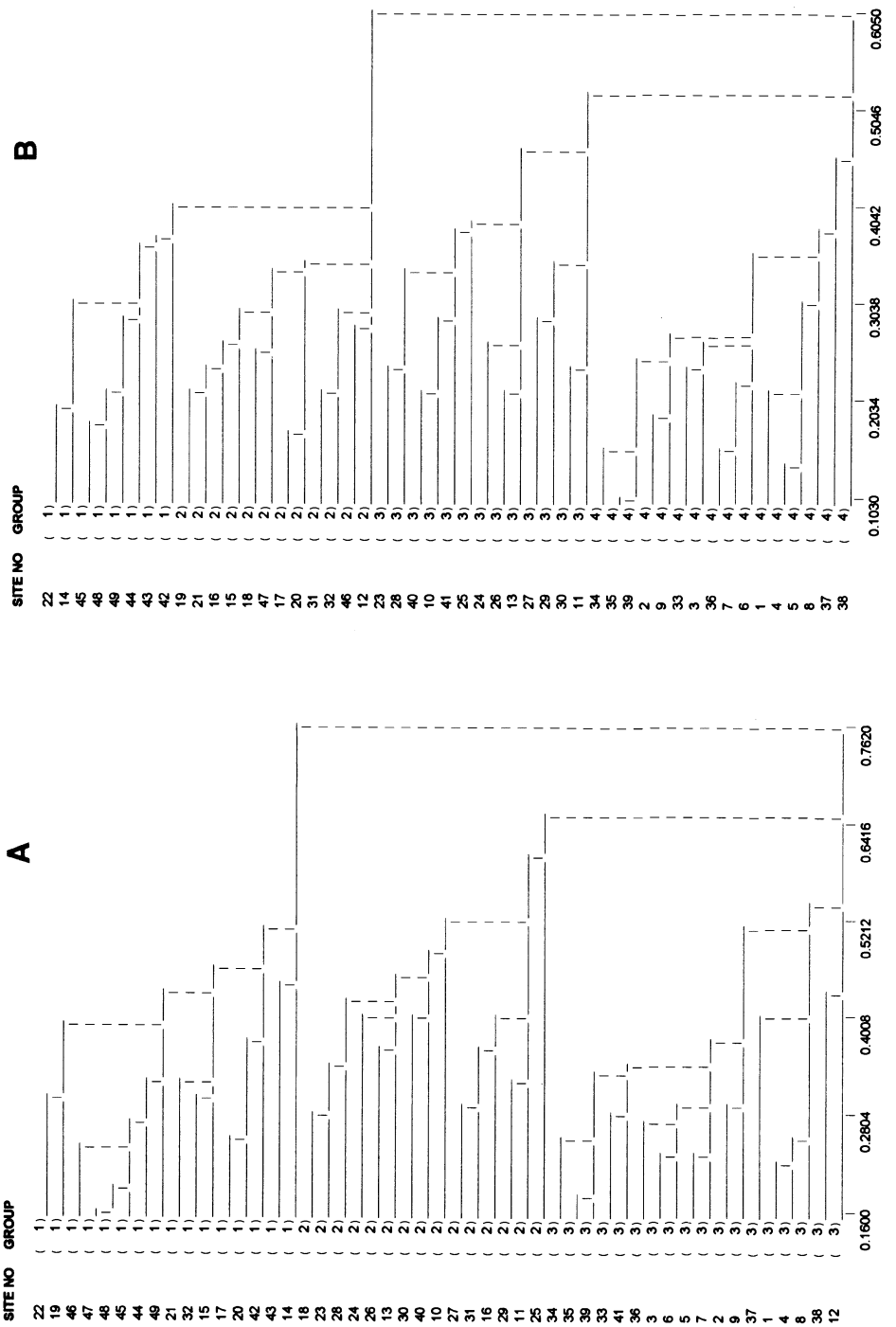

FIG. 2. UPGMA dendrograms for the species (A) and family (B) data. See Appendix 1 for the identity of the site numbers.

TABLE 2. Standardized discriminant function coefficients for the environmental variables used in the species- and family-level discriminant analyses. Variables are in descending order of selection. The number of functions is 1 less than the number of site groups (3 at species level, 4 at family level).

Variable	Function 1	Function 2	Function 3
Species level			
Conductivity	1.082	0.546	—
Altitude	0.813	0.695	—
Substrate heterogeneity	−0.549	0.186	—
Distance of site from source	−0.349	0.910	—
Longitude	−0.238	0.295	—
% of dispersion	85.0	15.0	
Family level			
Conductivity	1.100	−0.226	−0.390
Catchment area upstream of site	−0.891	−1.608	1.644
Mean annual discharge	0.173	1.356	−1.105
Latitude	0.081	0.693	0.788
% of dispersion	68.6	26.6	4.8

closely resembled Group 2 at the species level, and Group 4 was almost identical to Group 3 at the species level. A group similar to Group 1 at the species level could be distinguished, but at the family level this was further divided into 2 smaller groups: Group 1 (family) consisted almost entirely of Campaspe basin sites, while Group 2 (family) contained most of the Barwon basin sites, the remainder of the Campaspe basin sites, and a number of sites from the South Gippsland basin.

The DCA ordinations (not shown) were similar in pattern for the species and family data sets and showed excellent separation of the groups described above on the 1st 2 axes.

Discriminant analysis

Stepwise discriminant analysis selected 5 environmental variables for the species level model and 4 for the family level model (Table 2). The variable most strongly associated with the 1st discriminant function in each model was COND-L; ALT in the species model and CA-L in the family model were also important. Variables indicative of river size such as DIST-L and ALT in the species model and CA-L and MAD-L in the family model were associated strongly with the 2nd discriminant function. COND-L, which provided the best discrimination of sites in both data sets, was strongly correlated (r = 0.7–0.8) with gradients evident in DCA ordinations of the community data. The remaining variables selected had lower correlations with these ordinations.

The role of the predictive variables in discriminating the biological groups can be more clearly illustrated by examining their mean values for each of the groups (Table 3). At the species level, high values for COND-L distinguished Group 1 from Groups 2 and 3. Low values for DIST-L and SUBHET and intermediate readings for COND-L distinguished Group 2; high values for DIST-L, SUBHET, and LONG (most easterly sites) and low values for COND-L distinguished Group 3. Group 4 in the family-level discriminant model was clearly separated from the others by high values for CA-L and MAD-L and low readings for COND-L. Group 3 was generally characterised by smaller values for CA-L and COND-L than occurred at Groups 1 or 2. Readings for Groups 1 and 2 largely overlapped; Group 2, however, could be distinguished from Group 1 by higher values for COND-L.

Validation of predictive models

The communities at the calibration sites were well predicted by the modelling process (Table 4). All of the basins at the species level, with the exception of South Gippsland, recorded mean O/E scores >0.90, indicating that the discriminant models were capable of predicting communities at sites not used in constructing the model. Ratios for the family model were mar-

TABLE 3. Means (SE) for the environmental variables selected by discriminant analyses at the species and family levels. The means are given as untransformed values in the original units.

Variable	Group 1	Group 2	Group 3	Group 4
Species level				
Conductivity (μS/cm)	1143.3 (235.6)	277.2 (87.4)	84.1 (11.5)	—
Altitude (m)	201.3 (42.8)	200.0 (51.6)	191.4 (30.6)	—
Substrate heterogeneity	2.68 (0.27)	2.86 (0.35)	3.78 (0.31)	—
Distance of site from source (km)	45.53 (9.40)	21.50 (5.72)	94.90 (24.03)	—
Longitude	144.4 (0.20)	144.8 (0.50)	147.5 (0.23)	—
Family level				
Conductivity (μS/cm)	748.8 (195.6)	1199.5 (306.3)	177.5 (47.3)	79.6 (9.47)
Catchment area upstream of site (km^2)	872.6 (425.9)	706.6 (251.6)	194.1 (78.0)	2924.9 (1151.7)
Mean annual discharge ($ML \times 10^3$)	96.73 (31.8)	76.85 (20.6)	86.03 (27.0)	449.46 (152.6)
Latitude	37.27 (0.21)	38.33 (0.24)	38.24 (0.19)	37.08 (0.11)

ginally higher for all basins, except Otway, with 4 out of the 6 basins having mean ratios of about 1.0.

The mean number of taxa expected to occur in the Snowy and Ovens basins (Table 4) was higher than that in the other basins, corresponding with the higher faunal richness recorded for these 2 basins (Butcher 1991). The mean number of expected taxa at the species level was only marginally higher than that expected at the family level for all basins except the Snowy and Ovens.

Ratios were also calculated for the 6 disturbed sites (Table 5). The exact type of disturbance at each of these sites was not known. Nevertheless, the ratios were usually <0.7 at the family level and ≤0.6 at the species level, confirming that the 6 sites were indeed disturbed compared with the reference sites. The fact that higher ratios were found at the family level is consistent with the pattern found for the calibration sites.

The Yarra River study

Three groups of sites were identified for both spring reference data sets (Table 6) and, with few exceptions, the groups were essentially similar in structure to one another and to those groups previously identified at the family level for the combined data (Fig. 2B). Unlike the combined data, however, Group 1 was not subdivided. Stepwise MDA chose (in order of selection) COND-L, LAT, SLOPE-L, and TEMP as the best discriminating variables for the spring 1990 data; LONG, LAT, COND-L, and SLOPE-L were selected for the spring 1991 data.

Both discriminant models were used to predict community assemblages at the 18 test sites in the Yarra catchment (Table 7). The lowest O/E ratios were recorded at inner urban sites, e.g., Darebin Creek (0.11 and 0.09), whereas the highest were found at rural sites, e.g., Woori Yallock Creek (1.01 and 0.99). The ranking of sites

TABLE 4. Mean expected number of taxa (Exp.) and the mean O/E ratio (SD) for the calibration sites from each basin.

Basin	No. of sites per basin	Species model		Family model	
		Exp.	O/E	Exp.	O/E
Snowy	5	38.62	1.02 (0.13)	28.92	1.05 (0.09)
Ovens	4	36.57	0.93 (0.20)	28.31	1.00 (0.17)
Otway	4	27.74	0.90 (0.09)	25.65	0.83 (0.09)
Campaspe	3	29.21	1.05 (0.17)	25.03	1.06 (0.18)
South Gippsland	2	26.80	0.75 (0.18)	24.28	0.89 (0.04)
Barwon	2	29.22	0.99 (0.05)	27.95	1.12 (0.09)

TABLE 5. Mean expected number of taxa (Exp.) and the mean O/E ratio (SD) for the disturbed sites. $n = 5$ for each site.

	Species model		Family model	
Site no.	Exp.	O/E	Exp.	O/E
50	32.65	0.20 (0.03)	29.05	0.41 (0.03)
51	32.59	0.61 (0.02)	29.20	0.62 (0.03)
52	32.64	0.47 (0.01)	27.69	0.61 (0.03)
53	35.59	0.35 (0.02)	29.05	0.64 (0.05)
54	28.60	0.52 (0.02)	28.31	0.84 (0.05)
55	25.98	0.58 (0.02)	28.00	0.67 (0.02)

TABLE 6. Distribution of the reference sites within each group for the spring 1990 and 1991 data sets.

	Group 1		Group 2		Group 3	
Basin	1990	1991	1990	1991	1990	1991
Barwon	4	4	—	1	2	—
South Gippsland	2	2	3	4	1	—
Campaspe	8	8	—	—	—	—
Otway	2	1	7	9	1	—
Ovens	—	1	2	1	7	7
Snowy	—	—	1	—	9	10

by their O/E ratios was very similar for the 2 models. There were, however, some inconsistencies: ratios for Olinda Creek and the Yarra River at Woori Yallock deviated by up to 18% between models (Table 7). The numbers of expected taxa were much the same for both models.

The 18 sites appeared to span a continuum of potential disturbance with O/E ratios ranging from 0.1 to 1.0. All water quality variables (values for which increased as environmental deterioration increased) were inversely correlated with the O/E ratios from both models (Table 8). Thus, as the level of disturbance increased the ratios decreased, as would be expected. Highest correlations were recorded for zinc, faecal coliforms, ammonia, total organic carbon (TOC), and copper. The strength of the correlations was little different between models or between coefficients. The generally linear trends between (log-transformed) concentrations of 4 of the water quality variables and the O/E ratios (Fig. 3) were clear.

Variation in the water quality data was summarized by PCA. All of the variables except suspended solids were correlated highly (>0.6) with the 1st PCA axis (46.5% of variation explained). This axis therefore represented a gradient in water quality. Only suspended solids correlated strongly (0.67) with the 2nd axis (25.5% of variation). The O/E ratios for spring 1990 and 1991 correlated ($r = -0.68$ and -0.69, $p < 0.01$) with the 1st axis only, confirming that these ratios were sensitive to changes in water quality.

Discussion

The models described here were based on data from only the bankside habitat. Parsons and Norris (1996) showed that similar predictive models based on samples from a single habitat (main channel or bankside) were well able to detect biological impairment and gave O/E ratios at test sites that were similar to those from models based on an amalgamation of data from several habitats. They concluded there was a high level of redundancy in biological information from different habitats and that inclusion of more than 1 habitat in a model could hamper rather than help detection of impaired sites.

Despite the fact that the models were based on a fairly small number of reference sites, the assemblages predicted at the calibration sites matched closely those observed, as might be expected for sites assumed to be undisturbed. The mean O/E ratios at the calibration sites varied from 0.8 to 1.0 for all basins except South Gippsland (0.75 at the species level but 0.89 at the family level). Wright et al. (1993a) used a cut-off level of 0.79 for the O/E ratio (for number of taxa from the British RIVPACS model) to indicate impairment of invertebrate assemblages. (This cut-off level was based on extensive knowledge of environmental conditions at specific sites.) Ratios above this (band A according to the scheme of Wright et al. 1993a) indicated no disturbance, whereas those below (placed in 3 bands) signaled increasing levels of disturbance. The lower-than-expected O/E ratio for the South Gippsland basin was due to a single low value (0.62) at the species level. As the ratio at the family level for this site was distinctly higher (0.91), the status of the site is uncertain.

It is quite possible that the 0.79 cut-off point may not be appropriate for Victorian or other Australian rivers. The O/E ratios for the 6 disturbed sites were <0.67 (except one: 0.84 at the family level). According to the banding scheme

TABLE 7. The expected number of taxa and the O/E ratios for the spring 1990 and 1991 models at each of the Yarra sites. The sites are arranged from the lowest to highest O/E for 1990.

Location	Spring 1990		Spring 1991	
	Expected	O/E	Expected	O/E
Darebin Creek at Fairfield	8.87	0.11	11.48	0.09
Yarra River at Abbotsford	13.65	0.15	11.17	0.18
Gardiners Creek at Kooyung	11.35	0.26	10.28	0.29
Diamond Creek at Eltham	10.62	0.28	8.63	0.34
Yarra River at Ivanhoe	13.55	0.30	11.90	0.34
Brushy Creek at Wonga Park	12.77	0.31	11.25	0.36
Plenty River at Viewbank	—[a]	—[a]	10.71	0.47
Yarra River at Wonga Park	13.62	0.51	12.27	0.49
Yarra River at Coldstream	13.82	0.51	12.39	0.56
Mullum Mullum Creek at Warrandyte	8.87	0.56	11.42	0.53
Yarra River at Heidelberg	13.68	0.66	11.97	0.59
Yarra River at Warrandyte	13.64	0.66	12.24	0.57
Olinda Creek at Coldstream	8.88	0.68	10.61	0.85
Yarra River at Maxswells Rd	12.78	0.70	12.10	0.74
Yarra River at Woori Yallock	13.72	0.72	12.26	0.90
Yarra River at Templestowe	13.58	0.81	12.04	0.83
Watsons Creek at Kangaroo Ground	8.87	1.01	11.37	0.88
Woori Yallock Creek at Yellingbo	11.91	1.01	11.06	0.99

[a] No predictions possible for site because data for 1 discriminating environmental variable were not available

of Wright et al. (1993a), 6 of these 12 ratios fell within band B (0.58–0.78), 3 within band C (0.37–0.57), and 2 within band D (<0.37). Lack of detailed knowledge about the degree of disturbance at each of these sites precludes further comment. However, the ratios for these 6 sites at least spanned most of the possible range and were not confined to a limited region of the scale as a less sensitive measure might be. The O/E ratios for the 18 test sites from the Yarra basin spanned from 0.09 to 1.01. Their variation was clearly related to continuous rather than abrupt changes in water quality, as measured by variables that are commonly used to judge this (Hellawell 1986), suggesting that the ratios are indeed sensitive measures of disturbance.

The models did not always provide accurate predictions. The upper catchment of the Yarra basin is used for water supply and is essentially free of human disturbance. In addition to the data for the 18 Yarra sites we also obtained family data (from the EPA) for 8 sites on small streams in the upper Yarra region and using the 2 spring models calculated O/E ratios. These

TABLE 8. Correlation coefficients for the water quality variables (log transformed) versus the O/E ratios for the 18 Yarra sites. Probability levels have been adjusted to reduce type 1 errors as a result of multiple (8) comparisons (*$p < 0.05/8 = 0.006$).

Variable	Pearson		Spearman rank	
	Spring 1990	Spring 1991	Spring 1990	Spring 1991
Ammonia	−0.67*	−0.65*	−0.72*	−0.72*
BOD	−0.47	−0.37	−0.44	−0.38
Cu	−0.53	−0.62*	−0.66*	−0.65*
Faecal coliforms	−0.70*	−0.65*	−0.68*	−0.64*
Suspended solids	−0.26	−0.21	−0.41	−0.37
TOC	−0.61	−0.55	−0.56	−0.56
Total P	−0.40	−0.37	−0.53	−0.54
Zn	−0.74*	−0.76*	−0.78*	−0.76*

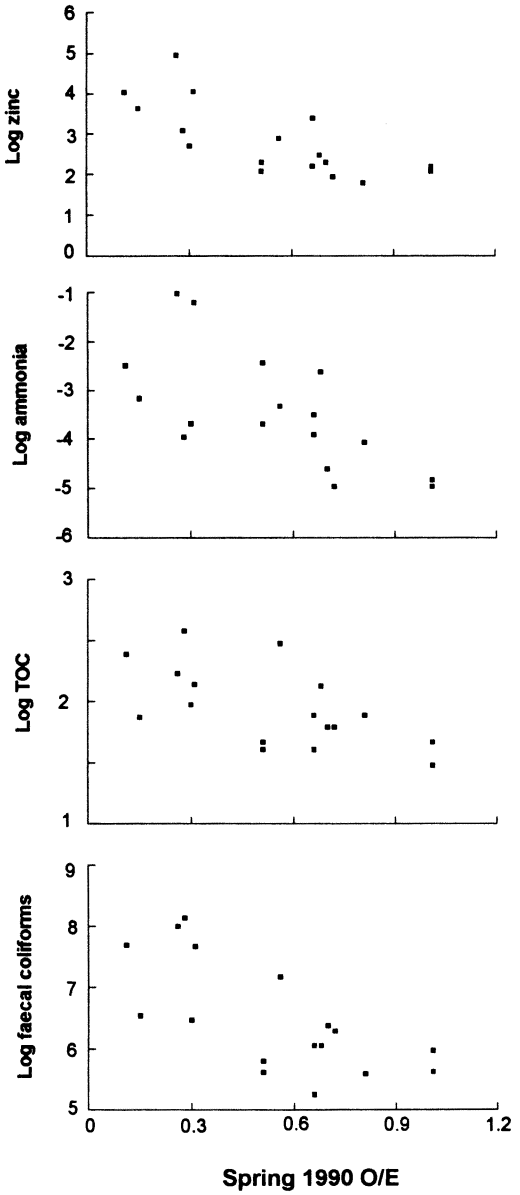

FIG. 3. Concentrations of zinc (μ/L), ammonia (mg/L), TOC (mg/L) and faecal coliforms (organisms/100 mL) versus the spring 1990 O/E ratios for the Yarra River sites. Natural logarithms are shown.

ranged from 0.54 to 0.90, with 6 sites having ratios <0.79. As all sites were undisturbed, one would expect the ratios to be close to 1.0; the fact that they were not, demonstrated that the family models did not predict accurately the community composition of these small streams. These sites were probably beyond the scope of the models in their current forms largely because there were no groups that were composed exclusively of sites on small streams. Such sites were present in the data sets and were mostly placed in Group 2 of the classifications for the spring data (Table 6). Their influence on the average composition of the taxa in these groups was, however, limited. It is the average composition that is reflected in the probabilities of occurrence of a taxon in a group and thus it is not suprising that O/E ratios for such sites were low. Wright et al. (1991, 1993b) have encountered similar problems with their RIVPACS models. Clearly these sorts of models have limits to their predictive abilities because sampling of reference sites will never be exhaustive.

There were few notable differences in performance between the species- and family-level models. The numbers of expected taxa that the models predicted were similar (Tables 4 and 5) except for sites in 2 basins (Snowy and Ovens) where the number of species expected clearly exceeded the number of families. The mean O/E ratios were slightly higher at the family level. Such differences may be important but can only be judged when models based on reference sites from many more river basins are available. Norris (unpublished) has shown that O/E ratios at the family level may be less variable than those at the species level, but this conclusion was based on data sets with a lower species and family richness than those we used. In our case, variability, as judged by the SD of the O/E (Tables 4 and 5), was much the same at both levels of taxonomic resolution.

The numbers of taxa expected from models based on data from 4 to 6 sampling occasions were higher than the numbers of taxa expected from models based on a single set of samples. For instance, the mean number of families expected from the full model (Table 4) was almost twice the number expected from the spring models (Table 7). This is probably a result of seasonal variation in the occurrence of taxa at both the species and family levels. By plotting cumulative numbers of taxa against sampling event (Fig. 4), it is clear that new species or families continued to be found after the 1st set of samples, and that about 3 sets of samples were necessary to record 80% of the taxa in a habitat at a site. These curves were based on the common taxa (110 species or 93 families) used in

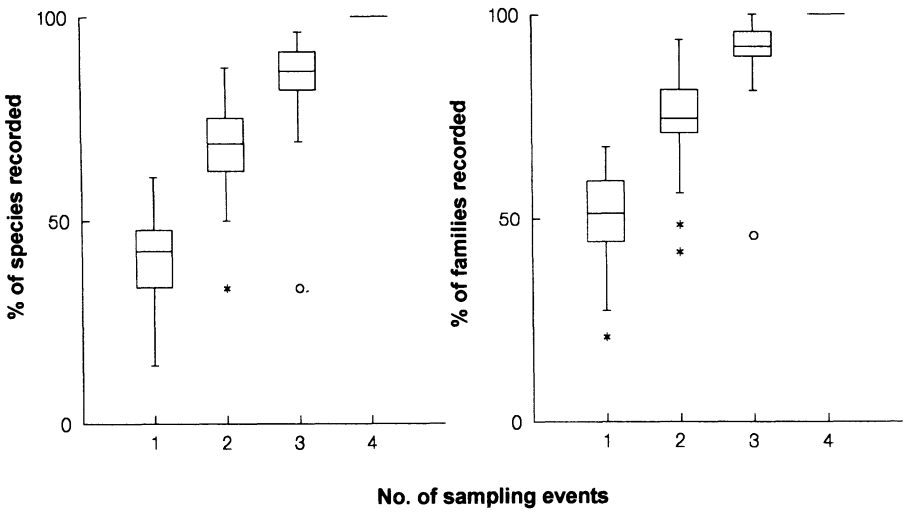

FIG. 4. Cumulative numbers of species or families (averaged over the 6 AWRC basins) versus sampling event. Horizontal lines are medians, boxes are interquartile ranges, and vertical bars are ranges, excluding outliers (*) or far outliers (O).

model construction. Similar assessments made for the species or families that occurred with a probability of 50% or more showed that cumulative numbers stabilised sometimes after 2 sets of samples but more usually after 3. Reexamination of macroinvertebrate data from 3 of the rocky sites in the upper catchment of the La Trobe River (Marchant et al. 1985) showed that of the species taken in 6 sets of samples over 2 y, only 40–50% occurred on the 1st sampling occasion and 70–80% after the first 3 sampling occasions; families, however, accumulated more rapidly with 70–80% being present on the 1st sampling occasion and 90% by the 3rd occasion. Thus the rate of accumulation of taxa at the reference sites does not seem to be unusually low. Differences may be due to the fact that only bankside habitats are represented in our data whereas the La Trobe samples represent main channel habitats with a rich fauna.

Contrary to the above remarks, the previous study on macroinvertebrate communities in unpolluted Victorian running waters (Marchant et al. 1994) concluded that temporal variation accounted for very little of the variation in the data. ANOVAs of DCA scores for the current sites (in individual basins) showed that about 10–20% of the variation on each of the 1st 2 DCA axes could be attributed to temporal variation. Despite this low contribution to overall variation in the data, temporal variation was still considered important because recruitment of the common taxa to either the species or family data sets was slow.

One result of the seasonal fluctuation in taxa is that models based on more than 1 set of samples will have more predicted taxa than those based on single sets of data and thus may be more sensitive at detecting changes in the fauna. Furse et al. (1984) demonstrated that similar discriminant models based on combined invertebrate data from 3 seasons resulted in better predictions than those based on data from a single sampling occasion. This is not to say that models based on single sampling occasions cannot provide useful predictions: the predictions for the 18 Yarra sites made sense in relation to changes in water quality. However, the actual numbers of taxa that were expected to occur, according to the spring models, were low (<14). When numbers of expected taxa become very low there may be so few taxa in a habitat that those missing simply by chance may result in a lower than expected O/E ratio. There may thus be a lower limit to the number of taxa with which these predictive models will work successfully.

Inevitably, predictive models are only as good as the reference-site data on which they are based. It is, of course, essential that sampling effort at test and reference sites must match exactly for predictions to be valid. Wright et al. (1991) have drawn attention to this issue for the RIVPACS models in the UK. In Victoria the

models will improve with more data, but the current versions demonstrate that successful predictions can be made from a modest set of reference sites. This is the first attempt to apply predictive models to river invertebrate communities over a broad geographic region outside the UK and over an area with a markedly different climate from that in the UK. There are important issues, such as the stability of model predictions for Victoria where hydrological conditions are markedly more variable than in Europe or North America (Lake et al. 1985), which obviously cannot be discussed until more experience with these models has been gained.

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APPENDIX 1. Location of reference and disturbed sites and site numbers as used in Fig. 1. Land use is indicated by a number (1–4); see footnotes to Table 1 (Vegetation) for explanation of numerical categories.

Site no.	Location	Land use
Snowy basin		
1	Snowy River at Orbost	2
2	Brodribb River at Sardine Creek Junction	4
3	Buchan River at Buchan	2
4	Snowy River at McKillops Bridge	4
5	Deddick River at Deddick	2
6	Suggan Buggan River at Suggan Buggan	4
7	Rodger River at Jackson Crossing	4
8	Snowy River downstream of Basin Creek	2
9	Brodribb River downstream of Orbost Pumping Station	2
10	Rodger River at Deddick Trail	4
South Gippsland basin		
11	Tarra River at Yarram	1
12	Agnes River at Agnes Falls	2
13	Tarra River at Fischers	1
14	Wilkur Creek at Leongatha	2
15	Franklin River at Toora	2
16	Merriman Creek at Seaspray	2
54	Bass River at Glen Forbes South	1
55	Tarwin River at Dunlop's Bridge	1
Barwon basin		
17	Barwon River at Pollcksford	2
18	East Barwon River at Forest	4
19	Leigh River at Mt Mercer	2
20	Barwon River at Inverleigh	1
21	Barwon River at Ricketts Marsh	2
22	Yarrowee Creek at Sebastopol	1
50	Birregurra Creek at Ricketts Marsh	1
51	Barwon River at Geelong	3

APPENDIX 1. Continued.

Site no.	Location	Land use
Otway basin		
23	Gellibrand River at Upper Gellibrand	2
24	Little Aire Creek at Beech Forest	2
25	West Airkins Creek at Wyelangta	4
26	Aire River at Beech Forest	3
27	Kennedy's Creek at Kennedy's Creek	2
28	Cumberland River at Lorne	3
29	Gellibrand River at Burupra	2
30	Gellibrand River at Bunkers Hill	4
31	Scotts Creek at Timboon	2
32	Curdies River at Timboon	1
Ovens basin		
33	Ovens River at Bright	1
34	Ovens River at Myrtleford	1
35	Fifteen Mile Creek at Greta South	1
36	Rose River at Matong North	4
37	King River at Docker	2
38	King River downstream of Lake William Hovell	3
39	Ovens River at Rocky Point	1
40	West Ovens River at Harrietville	4
41	King River upstream of Lake William Hovell	3
53	Ovens River at Peechelba	2
Campaspe basin		
42	Campaspe River at Rochester	1
43	Campaspe River downstream of Lake Eppalock	2
44	Stockyear Creek at Ashbourne	1
45	Campaspe River at Redesdale	2
46	Axe Creek at Longlea	3
47	Coliban River at Lyal	2
48	Wild Duck Creek at Mia Mia	2
49	Campaspe River downstream of Kyneton	1
52	Mt Pleasant Creek at Runnymeade	2

APPENDIX 2. Taxa in the species and family data sets (110 and 93 taxa respectively). Some taxa are distinguished by Victoria Environment Protection Authority code numbers. (a) = adult and (l) = larva for Coleoptera; these stages occupy different niches.

Taxon group	Taxa used in family data set	Taxa used in species data set
Hydrozoa	Hydridae	*Hydra* sp.
Turbellaria	Turbellaria	Turbellaria
Temnocephalidae	Temnocephalidae	
Nematoda	Nematoda	Nematoda
Nematomorpha	Nematomorpha	
Gastropoda	Hydrobiidae	*Potomopyrgus anitpodarum* (Gray)
		Fluvidona angasi (Smith)
	Ancylidae	*Ferrissia petterdi* (Johnston)
	Planorbidae	
	Planorbidae / Physidae	Planorbidae / Physididae spp.
Bivalvia	Corbiculidae	*Coriculina australis* (Deshayes)
	Sphaeriidae	*Pisidium casertanum* (Poli)
Oligochaeta	Oligochaeta	Oligochaeta
Hirudinea	Glossiphoniidae	
Hydracarina	Hydracarina	Hydracarina
Isopoda	Janiridae	*Heterias* spp.
Amphipoda	Ceinidae	*Austrochiltonia* spp.
	Gammaridae	*Austrogammarus multispinatus* Williams & Barnard
	Eusiridae	
Decopoda	Atyidae	*Paratya australiensis* Kemp
	Palaemonidae	
	Parastacidae	
	Hymenosomatidae	
Collembola	Collembola	
Ephemeroptera	Leptophlebiidae	*Atalophlebia* EPA sp. 1
		Atalophlebia EPA sp. 3
		Atalophlebia EPA sp. 9
		Atalophlebia EPA sp. 5
		Austrophleboides pusillus (Harker)
		Nousia sp.
		Koornonga sp.
		Ulmerophlebia sp.
	Caenidae	Caenidae Genus C sp.
		Caenidae Genus B sp.
	Baetidae	Baetidae Genus 2 EPA sp. 3*
		Baetidae Genus 1 EPA sp. 4*
		Baetidae Genus 1 EPA sp. 5*
		Baetidae Genus 2 EPA sp. 6*
		Centroptilum sp.
		Cloeon spp.
	Coloburiscidae	*Coloburiscoides* spp.
	Ameletopsidae	
	Oniscigastridae	*Tasmanophlebia* sp.
Odonata	Coenagrionidae	*Ischnura heterosticta* (Burmeister)
		Ischnura aurora (Brauer)
	Lestidae	
	Synlestidae	*Synlestes weyersi* Selys
	Gomphidae	*Austrogomphus ochraceus* (Selys)
	Aeshnidae	*Austroaeschna unicornis* (Martin)
	Synthemidae	
	Corduliidae	*Procordulia / Hemicordulia* spp.
	Libellulidae	

APPENDIX 2. Continued.

Taxon group	Taxa used in family data set	Taxa used in species data set
Plecoptera	Austroperlidae	
	Gripopterygidae	*Leptoperla primitiva* McLellan
		Leptoperla neboissi McLellan
		Dinotoperla fontana Kimmins
		Dinotoperla serricauda Kimmins
		Dinotoperla brevipennis Kimmins
		Illiesoperla spp.
	Notonemouridae	
Hemiptera	Hydrometridae	
	Gerridae	
	Veliidae	*Microvelia peramoena* Hale
		Microvelia dubia Hale
		Microvelia fluvialis Malipatil
	Mesoveliidae	
	Corixidae	*Micronecta australiensis* Chen
		Micronecta annae Kirkaldy
		Sigara spp.
	Naucoridae	
	Notonectidae	*Enithares woodwardi* Lansbury
	Nepidae	
	Pleidae	*Plea* spp.
Megaloptera	Corydalidae	
Coleoptera	Haliplidae	
	Gyrinidae	
	Dytiscidae	*Necterosoma penicallatus* Clark (a)
		Necterosoma sp. (1)
		Antiporus femoralis (Boheman) (a)
		Australphilus saltus Watts (a)
		Sternopriscus mundanus Watts (a)
		Lancetes sp. (1)
		Antiporus spp. (a)
	Hydraenidae	
	Hydrochidae	
	Hydrophilidae	*Berosus involutus* MacLeay (a)
	Scirtidae	
	Elmidae (1)	
	Elmidae (a)	*Notriolus victoriae* Carter & Zeck (a)
		Notriolus quadraplagiatus Carter (a)
		Austrolimnius resa Hinton (a)
	Psephenidae	*Sclerocyphon striatus* Lea (1)
Diptera	Tipulidae	
	Simuliidae	*Austrosimulium furiosum* (Skuse)
	Culicidae	
	Dixidae	
	Psychodidae	
	Tanypodinae	*Ablabesmyia* sp.
		Pentaneura spp.
		Apsectrotanypus spp.
		Procladius paludicola Skuse
		Paramerina levidensis Skuse
		Larsia sp.
	Aphroteniinae	
	Podonomiinae	
	Chironomini	*Riethia* sp.

APPENDIX 2. Continued.

Taxon group	Taxa used in family data set	Taxa used in species data set
		Dicrotendipes spp.
		Polypedilum tonnoiri Freeman
		Chironomus cloacalis Martin
		Polypedilum oresitrophus/seorsus
	Tanytarsini	*Rheotanytarsus* sp.
		Tanytarsus inextentus Skuse
		Cladotanytarsus spp.
		Tanytarsus fuscithorax Skuse
		Paratanytarsus spp.
	Orthocladiinae	Orthocladiinae sp.
		Thienemanniella trivatatta Goetghebuer
		Nannocladius sp.
		Cricotopus annuliventris Skuse
		Corynoneura scutellata Winnertz
		Parakiefferiella sp.
		Paratrichocladius pluriserialis Freeman
		Cricotopus sp.
	Ceratopogonidae	*Bezzia* sp.
	Stratiomyidae	
	Empididae	
	Muscidae	
Trichoptera	Hydrobiosidae	
	Glossosomatidae	
	Polycentropodidae	
	Hydroptilidae	*Oxyethira columba* (Neboiss)
		Hellyethira spp.
	Ecnomidae	
	Hydropsychidae	
	Limnephilidae	
	Tasimiidae	
	Odontoceridae	
	Helicopsychidae	
	Philorheithridae	
	Leptoceridae	*Triplectides truncatus* Neboiss
		Triplectides similis Mosely
		Triplectides volda Mosely
		Triplectides australis Navas
		Triplectides australicus Banks
		Triaenodes spp.
		Oecetis sp.
		Notalina bifaria Neboiss
		Notalina fulva Kimmins
		Notalina spira StClair
		Condocerus paludosus Neboiss
	Calamoceratidae	*Anisocentropus* sp.
	Atriplectidae	*Atriplectides dubius* Mosely
	Conoesucidae	*Costora delora* Mosely
		Conoesucus sp.
		Conoesucidae sp.
	Calocidae	
	Helicophidae	
Lepidoptera	Pyralidae	Pyralidae sp.

* Baetidae Genus 1 and 2 are taxa that were formerly referred to as *Baetis,* but are now no longer considered as part of *Baetis,* as currently defined (Dean and Suter 1996)

APPENDIX 3. The 18 Yarra sites and surrounding land use.

Location	Land use
Mullum Mullum Creek at Warrandyte	Urban–rural
Diamond Creek at Eltham	Urban
Plenty River at Viewbank	Urban
Darebin Creek at Fairfield	Urban
Gardiners Creek at Kooyung	Urban
Yarra River at Abbotsford	Urban
Yarra River at Ivanhoe	Urban
Yarra River at Heidelberg	Urban
Yarra River at Wonga Park	Urban–rural
Yarra River at Templestowe	Urban–rural
Yarra River at Warrandyte	Urban–rural
Yarra River at Coldstream	Urban
Watsons Creek at Kangaroo Ground	Rural
Olinda Creek drain at Coldstream	Rural
Brushy Creek at Wonga Park	Urban–rural
Yarra River at Maxwells Rd	Rural
Woori Yallock Creek at Yellingbo	Rural
Yarra River at Woori Yallock	Rural