

## Identification of morphological guilds in streams fish communities and their application in the estimation of biomass

K.M. Martin-Smith\*

Department of Zoology, University of Aberdeen, Tillydrone Avenue, Aberdeen AB9 2TN, Scotland

\*Address for communication: Danum Valley Field Centre, c/o Rakyat Berjaya Sdn. Bhd., P.O.Box 60282, 91112 Lahat Datu, Sabah, Malaysia

**ABSTRACT** Length/weight relationships were examined in a tropical freshwater fish community to facilitate biomass estimation. The relationships of body weight to standard length were determined for 21 species of freshwater fishes in Sabah, Malaysia (18 species of Cyprinidae, 1 species each of Anguillidae, Mastacembelidae and Bagridae). Multiple comparison of regression lines by analysis of covariance revealed two major functional groups within which species were indistinguishable. These groups were designated 'flattened' and 'heavy-bodied'. In addition there were two species with an 'eel-like' morphology. Common regression equations were generated for each group which allowed biomass to be estimated solely from length-frequency data, without the need for species identification. Biomass was estimated from species-specific regressions and from guild-specific regressions using data from surveys of four streams. The difference between these values was less than 5% for three streams with diverse fish communities. For a fourth stream with only four species biomass was significantly underestimated. When the length-frequency data were grouped in intervals the error of estimation increased as the interval size increased. Size data grouped into 2 or 3 mm intervals gave estimates of biomass indistinguishable from raw data. It is suggested that the use of morphological guilds is a valid tool for freshwater fish survey work in the old-world tropics.

**ABSTRAK** Satu kajian yang menggunakan hubungan panjang berat bagi menganggar biojisim komuniti ikan air tawar di kawasan tropika telah dijalankan. Hubungan berat badan dengan panjang piawai 21 spesies ikan air tawar (18 spesies Cyprinidae dan 1 spesies masing-masing bagi Anguillidae, Mastacembelidae dan Bagridae) di Sabah, Malaysia telah ditentukan. Perbandingan berbilang terhadap garis regresi menggunakan analisis kovarians menunjukkan bahawa spesies-spesies ikan ini tergulung dalam dua kumpulan utama, iaitu spesies yang mempunyai badan yang pipih dan badan yang tinggi. Di samping itu ada juga spesies yang agak memanjang seperti belut. Biojisim ikan telah ditentukan dengan menggunakan regresi spesies tertentu dan juga regresi kumpulan spesies tertentu. Biojisim menggunakan kedua-dua kaedah ini agak serupa bagi anak-anak sungai yang mempunyai kepelbagaian ikan yang tinggi, perbezaannya kurang daripada 5%. Sebaliknya bagi anak sungai yang mempunyai kepelbagaian yang rendah, perbezaan ini amat ketara sekali. Apabila data frekuensi panjang ini dikumpulkan dalam bentuk jeda, kesilapan anggaran meningkat dengan peningkatan saiz jeda. Akan tetapi saiz jeda 2 atau 3 mm memberikan anggaran biojisim yang mempunyai perbezaan paling kecil. Bergantung kepada kepelbagaian spesies ikan yang terdapat di habitat akuatik yang dikaji, penemuan awal mendapati kaedah mengumpulkan spesies ikan yang mempunyai morfologi yang sama adalah satu cara

yang boleh digunakan untuk menganggar biojisim ikan di kawasan tropika.

(morphological guilds, fish communities, biomass)

### INTRODUCTION

Comparison of the biomass (standing stock) of fish species is often used to determine the effects of different treatments on stream communities [1,2,3]. Recently, inferences about the effects of catchment management or changes in water quality in Malaysia have been based on measurements of standing crop of fishes [4,5]. The effects of different logging regimes on fish populations in North America have been assessed by comparisons of biomass between streams of different logging history [1,3]. Biomass has been used as an indirect estimate of production [6] and is an essential prerequisite for calculating production using the Ricker algebraic method [7].

Biomass can be measured directly in the field, but this is time-consuming when large areas need to be surveyed. Within a species length and weight are highly correlated [8]; thus length-frequency distributions can be used to estimate biomass [9]. This is relatively simple in temperate regions since regression data are available for most European and North American fishes [e.g. 10,11,12] but few investigations have been carried out on tropical fishes [but see 13,14,15,16]. In addition the highly diverse nature of tropical freshwater fish assemblages, often with numerous morphologically similar species [17] is a complicating factor. Length-weight relationships need to be generated for each species present and correct identification performed by field workers.

However, the fact that many tropical species are morphologically similar suggested that individual spe-

cies identification may be unnecessary if the objective of a study is to measure biomass only. Preliminary results from length-weight relationships of some freshwater fishes in Sabah indicated that the fish could be partitioned into two major morphological guilds [18]. The objective of this paper is to expand these preliminary findings and to experimentally test the validity of morphological guilds in biomass estimation.

## MATERIALS AND METHODS

### Study sites

Fishes were collected from streams and rivers in the vicinity of Danum Valley Field Centre (DVFC), Sabah, Malaysia. All streams in the area form part of the headwater catchment of the Segama River. Six streams were used in this study ranging in size from approximately 3-15 m in width with catchment areas of <1 km<sup>2</sup> to c. 40 km<sup>2</sup>. Fishes were also captured from the Segama River which is approximately 30 m wide and up to 5 m deep at this location. Well developed pools and riffles are present in many of the streams with substrate varying from bedrock and cobbles in the riffles to sand, silt and organic debris in pools. In-stream vegetation is not present and most of the streams are heavily shaded. This study is confined to fishes from pools only, since most of the riffle species are small and do not contribute significantly to the biomass of the entire system [19].

### Study species

Over 50 species of fish are found around DVFC [19,20]. However, many of these are present in low numbers or are too small to be reliably measured in the field (e.g. *Gastromyzon* and *Protomyzon* spp.). This study was confined to 21 species, 18 from the Cyprinidae, 1 each from the Anguillidae, Mastacembelidae and Bagridae. These are the most abundant species locally and together contribute between 80 and 95% of the biomass (Martin-Smith, unpublished data). Identification of fish was from standard taxonomic works [20,21]. The fishes and their authorities are given below.

Cyprinidae: *Barbodes collingwoodii* (= *Puntius collingwoodii*) (Günther), *Crossocheilus cobitis* (= *Epalzeorhynchus kalliurus*) (Bleeker), *Cyclocheilichthys apogon* (Valenciennes), *Cyclocheilichthys repasson* (Bleeker), *Dangila sabana* Inger & Chin, *Garra borneensis* (Vaillant), *Hampala*

*macrolepidota* Valenciennes, *Lobocheilos bo* (Popta), *Luciosoma pellegrini* Popta, *Nematabramis everetti* Boulenger, *Osteochilus microcephalus* (Valenciennes), *Osteochilus spilurus* (Bleeker), *Puntioplites bulu* (= *Puntius bulu*) (Bleeker), *Puntius sealei* (Herre), *Rasbora cf. ruttleri* Weber & de Beaufort, *Rasbora sumatrana* (Bleeker), *Tor douronensis* (Valenciennes), *Tor tambroides* Bleeker.  
Anguillidae: *Anguilla borneensis* Popta.  
Mastacembelidae: *Macrognathus keithi* (Herre).  
Bagridae: *Mystus baramensis* (Regan).

### Length-weight relationships

In small streams fishes were captured by electrofishing using pulsed DC at 300 V with a current of approximately 1.5 A. In deeper water (>1.2 m) fishes were captured using a cast net with stretched mesh size of 20 mm. Upon capture fishes were lightly anaesthetised by placement in a dilute solution of benzocaine. Standard length (SL) was measured to the nearest mm and fresh weight (WT) to the nearest 0.1 g before fish were returned to the water. Some species were far more abundant than others, therefore sample size varied according to species. A minimum of 30 individuals was considered acceptable for analysis, but varied up to n=170 for *L. bo* (see Table 1).

### Biomass estimation

As part of another study (Martin-Smith, unpublished data) fish surveys were conducted in four streams around DVFC coded as CSR, ST, WS and LLS. Depending on stream morphology between three and six pools were quantitatively sampled by electrofishing. Pools were blocked with stop nets, then three passes were made with the electrofisher in an upstream direction. The standard lengths of all fishes captured were measured to the nearest mm. Population estimates were made using the Zippin maximum-likelihood procedure [22]. Biomass was estimated from these data using (a) species-specific regressions on raw data, (b) guild-specific regressions on raw data, and (c) guild-specific regressions on data grouped into intervals of 2, 3, 5 or 10 mm. Comparisons between the different estimates of biomass were made using the species-specific estimate as the 'true' value.

### Data analysis

Fish length-weight relationships are of the form  $y = aM^b$

[8]. Log-transformation of the data therefore yields the equation  $\log y = b \log M + \log a$ , a linear relationship, with  $a$  and  $b$  representing the intercept and the slope of the line respectively. Thus, all data were log-transformed and least squares linear regressions performed on the transformed data with WT as the dependent variable. Plots of the residuals were used to test the homoscedasticity of the data [23]. Data from different streams were pooled, the assumption being made that length/weight relationships for any individual species were the same for different streams. Where the sample sizes were great enough this was tested by analysis of covariance (ANCOVA). Comparison between the slopes of regression lines for each species was also performed using ANCOVA. *Post-hoc* Tukey's honestly significant difference (HSD) tests were used to identify significantly different slopes, which were then removed stepwise from the analysis. The F-statistic for differ-

ences between intercepts was calculated for groups of species which did not have significantly different slopes, followed by *post-hoc* Tukey's HSD to identify species with significantly different intercepts [23]. Where regressions for groups of species were not significantly different, common regression lines were generated [23]. Guild-specific estimates of biomass were tested for significant difference from the species-specific estimate using two-tailed t-tests.

## RESULTS

### Length-weight relationships

The number of individuals sampled, the mean length, mean weight and the range of these values for each species are given in Table 1. Linear regressions on log-transformed data were highly significant ( $p < 0.001$ )

**Table 1.** Sample sizes, mean length, weight and range for species of some freshwater fishes from Sabah.

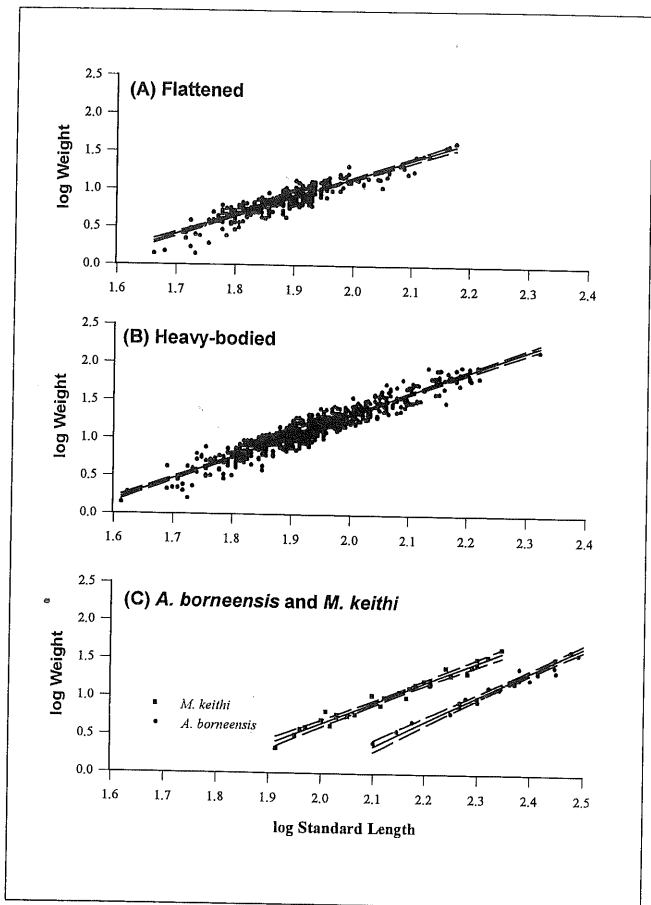
Species	Number of individuals	Mean SL (mm)	Range (min.-max.)	Mean WT (g)	Range (min.-max.)
<b>Cyprinidae</b>					
<i>B. collingwoodii</i>	30	74	55-142	13.4	6.2-81.7
<i>C. cobitis</i>	46	78	52-114	7.1	2.2-14.8
<i>C. apogon</i>	34	102	80-148	34.8	18.7-135.0
<i>C. repasson</i>	30	88	49-155	15.9	2.1-70.0
<i>D. sabana</i>	30	122	101-221	62.3	27.9-154.0
<i>G. borneensis</i>	107	72	53-98	6.9	3.8-20.5
<i>H. macrolepidota</i>	84	89	44-154	16.0	2.0-73.1
<i>L. bo</i>	167	88	52-149	14.1	2.0-68.8
<i>L. pellegrini</i>	30	116	82-150	19.8	6.3-42.2
<i>N. everetti</i>	118	77	48-98	7.9	1.5-16.2
<i>O. microcephalus</i>	134	83	56-141	15.8	5.0-82.0
<i>O. spilurus</i>	79	79	41-102	12.5	1.4-26.0
<i>P. bulu</i>	32	175	121-226	122.9	41.8-169.9
<i>P. sealei</i>	56	69	42-116	10.2	1.9-42.1
<i>R. cf. rutteni</i>	44	35	24-49	0.9	0.3-2.3
<i>R. sumatrana</i>	66	75	46-95	7.3	1.4-12.4
<i>T. douronensis</i>	77	99	52-165	25.9	2.4-91.2
<i>T. tambroides</i>	36	116	69-170	34.5	6.8-113.3
<b>Anguillidae</b>					
<i>A. borneensis</i>	30	224	140-310	18.1	3.6-43.0
<b>Mastacembelidae</b>					
<i>M. keithi</i>	30	146	82-222	14.4	2.1-45.2
<b>Bagridae</b>					
<i>M. baramensis</i>	41	120	50-210	31.3	2.2-149.1

for all species (Fig. 1, Table 2). No significant heteroscedascity was apparent from plots of the residuals. For those species for which between-stream differences could be examined (*G. borneensis*, *H. macrolepidota*, *L. bo*, *N. everetti*, *O. microcephalus*, *O. spilurus*, *T. douronensis*) there was no significant difference in the regression equations ( $F < 0.458$ ,  $p > 0.50$  in all cases). ANCOVA revealed significant differences between species for the slopes of the regression lines ( $F = 3.127$ ,  $df = 15$ ,  $p < 0.001$ ). *Anguilla borneensis* and *M. keithi* had clearly different morphologies and so were removed from the analysis. Both of these species are 'eel-shaped', with elongated bodies; thus fish are significantly longer for a given weight than the other species (Fig. 1 and Table 2). For the remaining species *post-hoc* Tukey's HSD showed

that there were two groups of species with significantly different values of *b*, the estimate of the slope, although one species, *N. everetti*, showed overlap between both groups. A subjective decision was made to place it in the first group which consisted of *C. cobitis*, *G. borneensis*, *L. pellegrini*, *R. cf. ruttleri* and *R. sumatrana*. These fishes are all flattened, either dorso-ventrally in the case of *C. cobitis* and *G. borneensis* or laterally in the case of the other species. *Nematabramis everetti* was placed in this group because the estimate of *b* was not significantly different from all the members of this group (as opposed to only *B. collingwoodii* and *P. sealei* in the second group), its flattened morphology and its lower regression coefficient. Within this group there were no significant differences between the values of the intercept of the re-

**Table 2.** Regression coefficients for length/weight relationships (with standard errors in parentheses) for some freshwater fishes from Sabah.

Species	R <sup>2</sup> (all significant at p<0.001)	b, slope of regression (SE)	log a, intercept of regression (SE)
<b>'flattened' group</b>			
<i>C. cobitis</i>	0.894	2.650 (0.136)	-4.184 (0.257)
<i>G. borneensis</i>	0.737	2.456 (0.142)	-3.748 (0.264)
<i>L. pellegrini</i>	0.851	2.652 (0.122)	-4.208 (0.243)
<i>N. everetti</i>	0.846	2.875 (0.113)	-4.542 (0.213)
<i>R. cf. ruttleri</i>	0.824	2.677 (0.146)	-4.223 (0.202)
<i>R. sumatrana</i>	0.787	2.748 (0.124)	-4.309 (0.229)
<b>'heavy-bodied' group</b>			
<i>B. collingwoodii</i>	0.950	2.907 (0.081)	-4.402 (0.171)
<i>C. apogon</i>	0.917	3.124 (0.102)	-4.997 (0.156)
<i>C. repasson</i>	0.980	3.075 (0.114)	-4.862 (0.221)
<i>D. sabana</i>	0.922	2.994 (0.123)	-4.881 (0.149)
<i>H. macrolepidota</i>	0.955	3.011 (0.071)	-4.740 (0.138)
<i>L. bo</i>	0.935	3.158 (0.065)	-5.042 (0.125)
<i>M. baramensis</i>	0.970	2.982 (0.082)	-4.781 (0.170)
<i>O. microcephalus</i>	0.916	3.022 (0.079)	-4.645 (0.151)
<i>O. spilurus</i>	0.944	3.173 (0.088)	-4.960 (0.165)
<i>P. bulu</i>	0.923	3.125 (0.094)	-4.901 (0.143)
<i>P. sealei</i>	0.941	2.900 (0.078)	-4.376 (0.166)
<i>T. douronensis</i>	0.971	3.059 (0.061)	-4.786 (0.120)
<i>T. tambroides</i>	0.966	3.040 (0.072)	-4.716 (0.133)
<b>'eel-like'</b>			
<i>M. keithi</i>	0.947	2.784 (0.077)	-4.930 (0.158)
<b>'eel'</b>			
<i>A. borneensis</i>	0.917	2.875 (0.105)	-5.552 (0.227)



**Figure 1.** Length/weight regressions (with 99% confidence limits) for morphological guilds of some freshwater fish species from Sabah.

gression line,  $\log a$ . The common regression line for the flattened fishes was calculated as:  $\log WT = 2.677 \log SL - 4.208$ . Within the second group of species with a common value of  $b$  there were no significant differences in the value of the  $\log a$ . All of these species had 'standard' cyprinid body shape ('heavy-bodied') with the common regression line:  $\log WT = 3.055 \log SL - 4.785$ .

#### Biomass estimation

The estimates of biomass using species-specific and guild-specific regressions on the raw data for the four streams surveyed are given in Table 3. For three of the streams (CSR, ST, WS) there were no significant differences between the estimates of biomass using either method (Table 4). The difference between the estimates for any individual pool was always less than 10% and the mean difference for the whole stream was 2.5-5.4%.

These three streams had diverse fish communities with between 6 and 15 species present in each sample location (mean = 11.3 species) and a total of >15 species present in each stream (Table 3). For a fourth stream (LLS) the species-specific regression gave estimates of biomass significantly higher than the guild-specific regression (Tables 3 and 4). This stream had a depauperate community with 3 or 4 species present at each sampling location (mean = 3.5 species) and a total of only 4 species present in the entire stream. These four species were *A. borneensis*, *P. sealei*, *Protomyzon whiteheadi* and *Betta unimaculata* of which *P. sealei* comprised >95% of the individuals and >90% of the biomass. There was a strong systematic bias between the species-specific and guild-specific regressions for this community.

Results from grouping the data into different size intervals and applying guild-specific regressions to the mid-point values are given in Table 5. For the reasons outlined above data from LLS stream are considered atypical and will not be considered further. Differences between values obtained with different interval sizes for individual sampling locations were unpredictable, but generally mean values for each stream showed greater deviation and spread for increasing interval size. Combining data from CSR, ST and WS streams, data grouped into 2 or 3 mm intervals gave estimates within 5% of the true value, while data grouped into 5 or 10 mm intervals gave estimates greater than 5%.

#### DISCUSSION

This study demonstrates that the measurement of an ecologically-important quantity, biomass, in a complex community can be simplified by the application of morphological guilds. Biomass estimates generated from a simplified set of length-weight relationships were not significantly different from those generated by a more complicated set of species-specific relationships. This is an extension of the guild concept that has important implications for fisheries management in the tropics. The use of guilds in management work is not new, but previous work has been restricted mainly to the use of trophic guilds [24]. Morphological guilds have been identified in the elucidation of feeding habits, water column position and behaviour [25,26,27] but not in the estimation of standing crop.

**Table 3.** Estimates of biomass of fishes from four streams using species-specific and guild-specific length/weight regressions.

Stream	Pool No.	No. Species	No. Fish	Biomass estimate (in g) from:		
				Species-specific regression	Guild-specific regression-	% difference
CSR	1	15	170	1156.4	1153.4	-0.3
	2	14	164	1030.8	978.9	-5.0
	3	13	188	1220.6	1230.8	0.8
ST	1	11	68	694.0	680.8	-1.9
	2	8	19	143.5	136.0	-5.2
	3	6	8	71.2	72.5	1.9
	4	10	97	981.6	964.3	-1.8
	5	9	28	359.8	364.3	1.3
	6	9	63	860.9	832.9	-3.3
WS	1	9	59	498.9	450.9	-9.6
	2	11	43	319.8	292.6	-8.5
	3	8	25	195.8	194.5	-0.6
	4	11	89	1033.2	1111.3	7.6
	5	14	58	510.2	523.6	2.6
	6	15	60	326.9	316.0	-3.3
LLS	1	3	40	46.9	37.1	-20.8
	2	4	172	611.5	451.2	-26.2
	3	4	98	182.6	131.5	-28.0
	4	3	51	59.5	45.4	-23.7
	5	4	119	471.0	363.9	-22.7
	6	3	53	170.9	121.9	-22.1

Survey work is invariably constrained by time or money and subjective management decisions have to be taken as to the sampling effort expended at particular localities: 'few, intensive' vs. 'many, superficial' [12]. The present study is offered as a technique to allow greater information to be gathered for the same sampling effort. Standing crop is an extremely important measurement in management work and if length-frequency data are required for other purposes (such as production estimation by the Bhattarachaya method) then the present technique requires no more than recognition of which morphological guild to place a fish in - something that requires little skill or training.

The present study relies on morphological similarity between members of a complex community. Much of this similarity may be due to taxonomic affinities within the community. In common with most freshwa-

ter fish assemblages in the old-world tropics, communities in Sabah are dominated by cyprinids [28]. It might be expected that many species within a family or subfamily show similarities in morphology. Most of the flattened group of fishes in the present study belong to the subfamily Danioninae (all except for *Garra*) whereas the heavy-bodied fishes are from the family Cyprininae [28]. Other communities dominated by different families e.g. characins in South America or cichlids in Africa may not conform to the general equations presented here, although it is postulated that similar morphological guilds exist in these other systems. Obviously, validation of this hypothesis is required.

The selection of suitable size intervals for measurement is of paramount importance when conducting survey work. [29] has shown that the detection of size-class modes is determined by the life history character-

**Table 4.** Results of paired t-test on mean biomass estimates generated using species-specific or guild-specific length/weight regressions from fishes in four Sabah streams.

Stream	No. Paired Observations	Degrees of Freedom	t-value	p-value (ns = not significant)
CSR	3	2	0.797	0.51(ns)
ST	6	5	2.032	0.10(ns)
WS	6	5	0.039	0.97(ns)
LLS	6	5	2.745	0.04

**Table 5.** Comparison of biomass estimates generated using length-frequency data grouped into differing size intervals (standard errors in parentheses).

Stream	Pool No.	Magnitude of percentage deviation from 'true' value when size frequency data grouped into intervals of:				
		1 mm (=raw data)	2 mm	3 mm	5 mm	10 mm
CSR	1	0.3	1.9	1.9	2.4	3.0
	2	5.0	5.8	5.6	6.3	7.4
	3	2.1	3.2	3.4	3.8	4.2
Mean for CSR	(SE)	2.5 (1.4)	3.6 (1.1)	3.6 (1.1)	4.2 (1.1)	4.9 (1.3)
ST	1	1.9	0.2	0.3	0.7	1.0
	2	5.2	0.8	1.0	4.9	2.3
	3	1.9	4.0	5.9	5.9	6.2
	4	1.8	0.1	0.2	1.6	3.5
	5	1.3	2.1	2.8	1.9	0.2
	6	3.3	6.8	6.9	6.7	5.9
Mean for ST	(SE)	2.6 (0.6)	2.3 (1.1)	2.8 (1.2)	3.6 (1.0)	3.2 (1.0)
WS	1	9.6	7.6	8.5	8.3	6.7
	2	8.5	10.8	11.8	12.1	12.4
	3	0.6	8.9	8.1	9.0	7.5
	4	7.6	7.9	7.5	9.6	12.9
	5	2.6	4.4	4.7	6.2	5.1
	6	3.3	1.0	0.9	1.8	1.0
Mean for WS	(SE)	5.4 (1.5)	6.8 (1.4)	6.9 (1.5)	7.8 (1.4)	7.6 (1.9)
Mean for all three above streams	(SE)	3.7 (0.8)	4.4 (0.9)	4.6 (0.9)	5.4 (0.9)	5.3 (1.0)
LLS	1	20.8	18.0	16.9	15.6	16.4
	2	26.2	23.8	24.3	23.6	22.9
	3	28.0	26.0	25.1	24.1	24.0
	4	23.7	19.7	19.4	16.2	15.4
	5	22.7	20.4	21.2	21.4	18.1
	6	28.7	23.4	24.4	23.6	22.0
Mean for LLS	(SE)	25.0 (1.3)	21.9 (1.2)	21.9 (1.4)	20.7 (1.6)	19.8 (1.5)

istics of each species. The present work shows progressively increasing errors with increasing interval size, but no significant difference between measurements to the nearest 1, 2 or 3 mm. However, even interval size of 5 or 10 mm gave results within 10% of the true value, which suggests that, in some circumstances where speed of data acquisition is paramount, very large size intervals compared to fish body size could be used to produce an acceptable estimate of biomass. It is suggested that for most purposes, measurement to the nearest 2 or 3 mm would represent an adequate compromise between speed and accuracy.

A shortcoming of using morphological guilds is shown by the estimate of biomass from the depauperate community in LLS stream where values were consistently underestimated using guild-specific regressions. A community dominated by a single or few species will show systematic bias when guild-specific regressions are applied, which may or may not result in a significant difference in the estimation of biomass, depending on whether the species-specific regression is close to the common equation and whether the mean size of the species involved is close to the mean size of individuals in the guild. In the case of LLS, *P. sealei* individuals were generally smaller than the mean of the heavy-bodied guild and the species-specific regression was different from the common equation. However, using guild-specific regressions in such a simple community would make little sense since the technique is designed to simplify complex communities.

In conclusion, the judicious application of common length-weight regressions for morphological guilds can considerably simplify the production of estimates of biomass in a tropical freshwater community in Sabah. It is suggested that this work can be extended to other assemblages in South East Asia as a tool in fisheries management work or in environmental impact studies.

**Acknowledgments** I would like to acknowledge Yayasan Sabah, Danum Valley Management Committee, Sabah Chief Minister's Department, Sabah Fisheries Department and Economic Planning Unit of the Prime Minister's Department for permission to conduct research in Sabah. My collaborators, En. Abdullah Samat of Universiti Kebangsaan Malaysia — Sabah Kampus and the Sabah Fisheries Department have been most helpful. The help of Dr. Lindsay Laird, Dr. Adrian Marshall, the field assistance of En. Karim Kasil, the criticisms of Dr. Mitchell Crook, James Gibbons and anonymous reviewers, and the financial support of the ODA and the Royal Society have been invaluable. This is publication no. A/135 of the Royal Society Southeast Asian Rainforest Programme.

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