

# Tools for identifying unexpectedly low microfossil count sums

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## Abstract

Microfossil counts are a key data type in palaeoecology. Recent work has raised the possibility that some authors might misreport an important quality control parameter, the counts sums, occasionally dramatically so. This paper introduces methods that can flag assemblages with potentially misreported count sums and finds that some assemblage datasets that fail these tests.

**Keywords:** Microfossil counts; quantitative methods

## 1. Introduction

Six percent of papers published in *Molecular and Cellular Biology* show evidence of inappropriate image duplication (Bik et al. 2018) either due to error or, more rarely, misconduct. It would be reckless to assume that the palaeoecological literature does not have equivalent problems: the low rate of retractions in the ecological and geological literature (Grieneisen and Zhang 2012) may partially reflect our limited ability to detect errors and misconduct rather than their prevalence.

Several numerical tools have been developed to identify questionable data. Deviations from the distribution of digits expected from the Newcomb-Benford law has been used to detect issues with scientific and financial data (Barabesi et al. 2018). Carlisle (2017) identified papers where the baseline differences in means for different treatments were surprisingly high or low given the variance of the data. Brown et al. (2017) developed the granularity-related inconsistency means (GRIM) test of whether means of integer data are consistent with the reported sample size. However none of these tests are directly applicable to microfossil assemblage data, one of the most common types of palaeoecological data.

A common assertion in papers reporting microfossil assemblage data is that a minimum of  $N$  microfossils were counted, where  $N$  is often fifty for chironomids and several hundred for pollen and diatoms. This is important because larger count sums are associated with smaller uncertainties, both in relative abundance of taxa and derived statistics such as transfer function reconstructions (Heiri and Lotter 2001). However, mistakes happen and metadata such as count sums

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can be forgotten once percentages are calculated. In addition, given the time-consuming nature of microfossil counting, especially when preservation is poor or concentrations are low, there may be an incentive to misreport the minimum count sum. The risk that count sums will be mis-reported is not just theoretical: Larocque-Tobler et al (2015) reported that their chironomid count sums were at least fifty head capsules; a subsequent corrigendum (Larocque-Tobler et al. 2016) acknowledged that count sums were actually as low as nineteen. Telford (2019a) reports some other cases where count sums may be much lower than reported.

If the genuine assemblage counts are archived for all taxa, it is trivial to identify undercounts. Unfortunately, count data might be falsified so that it appears to meet the reported count sum. A more common problem is that, regrettably, many palaeoecologists archive percent data without an indication of the count sum. This paper develops simple tests that can flag if the count data might have been misrepresented, or if the count sum of percent data is perhaps lower than reported.

The key insight that allows inference about the count sum is that assemblage data are expected to follow the typical features of a rank abundance curve. In particular, because there are many rare taxa in most communities (Darwin 1859), most community or assemblage samples will include taxa represented by a single individual, hereafter singletons, unless the sampling effort is high relative to the taxonomic richness (Coddington et al. 2009). In the occasional assemblages without singletons, the greatest common divisor should usually be one, i.e. few assemblages should have all counts divisible by an integer larger than one, especially if species richness is high.

In general, it is not possible to determine the sum from which percent were calculated, but the properties of community and assemblage counts make it possible to estimate it. Given that we expect the rarest taxon to be a singleton, the count sum  $N$  can be estimated as  $1/p_{min} \times 100$  where  $p_{min}$  is the percent abundance of the rarest taxon. This method will fail for assemblages without singletons. We also expect the percent  $p$  to be calculated from integer counts, therefore, there should be a count sum  $N$  such that  $p_i/100 \times N$  is, within rounding error, an integer for all  $i$  taxa. Possible values for  $N$  can be found by a direct search algorithm over the range of plausible values of  $N$ . An infinite number of possible count sums that are consistent with the percent exist, but the lowest will give the correct value of  $N$  except in cases where the greatest common divisor is greater than one. These tests are closely related to GRIM (Brown and Heathers 2017), as all rely on the granularity of percentages calculated from integer data.

This paper aims to test the methods presented above and present some cases with unexpected results. Some complications and caveats are discussed.

## 2. Methods

Publicly available datasets were downloaded from the Palaeodata Center, Neotoma, Pangaea and other sources. A range of ecological and palaeoecological

Table 1: Percent of bird counts with singletons and of greatest common divisor (GCD) of one, at different taxonomic levels.

Taxonomic level	Percent with singletons	Percent GCD = 1	Median richness
species	99.95	100.00	54
genus	99.85	100.00	46
family	95.69	100.00	25
order	82.62	99.42	9

data were sought to allow for difference in typical count sum and species richness. Fossil pollen assemblage in the Neotoma database (Williams et al. 2018) (downloaded 2019-05-03) with small count sums ( $< 50$ ), that appeared to be percentages, or were documented as back-transformed from digitised data were excluded. Datasets with percent data where the minimum count sum was not reported in the associated paper were excluded. Datasets discussed by Telford (2019a) as possibly having under-reported count sums were also excluded to avoid double reporting. Datasets with possible mis-reporting are anonymised, but no attempt is made to diagnose whether errors or misconduct are responsible. This paper does not attempt to be an exhaustive survey of all the data available.

All analyses were done in R version 3.4.4 (R Core Team 2018) and used the packages extraDistr version 1.8.10 (Wolodzko 2018), numbers version 0.7.1 (Borchers 2018), and countSum 0.0.3 (Telford 2019b). Code to replicate all the analyses shown above is archived at <https://github.com/richardjtelford/count-check.ms>.

### 3. Results

#### 3.1. Prevalence of singletons

The vast majority of the over 65,000 bird counts from the North American breeding bird survey (Pardieck et al. 2018) have singletons at the species level (Table 1). To explore the effect of taxonomic richness on the prevalence of singletons, I aggregate the birds counts to progressively lower taxonomic resolutions. As richness declines, the proportion of counts having singletons declines (Table 1), reaching a moderate proportion at the order level, where most of the counts lacking singletons have fewer than five taxa. The vast majority of counts have a greatest common divisor of one, except when taxonomic richness is low.

To test the sensitivity of the prevalence of counts without singletons to the count sum, I re-sample the counts with 400 or more observations to smaller count sums using a multivariate hypergeometric distribution. At the order level, the proportion of counts with singletons increases steeply until it reaches a maximum at about 200, thereafter is declines slowly (Fig. 1). The prevalence of counts with singletons is low for small counts because it is possible that only the common taxa are counted; with larger counts, the chance of counting a single individual of a rare taxon increases. With even larger counts the prevalence of counts with

110 singletons decreases due to saturation as singletons become doubletons and few  
 111 new taxa are found.

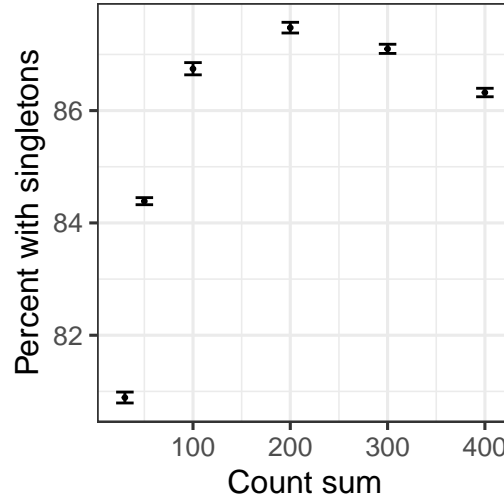


Figure 1: Effect of count sum on the proportion of bird counts without singleton orders. Results are the mean of ten trials, error bars are two standard errors.

112 The 862 diatoms counts from Owen’s Lake span a wide range of count sums  
 113 (1 – 701) as, if concentrations were low, the requirement that at least 300 valves  
 114 were counted, was replaced by a minimum area of slide to count (Bradbury 1997).  
 115 Discounting the 20 mono-specific assemblages (all with very low count sums),  
 116 97.39% of assemblages have singletons with a median number of singletons per  
 117 assemblage of five. Assemblages with count sums above 50 have a higher chance  
 118 of having singletons (98.18% vs 89.04%). 99.52% of assemblages have a greatest  
 119 common divisor of one, the remainder have a greatest common divisor of two.  
 120 Assemblages with a greatest common divisor above one all have low taxonomic  
 121 richness.

122 The 1775 assemblages in the North American testate amoeba training set  
 123 with available count data (Amesbury et al. 2018) have count sums between 52  
 124 and 456 tests (median = 151), and taxonomic richness ranges between 2 and  
 125 31 (median = 15) taxa. 94.87% of the assemblages have at least one singleton  
 126 (median 4) and 99.72% of assemblages have a greatest common divisor of one.  
 127 Of the five assemblages with a greatest common divisor above one, three have  
 128 fewer than five taxa; four have a greatest common divisor of two, and the other  
 129 one has a greatest common divisor of three.

130 The pollen data from the Neotoma database included over 182 thousand  
 131 assemblages in 4130 datasets. Nearly all assemblages have singletons (97.04%)  
 132 and a greatest common divisor of one (99.64%). The assemblages with a greatest  
 133 common divisor above one are not randomly distributed among the datasets:  
 134 96.63% of the datasets have no such assemblages. Some data sets with a high  
 135 proportion of assemblages with a greatest common divisor above are older

136 datasets which may, despite the available metadata, have been digitised with the  
 137 loss of rare taxa and precision. For example, one dataset includes 84 assemblages  
 138 with a median richness of 16 taxa. Count sums vary between 69 and 3201. The  
 139 greatest common divisor is three for all assemblages, that is all 1300 counts  
 140 in the dataset are divisible by three. Excluding such datasets would further  
 141 increase the proportion of assemblages with singletons. Some other Neotoma  
 142 datasets are discussed in a subsequent section.

### 143 *3.2. Estimating the percent sum*

144 The Owen’s Lake dataset (Bradbury 1997) also includes percentages for each  
 145 taxa, allowing the count sums estimated from the percent data to be verified.  
 146 Excluding mono-specific assemblages, for which no meaningful estimate of the  
 147 count sum is possible, the minimum percent method and the direct search  
 148 method correctly estimate the count sum for, respectively, 97.39% and 99.52%  
 149 of the assemblages. The few assemblages that fail the direct search method are  
 150 species poor and have low count sums.

151 The 22 chironomid head capsule assemblage dataset from Last Chance Lake  
 152 (Axford et al. 2017) also includes both the count sums and the percentage of each  
 153 taxa. The percentages are given to two decimal places: to account for rounding  
 154 errors, the countSum package uses the smallest and largest values consistent  
 155 with the reported percentage. With the minimum percent method the estimated  
 156 count sums are, within error, either identical to the reported count sum or twice  
 157 as much (Fig. 2). With the direct search method, the estimated count sums are  
 158 all exactly twice the reported count sum. The factor of two difference is because  
 159 all the counts include half head capsules (but only sometimes is the rarest taxon  
 160 represented by a half head capsule). Reporting half microfossils is common  
 161 for several microfossil groups, including chironomids and pollen (especially for  
 162 bisaccate conifers); occasionally other fractions are reported. Half counts make  
 163 the estimated count too high by a factor of two, so do not risk incorrectly flagging  
 164 count sums as being too small. The direct search method is more precise than  
 165 the minimum percent method as the rounding error is relatively smaller on the  
 166 larger percent values the method uses.

### 167 *3.3. Unexpected count data*

168 Some of the pollen data in the Neotoma database have an inexplicably high  
 169 proportions of assemblages with a greatest common divisor greater than one.  
 170 Here I focus on four datasets produced by the same research group. All the  
 171 datasets, which are relatively recent, include information on the spike used to  
 172 calculate pollen concentration, so cannot have been digitised. The four datasets  
 173 have some assemblages with a greatest common divisor of two interspersed,  
 174 sometimes regularly, amongst assemblages with the expected greatest common  
 175 divisor of one. The assemblages with a greatest common divisor of one typically  
 176 have several singletons (Table 2)).

177 Assemblages with a greatest common divisor of one typically have a higher  
 178 taxonomic richness than assemblages with a greatest common divisor of two

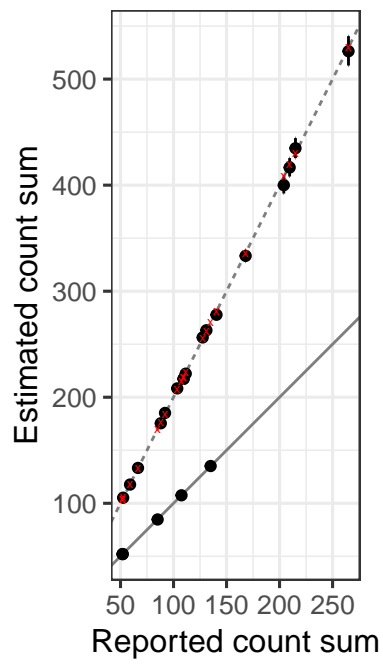


Figure 2: Estimated and reported chironomid count sums by the minimum percent method (solid symbols with error bars) and the direct search method (red crosses) from Last Chance Lake (Axford et al. 2017). Lines show the 1:1 (solid) and 2:1 (dashed) relationships.

Table 2: Caption

dataset	No. assemblages	Median no. taxa	GCD = 1	Median no. singletons (GCD = 1)
1	53	36	0.49	16
2	83	36	0.61	17
3	27	19	0.70	7
4	41	19	0.93	10

(Fig. 3). The latter have a richness that is typically of the former with count sums half as large.

One assemblage with a greatest common divisor of two has 73 taxa. Assuming the distribution of counts is (at least locally) uniform, the probability of  $n$  counts being divisible by  $k$  is  $1/k^n$ : for a single assemblage with this many taxa, the probability is 1 in  $10^{21}$ . The probability that these counts reflect the true nature of the pollen assemblages is exceedingly low; it is far more likely that the data have been mishandled at some stage in some way.

### 3.4. Unexpected percent data

Dataset diatom1 includes 35 diatom assemblages with a median richness of 19 taxa. The associated paper reports that at least 400 valves were counted from each assemblage, which means that singletons should have a relative abundance of 0.25% or less. However, the rarest taxon in two assemblages have a relative abundance of 3.23%, and the relative abundance of all other taxa in these assemblages are, within rounding error, integer multiples of this. If the count sums actually are at least 400, this would imply that each species count in these assemblages is an integer multiple of at least 13. This seems unlikely. Alternatively, the actual count sum for these assemblages could be as low as 31 valves. In total, six assemblages appear to have a count sum below 400 valves.

The archived data include 56 taxa that have a maximum abundance of at least 1.25%; this is about half of the 109 taxa reported in the paper. This pruning of rare taxa will increase the risk of counts without singletons, which would cause the minimum percent method to fail, but will have little impact on the direct search method.

Dataset diatom2 has 71 assemblages with a median richness of 57 taxa. The associated paper reports that the diatom counts included 400–500 valves per assemblage except for four diatom-poor assemblages with at least 100 valves. The direct search method estimates that twelve assemblages have a count sum of less than 400, and three have less than 100. The direct search and minimum percent methods agree, within rounding error, on the estimated count sums, implying that either all assemblages have singletons and count sums are low in some assemblages, or that the greatest common divisor of the raw counts is greater than one. This means that for the assemblage with the minimum percent is 7.14, which has seven taxa, all counts would need to be multiples of 8 for the count sum to be at least 100.

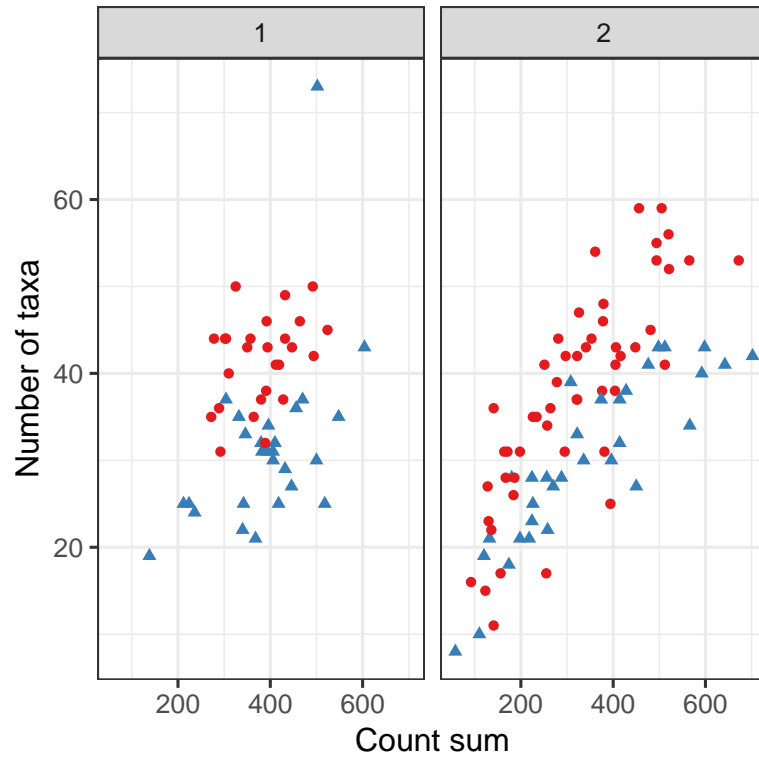


Figure 3: Number of taxa against count sum for assemblages with a greatest common divisor of one (red circles) or two (blue triangles). All four datasets show the same pattern, but it is clearest in datasets 1 and 2 which have the highest proportion of assemblages with a greatest common divisor of two.



214 Dataset chironomid1 has 55 assemblages. Although the associated paper  
215 reports that assemblages with count sums below 50 were discarded, the direct  
216 search method estimates that three assemblages had count sums between 38 and  
217 40. These assemblages are diverse (richness between 15 and 17 taxa), so it is  
218 unlikely that the true counts are double that estimated here and the greatest  
219 common divisor is two.

220 Palaeoceanographic dataset marine1 has 160 assemblages with a median  
221 taxonomic richness of 34.5 taxa. The associated paper reports that assemblages  
222 with count sums below 100 were omitted, and that there were 20 assemblages with  
223 count sums below 200. The direct search method estimates that five assemblages  
224 have count sums below 100 (this excludes one mono-specific assemblage), with  
225 count sums as low as 34. With this dataset, the direct search and the minimum  
226 percent method give identical results for some assemblages but highly divergent  
227 estimates for others, with the direct search method sometimes giving estimates  
228 of several thousand, in one case over two orders of magnitude higher than the  
229 minimum percent method. Some of the divergence appears to be because some,  
230 mainly low diversity, assemblages lack singletons. The most extreme divergences  
231 appear to be data entry errors with incorrect rounding, perhaps during taxonomic  
232 revisions of the percent data rather than the raw counts.

## 233 4. Discussion

234 Analysis of the breeding bird, Owen's Lake, testate amoeba and pollen  
235 data sets has shown that, as expected, the vast majority of community and  
236 assemblages counts should have singletons, and even more should have a greatest  
237 common divisor of one. This means that these characteristics are potentially  
238 useful for identifying data where the count sum is misreported.

239 My search through archived microfossil data found several datasets where  
240 count sums are, or appear to be, smaller than that reported. Some of the count  
241 sums appear to be an order of magnitude below what was reported. The percent  
242 datasets examined are a convenience sample of available data that met the  
243 inclusion criteria. As such, this analysis cannot be used to accurately determine  
244 the prevalence of datasets with possible undercounts, but it appears that a  
245 non-negligible fraction of the literature is affected. It is possible in some cases  
246 that the assemblages with low counts were omitted or merged prior to analysis,  
247 but the number of assemblages reported was not updated. Care was taken to  
248 identify any such cases by, for example, examining stratigraphic diagrams to see  
249 if the low count assemblages were included. In some cases, the assemblages with  
250 low apparent counts can be seen in the published stratigraphic diagrams.

251 It is also possible that the apparently low count sums are a false positive.  
252 This can only happen in assemblages that have a greatest common divisor greater  
253 than one, which is very rare, especially for taxonomically diverse assemblages. If  
254 a dataset contains several taxonomically diverse assemblages that have a greatest  
255 common divisor of two (or especially if greater than two) doubts should be raised  
256 about whether the counts sums are accurately described.

257 Microfossil percent data are often given to two decimal places. This is  
258 sufficient precision for the direct search method to have utility with counts sums  
259 of several thousand. Some data are only given to the nearest percent, which  
260 means that neither method has utility with count sums above 100.

261 The direct search method will fail if the dataset includes taxa calculated  
262 with different count sums, for example pollen sums of trees, shrubs and upland  
263 herbs and a pollen and spore sum that also includes pteridiophytes. It should  
264 be possible to identify such cases from the meta-data and knowledge of usual  
265 practice with different proxies. It will also fail, as show by dataset marine1, if  
266 percentages are incorrectly calculated or rounded.

267 Some taxonomic groups have microfossils that often come in groups of  
268 attached individuals. For example, for each diatom cell has two valves which are  
269 the counting unit. These valves usually separate during processing, but paired  
270 valves are often found, and some taxa such as *Aulacoseira* produce long chains  
271 of strongly bound valves. This might make singletons slightly less likely. The  
272 results from Owen's Lake suggest that this is not an important problem, as most  
273 assemblages have many singletons.

274 Small undercounts in a few assemblages will have minimal impact on the  
275 precision of any palaeoenvironmental reconstruction or other statistics derived  
276 from the assemblage. Substantial undercounts will potentially seriously effect  
277 the precision of the results. Such undercounts might constitute a data handling  
278 error, for example, if samples with low counts were supposed to be merged but  
279 that step was forgotten. Substantial and pervasive under-counting could be  
280 construed as scientific misconduct due to either negligence or falsification, and  
281 action to correct the literature is probably required.

282 Some papers do not report count sums. When this important quality metric  
283 is omitted, the reader should be able to assume that the standard minimum  
284 count sum for the taxonomic group has been used (i.e. 50 for chironomids, several  
285 hundred for pollen and diatoms). If the actual count sums are materially below  
286 this, then this potentially constitutes falsification by omission (Fanelli 2013).

## 287 5. Conclusions

288 A non-negligible fraction of the archived assemblage data includes counts  
289 that appear to have a count sum below that reported in the paper. Some of the  
290 apparent counts are small enough that the uncertainty of the count and derived  
291 statistics will be substantially larger than expected. These results highlight the  
292 importance of archiving both the raw data and the code required to process the  
293 data.

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