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Comparison of sediment biomarker signatures generated using time-integrated and discrete suspended sediment samples

Hari Ram Upadhayay*, Steven J. Granger, Adrian L. Collins

Net Zero and Resilient Farming, Rothamsted Research, North Wyke, Okehampton, EX20 2SB UK.

*Correspondence:

Hari Ram Upadhayay (hari.upadhayay@rothamsted.ac.uk)

Tel: +44 (0)1837512260

1 Abstract

2 Sediment source fingerprinting using biomarker properties has led to new insights in
3 our understanding of land use contributions to time-integrated suspended sediment samples at
4 catchment scale. A time-integrated mass-flux sampler (TIMS; also known as the ‘Phillips’
5 sampler), a cost-effective approach for suspended sediment collection *in situ*. Such samplers
6 are being used to collect sediment samples for source fingerprinting purposes, including by
7 studies using biomarkers as opposed to more conventional tracer properties. Here, we assessed
8 the performance of TIMS for collecting representative sediment samples for biomarkers during
9 high discharge events in a small lowland agricultural catchment. Concentrations of long odd-
10 chain n-alkanes ($>C_{23}$) and both saturated free and bound fatty acids (C_{14} - C_{32}), as well as
11 compound-specific ^{13}C were compared between sediment collected by both TIMS and auto-
12 samplers (ISCO). The results showed that concentrations of alkanes, free fatty acids and bound
13 fatty acids are consistently comparable between TIMS and ISCO suspended sediment samples.
14 Similarly, compound-specific ^{13}C signals were not found to be significantly different in the
15 suspended sediment samples collected using the different samplers. However, different
16 magnitudes of resemblance in biomarker concentrations and compositions between the samples
17 collected using the two sediment collection methods were confirmed by overlapping index and
18 symmetric coordinates-based correlation analysis. Here, the difference is attributed to the
19 contrasting temporal basis of TIMS (time-integrated) vs ISCO (discrete) samples, as well as
20 potential differences in the particle sizes collected by these different sediment sampling
21 methods. Nevertheless, our findings suggest that TIMS can be used to generate representative
22 biomarker data for suspended sediment samples collected during high discharge events.

23 **Keywords** Source fingerprinting, Alkanes, Fatty acids, Sediment, Biotracers

24

25 Introduction

26 Excessive suspended sediment in aquatic ecosystems can have significant impacts on
27 their water quality and integrity (Bilotta & Brazier 2008, Yi et al. 2008). Human activity,
28 particularly land use change, combined with the increasing occurrence of extreme precipitation,
29 has caused a significant increase in soil erosion and sediment delivery to many aquatic systems
30 (Owens, 2020). Elevated suspended sediment concentrations (SSC) contribute directly to the
31 degradation of aquatic systems through reductions in ecosystem productivity resulting from
32 elevated turbidity and concomitant decreased light transmission through the water column
33 (Walling and Collins, 2016) and indirectly, via associated nutrients and contaminants which
34 bind to fine-grained sediments causing additional reductions in water quality.

35 Although much is known about the soil erosion processes and rates that occur in
36 agricultural and forest systems (Labrière et al. 2015, Montgomery 2007), attention has shifted
37 to understanding the relative contributions of different land use types to total suspended
38 sediment fluxes at the catchment scale (Collins et al. 2020, Collins et al. 2017). Here, improved
39 understanding of which land uses are dominant in contributing to elevated sediment fluxes can
40 support better targeting of management. Various tracers, such as radionuclides, stable isotopes,
41 mineral magnetics, colour, and biomarkers have been used to characterise sediments which,
42 have in turn, led to new insights in the understanding of the contributions of the different
43 sources areas of suspended sediment in catchments (Collins et al. 2020). These tracers can
44 provide information on the delivery pathways and slope-to-channel connectivity at catchment
45 scale (Upadhyay et al. 2020). Where tracers are applied using the sediment source
46 fingerprinting approach, the contributing sediment source areas are deconvoluted using an
47 unmixing model by comparing the composite tracers of the suspended sediment directly with
48 those of the potential catchment sediment sources. The reliability and robustness of this
49 approach therefore, depends upon the collection of a representative suspended sediment

50 sample, meaning that the sampling of suspended sediment for the analysis of tracers (i.e.,
51 fingerprint properties) is a critical task.

52 One widely-used method for collecting suspended sediment samples is the deployment
53 of a time-integrated mass-flux sampler (TIMS), also known as a 'Phillips' sampler (Phillips et
54 al. 2000). The TIMS collects suspended sediment due to the large reduction in water flow
55 velocity that occurs within it, compared to that of the watercourse. This is because the flow
56 inlet of the sampler is far smaller than the sampler's main chamber diameter. The sediment
57 sample collected by the TIMS integrates a sample of the suspended sediment flux throughout
58 the sampling period (low to high flows) and has been reported to collect representative
59 suspended sediment samples in the case of geochemical, physical and magnetic properties
60 (Russell et al. 2000, Smith & Owens 2014), for diatom communities (Foets et al. 2020) and for
61 quantifying suspended sediment transfer(Reference). One drawback to the TIMS however, is
62 that it has been shown to preferentially collect coarse sediment grains which can potentially
63 lead to an underestimation of the total suspended sediment flux at catchment scale (Perks et al.
64 2014, Smith & Owens 2014). Nevertheless, the TIMS is simple, cost effective, and easy to
65 deploy in a wide range of riverine environments and, as such, widely used to collect sediment
66 for sediment source apportionment.

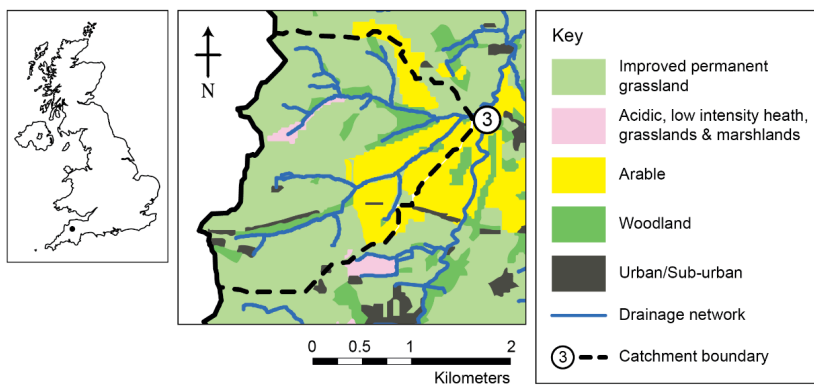
67 To date, no studies have examined whether sediment collected using TIMS is
68 sufficiently representative for the application biomarker analysis in conjunction with the
69 sediment source fingerprinting approach. This evidence gap is important since a growing
70 number of source fingerprinting studies are using biomarkers, as opposed to more conventional
71 sediment properties (Gibbs, 2008; Upadhayay et al., 2017; Collins et al., 2020). The potential
72 underrepresentation of fine-grained sediment in samples collected using TIMS noted by
73 previous studies could also create a bias when using biomarkers to trace suspended sediment
74 sources. This is because biomarkers, like other tracers, tend to adsorb preferentially to the fine-

75 grained particles (Upadhayay et al. 2020). Given this context we present a detailed evaluation
76 of the biomarker tracer composition of suspended sediment collected using TIMS compared
77 to that collected using a conventional auto-sampler in a field setting.

78 **Materials and Methods**

79 *Study catchment description*

80 The study was undertaken within the upper River Taw observatory (URTO), an
81 instrumented catchment within the headwaters of the River Taw in southwest England
82 (<https://www.rothamsted.ac.uk/projects/upper-river-taw-observatory-urto>) more details about
83 which can be found in Granger et al. (2023). In short, the URTO consists of a 19 km stretch
84 of the river that drains an area of 41.3 km² which is monitored at the catchment outlet for
85 discharge (Q) and various other physio-chemical parameters, including turbidity, on a 15-
86 minute timestep. Two further nested sub-catchments are monitored within the URTO which
87 are 4.4 and 1.7 km² in size. This study was undertaken using the 4.4 km² catchment referred to
88 as Catchment 3 in Granger et al. (2023) and hereafter (Figure 1). River hydrology is primarily
89 surface water driven and Q tends to be flashy in response to rainfall events while base flow is
90 maintained during extended dry periods by water released through rock fissures. The soils of
91 the study catchment are typically poorly draining, seasonally waterlogged clay-rich gley soils
92 and brown earths and the dominant land use was improved grassland (71%) for animal grazing,
93 but with a significant proportion of arable land (18%) and some woodland (10%) (Fig. 1).



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94
95 **Fig. 1** Location of the Upper River Taw Observatory within the UK and the land use in the
96 nested sub-catchment (Catchment 3)

97
98 ***Storm event sampling***

99 Storm events were targeted based on meteorological forecasts. Prior to a predicted
100 event, two TIMS were placed in stream flow at the outlet to Catchment 3. Sample lines of
101 automated samplers (Teledyne ISCO, NE, U.S.A.) were also placed instream and autosamplers
102 were set to collect 1 L samples at timesteps of either 30 or 60 minutes depending on the
103 expected duration and size of the forecast wet weather event. The autosamplers were also
104 configured to ensure that sample collection occurred at the same time as a Q and turbidity
105 measurement was taken. Once Q had dropped to a safe level, the TIMS were removed from the
106 channel and their contents bulked into a collection barrel. Autosamplers were also stopped at
107 this time and their samples taken back to the laboratory along with the TIMS samples.

108 ***Sample processing***

109 Once back at the laboratory, autosampler samples had a 250 ml sub-sample removed
110 for measurement of various chemical and physical parameters including SSC through the
111 filtration and subsequent drying at 105°C of a known sample volume on a pre-weighed GF/C
112 filter paper (UK Standing Committee of Analysts, 1980). The SSC data from these, and other

113 sampled storm events at Catchment 3, were then combined with the turbidity measurements
114 recorded at those times to develop a calibration curve which enabled all recorded 15-min time
115 step turbidity measurements to be converted to SSC. The remaining 750 ml of each autosampler
116 sample was bulked in barrels. Both bulked samples were left for several days in a refrigerated
117 environment to allow sediment to settle. Once the bulk of the sediment had settled to the bottom
118 of the barrels, the remaining water was removed and passed repeatedly through a portable
119 centrifuge to collect any remaining fine-grained particulate material. This material was then
120 added to the previously separated sediment and water was further removed using a laboratory
121 based static centrifuge until the material was about 500 ml in volume. This material was then
122 frozen at -20°C and subsequently freeze dried before being sieved through a 32 µm mesh. The
123 suspended sediment samples collected by the autosampler and TIMS, are hereafter referred to
124 as ISCO and TIMS sediment, respectively.

125 ***Biomarker extraction and analysis***

126 Bulk sediment carbon (C) and nitrogen (N) content and their stable isotope ratios were
127 measured using a Carlo Erba NA2000 elemental analyser (CE Instruments, Wigan, UK)
128 interfaced with a PDZ Europa 20-22 isotope ratio mass spectrometer (SerCon Ltd., Crewe,
129 UK). The isotopic results were expressed as natural abundance (δ) in parts per mil (‰)
130 compared to international standards. The elemental and isotopic reference standard used was
131 IAR001 (%N = 1.791; %C = 40.46; $\delta^{15}\text{N}$ = 2.51‰; $\delta^{13}\text{C}$ = -25.99‰), a wheat flour standard
132 sourced from Iso-Analytical, and calibrated against IAEA-N-1 and IAEA-CH6. The analytical
133 precision for elemental and isotopic reference standards were 0.42% and 0.2‰ for C and 0.03%
134 and 0.2‰ for N, respectively.

135 The detailed methodology for the biomarker extraction from sediment samples and
136 subsequent analyses can be found in Upadhayay et al. (2022). Briefly, total free lipids
137 (combined fatty acids (FA) and alkanes) were extracted from the sediment samples using

138 dichloromethane:methanol (9:1) by an accelerated solvent extraction machine (Donex 350)
139 with three extraction cycles at 100°C. Hydrolysable FAs (also known as bound fatty acids)
140 were then released from solvent extracted residues (~1 g; spiking with C₁₉ FA) by treatment
141 with 0.5 M KOH in methanol:water (9:1; 100°C for 2 h) using a reflux method. The
142 concentrations of alkanes were quantified using an Agilent 7890A GC with a flame ionization
143 detector, whereas free (FFA) and bound (BFA) fatty acid concentrations were determined using
144 an Agilent 6890 N/5973 N GC Mass Spectrometer. The reliability of the extraction process
145 was checked by running a sediment sample spiked with an external standard containing FA C₁₉
146 and alkane C₃₄. The compound-specific $\delta^{13}\text{C}$ signatures of alkanes, FFAs and BFAs were
147 determined using a Finnigan Mat 6890 GC coupled to a Finnigan Mat Delta Plus IRMS via a
148 Combustion III interface and the $\delta^{13}\text{C}$ was expressed relative to Vienna Pee Dee Belemnite
149 (VPDB). The stability and linearity of the system were better than 0.06‰. The $\delta^{13}\text{C}$ standard
150 deviation from the standards was $\pm 0.35\%$. The $\delta^{13}\text{C}$ values of FAs were corrected for the
151 contribution of $\delta^{13}\text{C}$ values of the added methyl group during derivatisation. For the purposes
152 of this study, we considered only long (>C₂₃) odd-chain n-alkanes, saturated FFAs and
153 saturated BFAs (C₁₄-C₃₂) due to their relevance for sediment source apportionment using the
154 fingerprinting approach (Collins et al. 2020, Upadhayay et al. 2017).

155

156 ***Statistical analysis***

157 A two-sample t-test was used to differentiate between ISCO and TIMS sediment for
158 bulk C and N properties, biomarker content and compound specific $\delta^{13}\text{C}$. The overlapping
159 index (similar area-under-the-curve of density distributions) was estimated (Pastore &
160 Calcagnì 2019) for quantifying similarities or differences between biomarker/isotope
161 distributions in TIMS and ISCO sediment samples. The overlapping index ranges from 0 to 1,
162 where 1 represents 'similar' in terms of variable distribution and 0 indicates 'distinct'. This

163 index does not assume the normality of distributions nor any other distributional form and
164 works properly even in the presence of multimodality (Pastore & Calcagni 2019). Besides
165 absolute biomarker concentrations, biomarker data were also considered in terms of their
166 composite nature as each biomarker is part of the whole and provides relative information.
167 Therefore, symmetric coordinates (a specific type of log-ratio transformation) (Kynčlová et al.
168 2017, Reimann et al. 2017) were calculated before correlation analysis, which was conducted
169 separately for alkanes, FFAs and BFAs of the ISCO and TIMS sediment. This approach was
170 adopted since it addresses the potential for the hidden influence of unaccounted biomarkers in
171 the composition. All statistical analysis were performed in R (R Core Team 2022) using
172 packages “robComposition” (Templ et al. 2011) and “Overlapping” (Pastore 2018). All figures
173 for presenting results were designed using the package “ggplot2” (Wickham 2009).

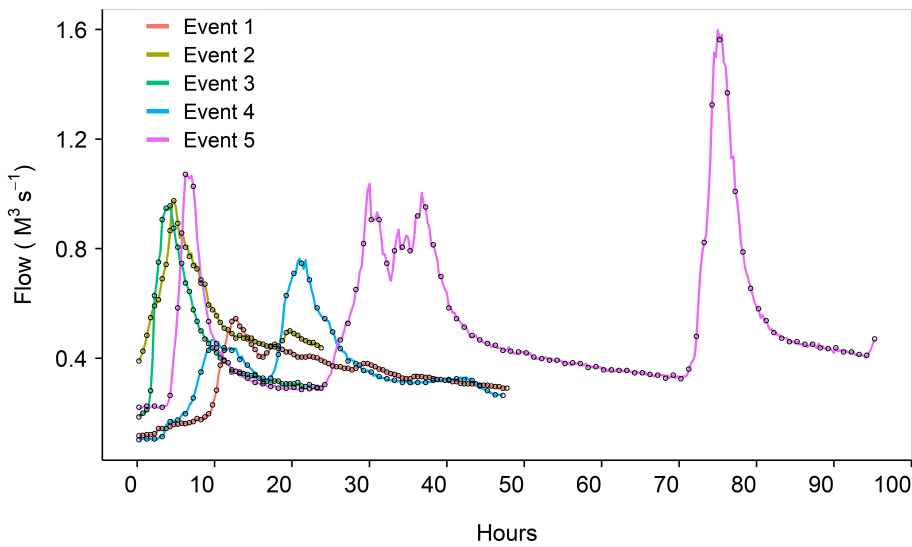
174 **Results and Discussion**

175 *Event characteristics*

176 Summary data for the five events reported in this study are contained within Table 1.
177 The five storm events differed in magnitude with peak recorded Q ranging between 0.5 to 1.6
178 m³ s⁻¹; the smallest event being Event 1 and the largest Event 5. While higher Q is typically
179 associated with higher SSC this was not observed in the case of the study events. While Event
180 5 had the highest recorded peak Q and the highest recorded peak SSC, events with lower peak
181 Q values sometimes had higher SSC concentrations than those events with higher peak Q (e.g.,
182 Events 3 and 4). These hydro-sedimentological responses can be due to a number of different
183 factors such as land cover and use, antecedent soil moisture and rainfall intensity, all of which
184 affect soil erosion and sediment connectivity to the stream channel (Upadhayay et al. 2022).
185 Events 1 to 3 represent simple hydrographs (Fig. 2) with rapidly rising Q in response to rainfall,
186 and a most attenuated decrease in Q. Events 4 and 5, however, are multi-peaked hydrographs

187 (Fig. 2) representing periods of time where Q rises and falls in response to different periods of
188 rainfall. In all cases, peak SSC occurred on, or just before, peak Q.

189 The masses of material collected by the TIMS and ISCO sampling approaches were measured
190 simply by measuring the mass of material left after freeze drying. Typically, the mass of
191 material collected by each approach increased with the increasing load of suspended sediment
192 transported during each event.



193
194 **Fig. 2** Hydrograph of five high storm events used to collect sediment by deploying ISCO and
195 TIMS in Lower Ratcombe stream. Open circles indicate ISCO sampling times

196

197

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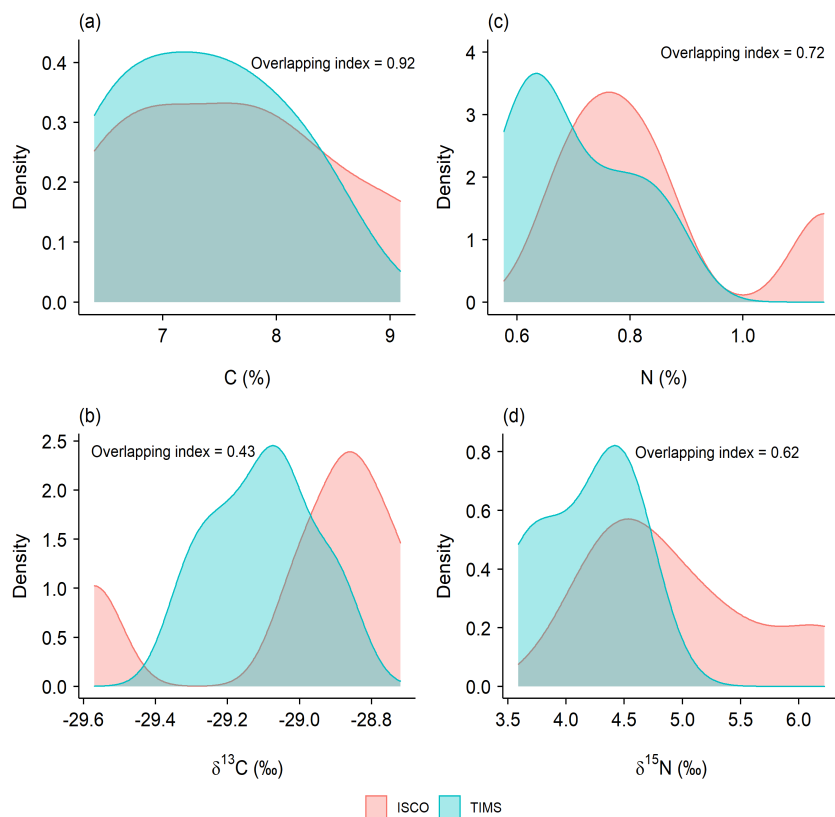
199 **Table 1** Summary data for the five storm events sampled using both ISCO and TIMS sampling
 200 methodologies.

Event ID	Date	Sampling duration	Flow (m ³ s ⁻¹)	SSC (mg l ⁻¹)	Event suspended sediment load (t)	ISCO Sampler frequency	Sediment sample mass (g)		Event load sampled by TIMS (%)
							ISCO	TIMS	
1	06/11/2018	47h 30min	0.1 – 0.5	0 - 128	1.3	30min	1.6	2.1	1.6 x 10 ⁻⁴
2	18/12/2018	23h 30min	0.4 – 1.0	9 - 101	1.5	30min	1.3	2.4	1.6 x 10 ⁻⁴
3	12/03/2019	23h 30min	0.2 – 1.0	6 - 490	3.9	30min	-	-	-
4	25/10/2019	47h 0min	0.1 – 0.8	4 - 546	6.3	1h	3.2	11.4	1.8 x 10 ⁻⁴
5	13/01/2020	95h 0min	0.2 – 1.6	6 - 826	18.9	1h	4.6	12.7	6.7 x 10 ⁻⁵

201

202 ***Bulk sediment data***

203 The C and N content of the suspended sediment samples collected using the ISCO (7.6
 204 ± 1.0%, 0.8 ± 0.2%, respectively) and TIMS (7.3 ± 0.8%, 0.7 ± 0.1, respectively) were not
 205 statistically different. However, when the data was compared using the overlap of the area-
 206 under-the-curve of density distributions (Fig. 3), differences were more apparent. While the C
 207 content of suspended sediment collected using the two different methods appears similar
 208 (overlapping index = 0.92), the N content of the samples was less so (overlapping index = 0.72)
 209 (Fig. 3 a and c). While there is no evidence in the literature pertaining to differences in the bulk
 210 N content of suspended sediment collected using these different methods, researchers have
 211 reported that sediment collected using TIMS compared to other sampling approaches can have
 212 both similar (Russell et al., 2000) and dissimilar (Keßler et al., 2020) bulk C contents. The two
 213 different sediment samples were also not significantly different in the case of their δ¹³C and
 214 δ¹⁵N signatures. However, values of 0.43 and 0.62 for the overlap index for the density
 215 distributions of δ¹³C and δ¹⁵N values (Fig. 3 b and d), respectively, suggest that the isotopic
 216 values in sediment collected using the two different approaches differed, possibly due to the
 217 corresponding differences in the temporal basis of the samples (i.e., time-integrated vs discrete)
 218 as well as potential differences in the particle size distributions of the different samples.



219
 220 **Fig. 3** Comparisons of the density distributions of carbon (a) and nitrogen (c) content and
 221 their respective isotope values (b) and (d) in the ISCO and TIMS sediment samples, using the
 222 overlapping index

223 ***Compound-specific signatures***

224 *Comparison of general concentrations*

225 The results for the concentrations of alkanes, FFA and BFA in the suspended sediment
 226 samples collected using the ISCO and TIMS generally showed no significant differences
 227 (Table 2). Concentrations of BFA C₂₆ and C₂₈ were, however, significantly higher in sediment
 228 collected using the TIMS compared to the ISCO. Despite the similarity of the alkane, FFA, and
 229 BFA concentrations between the TIMS and ISCO sediment samples, compounds were found

230 to differ when examined using the overlap of the area-under-the-curve of density distribution.
 231 More specifically, for alkanes, the overlap ranged between 0.49 – 0.82, for FFAs the overlap
 232 was slightly higher, ranging between 0.65 – 0.92, while the overlap range for BFA was
 233 extremely wide ranging from 0.19 – 0.82.

234

235 **Table 2** Distribution of biomarkers content and their $\delta^{13}\text{C}$ values in the ISCO and TIMS
 236 sediment samples. Bold figures indicate significantly different at $\alpha = 0.05$.

Compound	C-chain length	Content ($\mu\text{gC/g}$ sediment)		Overlapping index	$\delta^{13}\text{C}$ (‰)		Overlapping index
		ISCO	TIMS		ISCO	TIMS	
Alkanes	C ₂₃	1.0 ± 0.2	1.2 ± 0.4	0.82	-32.4 ± 1.3	-32.4 ± 2.0	0.39
	C ₂₅	3.4 ± 1.6	3.2 ± 0.6	0.71	-32.1 ± 1.5	-32.2 ± 1.3	0.83
	C ₂₇	8.5 ± 3.1	8.4 ± 1.1	0.71	-32.3 ± 1.3	-32.5 ± 1.4	0.85
	C ₂₉	11.0 ± 3.3	10.6 ± 1.3	0.49	-34.8 ± 1.6	-34.9 ± 1.5	0.96
	C ₃₁	9.1 ± 2.7	8.4 ± 1.3	0.78	-35.9 ± 1.1	-36.2 ± 1.7	0.82
	C ₃₃	3.8 ± 1.3	3.2 ± 0.5	0.73	-35.3 ± 1.5	-36.3 ± 0.6	0.55
Free fatty acids	C ₁₄	10.0 ± 4.9	5.5 ± 2.9	0.65	-29.3 ± 1.3	-30.6 ± 0.6	0.49
	C ₁₆	51.6 ± 16.1	36.6 ± 11.1	0.59	-30.1 ± 1.0	-30.4 ± 0.4	0.84
	C ₁₈	51.4 ± 30.2	34.5 ± 20.9	0.65	-31.5 ± 1.1	-31.5 ± 0.4	0.65
	C ₂₀	12.7 ± 4.1	10.3 ± 3.4	0.78	-33.5 ± 0.7	-34.2 ± 0.3	0.53
	C ₂₂	23.0 ± 3.8	21.2 ± 3.7	0.85	-34.4 ± 0.8	-34.8 ± 0.4	0.78
	C ₂₄	28.5 ± 3.9	26.8 ± 3.7	0.89	-34.3 ± 0.6	-34.9 ± 0.3	0.49
	C ₂₆	38.1 ± 6.7	35.5 ± 5.2	0.92	-35.5 ± 0.6	-35.6 ± 0.3	0.81
	C ₂₈	35.5 ± 4.5	36.0 ± 5.1	0.91	-35.5 ± 0.5	-35.5 ± 0.3	0.87
	C ₃₀	25.5 ± 3.9	26.0 ± 3.4	0.92	-36.4 ± 0.4	-36.4 ± 0.4	0.88
	C ₃₂	11.5 ± 2.5	11.5 ± 1.8	0.70	-37.6 ± 0.5	-37.5 ± 0.4	0.65
Bound Fatty acids	C ₁₄	16.3 ± 4.9	12.7 ± 4.2	0.82	-32.3 ± 0.6	-33.7 ± 0.8	0.42
	C ₁₆	94.9 ± 12.9	99.3 ± 45.7	0.63	-31.5 ± 0.8	-32.5 ± 0.6	0.39
	C ₁₈	40.0 ± 5.2	45.9 ± 21.1	0.62	-32.1 ± 0.4	-31.9 ± 0.4	0.83
	C ₂₀	8.3 ± 1.1	9.4 ± 0.8	0.41	-34.1 ± 0.8	-33.8 ± 0.7	0.78
	C ₂₂	14.4 ± 2.7	19.6 ± 5.4	0.37	-34.0 ± 0.5	-34.1 ± 0.4	0.56
	C ₂₄	10.8 ± 2.0	14.1 ± 2.5	0.19	-34.7 ± 0.2	-35.0 ± 0.9	0.58
	C ₂₆	8.2 ± 2.0	11.1 ± 1.7	0.56	-35.2 ± 0.5	-34.9 ± 0.5	0.88
	C ₂₈	7.2 ± 1.7	10.1 ± 1.4	0.47	-34.6 ± 0.5	-34.9 ± 0.4	0.87
	C ₃₀	3.1 ± 0.8	4.4 ± 0.9	0.68	-35.0 ± 0.7	-35.5 ± 0.9	0.72
	C ₃₂	1.2 ± 0.2	1.6 ± 0.5	0.28	-32.0 ± 0.2	-32.7 ± 0.7	0.16

237

238

239

240 *Compound-specific n-alkanes*

241 Alkanes are neutral lipids derived from plant waxes with different numbers of C atoms
242 in the molecules that are indicative of different origins. Long-chain ($>C_{27}$) n-alkanes are
243 derived from the waxes of terrestrial plants (Chikaraishi & Naraoka 2003), medium-chain
244 length ($C_{21} - C_{25}$) n-alkanes are produced by lower plants and aquatic macrophytes (Tolosa et
245 al. 2013), while short chain-length ($C_{15} - C_{19}$) n-alkanes are typically derived from aquatic
246 algae (Bianchi & Canuel 2011). Differences in the n-alkane composition between the ISCO
247 and TIMS sediment samples are illustrated in Fig. 4 (a) and (b). We observed strong
248 correlations of n-alkanes, with three clusters in the ISCO samples (C_{27}/C_{25} , C_{33}/C_{31} and C_{23}/C_{33})
249 but only two major clusters ($C_{27}/C_{29}/C_{31}$ and $C_{23}/C_{25}/C_{33}$) in the TIMS sediment samples. This
250 indicates that the ISCO and TIMS sediment samples are different in terms of alkane
251 composition. The study catchment is dominated by grassland and arable land uses (89%) (Fig.
252 1) and C_{31} and C_{33} n-alkanes have been reported to be dominant in such environments (Schäfer
253 et al. 2016). This suggests that sediment collected by the ISCO sampling approach better
254 represents the land use of the study catchment in terms of the composition of the n-alkane
255 signature.

256 *Compound-specific fatty acids*

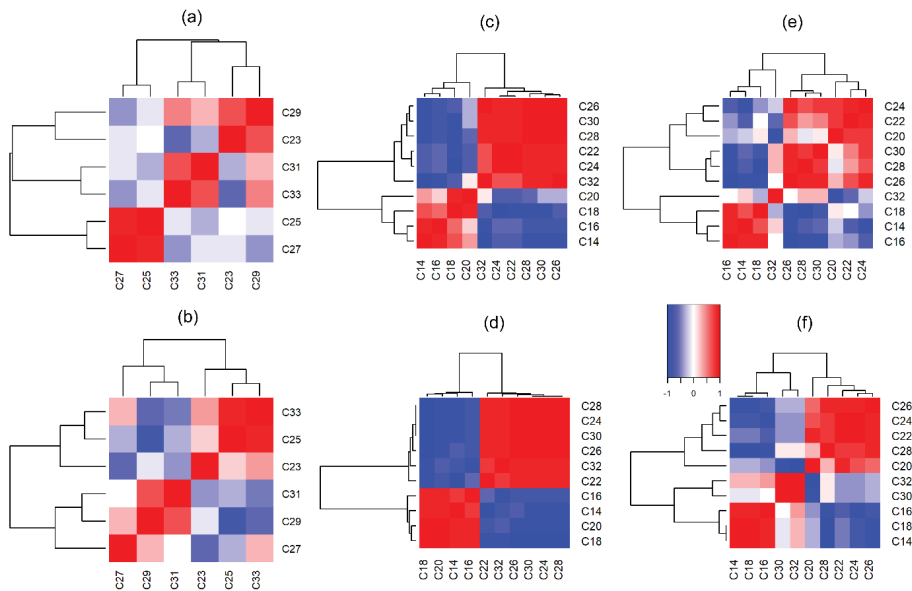
257 Differences also existed between the FFA composition of the ISCO and TIMS sediment
258 samples (Fig. 4 (c) and (d)). We observed two major clusters ($\leq C_{20}$ and $\geq C_{22}$) in the ISCO and
259 TIMS sediment samples consistent with their potential sources. Short-chain FFAs ($\leq C_{20}$) are
260 produced by all plants and also microorganisms, whereas long-chain FFAs ($>C_{22}$) are mostly
261 derived from vascular terrestrial plants (Chikaraishi 2014, Upadhayay et al. 2017) and therefore
262 long chain FFAs are good indicators of terrestrial sediment sources. Long-chain FAs were more
263 highly correlated with each other in the TIMS sediment samples compared to those collected

264 using the ISCO, with two major clusters of FFA observed in both the TIMS and ISCO
265 sediments (Fig. 4 (c) and (d)). The strong correlation in long-chain FFA is consistent with the
266 higher abundance of $>C_{22}$ FFA reported in grass/arable land compared to deciduous forest
267 (Schäfer et al. 2016, Zocatelli et al. 2012) and suggests that the TIMS collected a more
268 representative sample of sediment than the ISCO in terms of FFAs. Such FFAs are relatively
269 newly produced plant products and are delivered, along with fine-grained sediment, to
270 watercourses.

271 Bound FAs, which represent FAs not extracted by the solvents used to extract FFAs,
272 include both the breakdown products of other lipids and also previously FFAs which have
273 become strongly associated with soil particles (Upadhyay et al. 2022). This BFA pool
274 typically represents a relatively older FA pool than FFAs, often with a lower $\delta^{13}C$ signature
275 due to fractionations associated with FA cycling. Fatty acids can undergo selective microbial
276 degradation in soil, such as odd-C numbered FAs produced by microbial α -oxidation of even-
277 C numbered FAs (Matsumoto et al. 2007). Different clusters were observed in the BFAs
278 compared to the FFAs for the ISCO and TIMS sediment samples (Fig. 4 (e) and (f)).
279 Importantly, the clusters found in the BFAs ($C_{16}/C_{14}/C_{18}$, $C_{26}/C_{28}/C_{30}$ and $C_{20}/C_{22}/C_{24}$) were
280 consistent with their potential land use sources in the study catchment. The results exhibited
281 three clusters of BFAs based on correlation analysis in the TIMS sediment samples (C_{14}/C_{18} ,
282 C_{20}/C_{28} and C_{30}/C_{32}), still consistent with their potential catchment sources. Overall, the C_{26}
283 and C_{28} FA signatures in the TIMS sediment samples (Table 2) were found to be similar to
284 those of the grassland surface soils (e.g., C_{max} is at C_{26} for long-chain fatty acids) close to the
285 study catchment (unpublished data). This further suggests that TIMS can collect representative
286 sediment-associated FA signatures in the study catchment.

287 The $\delta^{13}C$ values of the n-alkanes, FFA and BFA were not significantly different for the
288 ISCO and TIMS sediment samples. The $\delta^{13}C$ values of the biomarkers suggested that they

289 originated from C3 plants (Matsumoto et al. 2007). However, although the $\delta^{13}\text{C}$ values of the
 290 biomarkers in the TIMS and ISCO sediment samples were not significantly different, they were
 291 not highly similar based on the overlap of the area-under-the-curve of the corresponding
 292 density distributions. Here, the overlapping index ranges were 0.39 - 0.96, 0.49 - 0.88 and 0.16
 293 - 0.88 for n-alkanes, FFAs and BFAs, respectively (Table 2). This clearly suggests that the $\delta^{13}\text{C}$
 294 distributions differ between the ISCO and TIMS sediment samples.



295
 296 **Fig. 4** Heat-map of correlations based on symmetric coordinates for the alkane ((a) and (b)),
 297 free fatty acid ((c) and (d)) and bound fatty acid ((e) and (f)) data for the ISCO (upper panel)
 298 and TIMS (lower panel) sediment samples. Biomarkers along the axes are sorted according to
 299 the results of the cluster analysis.

300 **Implications for sediment source assessment**

301 The mass of material collected by the ISCO autosamplers is dependent upon the sample
 302 frequency and volume. In our study, the time normalised mass of sediment collected by ISCO

303 was between 28 to 38% less material than the TIMS (Table 1). This means that more material
304 was available for the extraction of biomarkers and other analytes when sediment was sampled
305 using the TIMS. This is one reason why TIMS have been adopted so widely for sediment source
306 fingerprinting purposes (Collins & Walling 2004). One potential issue identified for the TIMS
307 sampler, however, concerns the underrepresentation of the finest particles in the time-
308 integrated sediment sample (Foets et al. 2020, Smith & Owens 2014), although, findings are
309 contradictory in the sense that some researchers have reported similar particle size distributions
310 in TIMS sediment samples compared with other samples (Goharrokhi et al. 2019).

311 Both biomarker content (Chen et al. 2016) and their stable isotope ratios (Upadhayay
312 et al. 2022) have been used for sediment source apportionment. This study has shown that the
313 biomarker content and the $\delta^{13}\text{C}$ are not significantly different for sediment samples collected
314 using the ISCO autosampler and the TIMS, but that the distribution of different biomarkers
315 was often different (Table 2). Moreover, biomarker composition is not similar for the ISCO
316 and TIMS sediment samples (Fig. 3) which may indicate biases in the different relative source
317 contributions to the sediment collected by these different sample collection approaches.
318 Therefore, researchers should be cautious when using different sediment sampling approaches
319 when drawing conclusions on the sediment source area contributions using biomarkers and
320 associated indices. To the best of our knowledge, this is the first study comparing biomarker
321 contents and their stable isotope ratios in samples collected using ISCO and TIMS approaches.
322 We inevitably must interpret our data based on the knowledge of what we would expect to find
323 given the known potential sediment sources in the study catchment. Here, the n-alkane and FA
324 concentrations and compositions in sampled sediment depends on the predominant vegetation
325 type of the study catchment and the potential corresponding sediment sources therein. Based
326 on the catchment land use information, we argue that TIMS can collect representative samples
327 for generating sediment-associated biomarker signatures in the study catchment during the high

328 discharge events responsible for soil erosion and sediment delivery, especially in the case of
329 FFA and BFA. However, one potential issue with the TIMS (and indeed the ISCO) is that
330 differences in the geochemical compositions of sediment collected in shallow and deep water
331 using the sampler have recently been reported and attributed to hydrodynamic sorting (Lučić
332 et al. 2021). Further research is therefore warranted to explore how the position of TIMS in the
333 water column and channel cross section, especially in larger river systems, impacts on the
334 biomarker composition and compound-specific stable isotope values assembled for sediment
335 samples.

336 **Conclusions**

337 Alkanes and FAs are biomarkers with increasing adoption in sediment source
338 apportionment studies for aquatic ecosystems. In this study, we have provided insights into the
339 comparability of biomarker content and their ^{13}C signals in sediment samples collected using
340 an ISCO autosampler and a TIMS. We found that whilst biomarker content and the
341 corresponding ^{13}C signals were not significantly different in the sediment samples collected
342 using the ISCO and TIMS approaches, biomarker distributions and compositional patterns
343 were often not similar. Heterogeneity in biomarker composition might emerge in ISCO and
344 TIMS sediment samples due to differences in the corresponding sediment sampling intervals.
345 The sediment collected using an ISCO represents discrete sediment samples taken at a constant
346 time interval in contrast to the TIMS which continuously samples sediment *in-situ* throughout
347 the period of deployment. More work is needed to explore the sensitivity of source
348 apportionment estimates to the potential contrasts in biomarker signatures generated using
349 different sediment sampling procedures. Overall, the TIMS was found to collect a
350 representative sediment sample based on biomarkers content. As such, the use of TIMS to
351 collect time-integrated sediment samples for analysis of biomarker signatures can broaden our

352 knowledge of sediment sources in catchments impacted by various anthropogenic and natural
353 perturbations.

354

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361 **Data availability**

362 The datasets analysed in this study are available from the corresponding author on request.

363 **Compliance with ethical standards**

364 Ethical approval: Not applicable; Consent to participate: Not applicable; Consent to publish:
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366 **Statements and Declarations**

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372 Sample collection and preparation were performed by [Steve Granger]. Biomarker extraction
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377

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Commented [SG1]: Some of these Journal titles have been shortened/abbreviated, while others remain in full. I suspect the journal will stipulate one of the other