Digitally improving the identification of aquatic macroinvertebrates for indices used in biomonitoring

Ruan C.J. Koen[1*], Frederik J. Koen[1], Nicholas B. Pattinson[2], Chris W.S. Dickens[3], and P. Mark Graham[2,4,5]

[1]*North-West University (NWU), Potchefstroom, South Africa*
[2]*GroundTruth, Pietermaritzburg, South Africa*
[3]*International Water Management Institute (IWMI), Colombo, Sri Lanka*
[4]*University of Kwa-Zulu Natal (UKZN), Pietermaritzburg, South Africa*
[5]*United Nations University, KZN Regional Centre of Expertise (UNU-RCE), South Africa*

INFO

ABSTRACT

This report provides an overview of the mini Stream Assessment Scoring System (miniSASS) and South African Scoring System Version 5 (SASS5) as biomonitoring techniques for assessing the ecological condition of streams and rivers based on the identification of aquatic macroinvertebrates. While miniSASS relies on minimally trained citizen scientists to identify macroinvertebrates at the Order-level, SASS5 utilizes expertly accredited practitioners for finer resolution, even up to the family-level. However, the reliance on citizen scientists for miniSASS identification introduces limitations in terms of precision, accuracy, and reliability. To address these limitations, ongoing developments within the CGIAR Initiative on Digital Innovation include the creation of a miniSASS smartphone application, an upgraded website, an interactive online course, and a machine-learning identification algorithm to assist with photo identification. Additionally, a revised dichotomous key has been developed to improve operator identification during miniSASS surveys. Furthermore, the potential for upscaling the machine-learning identification algorithm to assist in identifying the 91 family-level taxa used in SASS5 assessments has been explored. The outcomes of these developments and explorations presented in this paper aim to enhance the overall effectiveness and reliability of both the miniSASS and SASS5 techniques. By leveraging digital innovation and incorporating machine-learning technology, we anticipate the efficiency, accuracy, and accessibility of biomonitoring assessments will significantly improve, ultimately contributing to a better understanding and management of our aquatic ecosystems.

1. Introduction

1.1. Background

Within the CGIAR Initiative on Digital Innovation, GroundTruth, in conjunction with the International Water Management Institute (IWMI) and North-West University (NWU), are researching and developing digital innovations pertaining to the mini stream assessment scoring system (miniSASS) (Pattinson et al. 2023). The concept of miniSASS was developed in South Africa, based on the South African Scoring System (SASS) Version 5 (Dickens and Graham 2002; Graham, Dickens, and Taylor 2004), where one could sample aquatic macroinvertebrates and infer the ecological condition of a stream or river from the different relationships (i.e., specific, different sensitivities and tolerances) that different taxa of aquatic macroinvertebrates share with their environment (Dickens and Graham 2002; Morse et al. 2007; Ndatimana et al. 2023; Odountan et al. 2019; Paisley et al. 2014).

Both miniSASS and SASS5 rely on sampling and accurately

identifying the aquatic macroinvertebrates in a stream or river. For miniSASS, the macroinvertebrates need to be identified to an Order-level grouping (Graham et al. 2004), while for SASS5 the resolution is much finer, for most taxa going to family-level groupings (Dickens and Graham 2002). MiniSASS has been recognized as a promising tool both locally in South Africa (Graham and Taylor 2018), as well as internationally for reporting on the Sustainable Development Goals (SDGs) (Taylor et al. 2022).

MiniSASS is a low-cost, relatively simple technique, with no requirement for laboratory analyses; miniSASS surveys result in a real-time estimate of river health (Graham et al. 2004; Taylor et al. 2022). SASS5, which is designed for Southern Africa but also employed elsewhere by both private and government entities, is used for assessing the ecological condition of streams and rivers with greater certainty than offered by the more simplistic miniSASS (Bere and Nyamupingidza 2014; Fourie et al. 2014). In SASS5, the assessment results are computed as two index scores, the average score per taxon (ASPT), and the SASS5 score (Dickens and Graham 2002). These scores can also be used to inform a macroinvertebrate response index (MIRAI), which details the observed families against expected, and results in an ecological classification of the stream or river on a scale from natural or pristine through to severely modified (for further detail, see Thirion 2007).

1.2. Challenges

MiniSASS has limitations regarding its precision and accuracy, since it relies on identification of aquatic macroinvertebrates by minimally trained citizen scientists – identification which can be subject to error. For miniSASS, the score can change significantly based on misidentification. For example, a miniSASS survey in a rocky stream that finds four groups including 'Worms' [score 2], 'Minnow mayflies' [score 5], 'Snails / clams / mussels' [score 4] and 'Damselflies' [score 4], changes from an average score of 3.75 (very poor condition) to an average score of 7 (good condition) if the fourth group is misidentified as 'Stoneflies' [score 17]. Ultimately, doubt over the accuracy, validity, and reliability of river health assessments generated using miniSASS detracts from its use, impact, trustworthiness, and broader uptake.

For miniSASS to be regarded with scientific credibility, the data must be considered high quality, trustworthy and accurate (Arndt et al. 2022; Buytaert et al. 2014; Hulbert et al. 2019). Concerns over identification error are not considered a large issue for SASS5, where practitioners in southern Africa are generally well-trained and may even be examined on their identification abilities before being accredited in use of the SASS5 technique. However, identification can always be improved to minimize error and speed up identification.

Another limitation inherent with miniSASS and SASS5 was traditionally that data was captured manually in-field. The data would then need to be manually uploaded to the miniSASS website at a later stage, creating not only room for error in data capture, but also the potential that the data would not be captured in a database at all if the person who did the survey never uploaded it.

1.3. Innovation Opportunities

Recently, SASS5 has had a mobile application (app) launched that assists with data capture in-field, improving both the accuracy and speed of data capture, as well as the efficiency of data reporting[1]. However, there remains a clear need for digital innovation in the arena of aquatic biomonitoring with miniSASS and, potentially, SASS5. There are various ongoing developments within the CGIAR Initiative on Digital Innovation concerning miniSASS, including research and development of a miniSASS smartphone app, an upgraded miniSASS website[2], an online, interactive course for miniSASS[3], and a machine-learning (ML) identification algorithm for deep neural network assistance with identification of the aquatic macroinvertebrates from photographs taken by the miniSASS operator taken in-field (for more details, see Pattinson et al. 2022). Further to those developments, it was recognized that miniSASS operator identification (which happens in addition to the ML identification of photographs, creating two layers of identification security to improve identification and data reliability) would be improved by development of a revised, digitally interactive dichotomous key for miniSASS. This was determined because the original dichotomous key (a static, illustrated document) still left room for confusion or misidentification where branches in the key were not easy to understand or interpret for novice users. Revising the key into a digitally innovative format aimed to make using it more

---

[1] Forthcoming; the announcement video clip available at https://www.youtube.com/watch?v=T2yADWef0sw
[2] https://minisass.org/en
[3] https://groundtruth.plutolmsapp.com/enrol/index.php?id=374

friendly, intuitive, and accurate for a miniSASS operator, thus improving their identification accuracy and confidence, especially for novice operators.

Separately, the development of ML identification of aquatic macroinvertebrates from photographs for miniSASS also raised the possibility of using the technique during SASS5 assessments. Therefore, the potential for extension of the ML identification algorithm to SASS5 level to potentially assist in identifying the 91 family-level taxa used for SASS5, was explored. This report relays the outcomes of those processes and explorations.

2. A digital, interactive dichotomous classification key for miniSASS

With the launch of the miniSASS mobile app, in-field data collection has been digitally enhanced. MiniSASS operators can now collect photographs of the sample site, capture a range of anecdotal data (e.g., clarity tube measurements, dissolved oxygen levels, or qualitative descriptions), and, most importantly, capture photographs of the macroinvertebrates they sample. Within the mobile app, there is a built-in ML algorithm that provides identification predictions for the aquatic macroinvertebrates sampled based on the photographs the operator takes of each one. This both helps guide the operator in their identifications and provides its own objective identifications and resulting miniSASS score. However, the miniSASS operator still needs to identify all their specimens manually as well. This is where the dichotomous key is relevant – it assists a miniSASS operator to manually identify all their specimens accurately. The result is that each miniSASS assessment completed using the mobile app will have photographs of all the specimens found, coupled with separate (though ideally identical) identifications and miniSASS scores based first on the operator's identifications (assisted by the dichotomous key), and second on the ML algorithm's identification predictions.

2.1. The original miniSASS dichotomous key

A dichotomous key is a tool or method used to aid in the identification of organisms. Dichotomous keys comprise decision tree systems, whereby the user is offered pairwise decisions at each branch, deciding on which diagnostic features align with the organism as they move along the tree. The traits that split each decision of the tree range widely, from specific morphological or physiological characteristics, to general identifiers such as belonging to a certain high-level taxonomic group. The features are organismal traits that

cascade in specificity, with each split along the decision tree growing more specific until a unique identity can be reached.

Within a dichotomous key, the decision-making process starts at a single node. Thereafter, the decisions progress stepwise via paired splits, where the user selects which of two branches they will continue down at each decision node. Ultimately, by progressing to the conclusion of these pairwise identifier splits, the user ends up with the logical identification of the organism to a specified or desired taxonomic level.

Within miniSASS, users are required to identify all the aquatic macroinvertebrates they sample and assign them as belonging to one of 13 miniSASS groupings. The groups are at roughly Order level, though they do not all correspond perfectly with Order-level taxonomy given the taxonomic difficulties associated with global classification of aquatic macroinvertebrates (Bouchard Jr et al. 2005; Guareschi and Wood 2019; Jones 2008). The miniSASS groups found are then used to determine the miniSASS score and the inferred ecological condition of the stream or river being surveyed. Naturally, this process necessitates that miniSASS operators are able to identify all the aquatic macroinvertebrates they sample. This is where the miniSASS dichotomous key is required to aid in classifying each of the organisms found into their relevant miniSASS group. To-date, miniSASS operators have been provided with a dichotomous key that they can use in-field (Figure 1).

2.2. Issues with using the dichotomous key

The development of the miniSASS mobile app raised the possibility to digitize the key, so that it could be navigated intuitively on the app, without the need for a static print-out.

To transcribe the original miniSASS dichotomous key would require each of the decision nodes to be displayed in a separate interface, together with their relevant ancillary descriptive data. The ancillary information comprises short descriptions of the diagnostic features separating the node decision branches, as well as images of the relevant trait where possible (e.g., images of each of the different morphological features that separate out at a decision node). A system with this design would substantially increase the size of the app, creating issues for downloading, mobile data use, and storage space on the smartphones carrying the app.

In addition to the concerns over the practicality and appropriateness of directly digitizing the original key, there are issues with decision nodes that are based on technically incorrect information, or ambiguities over the focal feature. This arose given that complex information, particularly
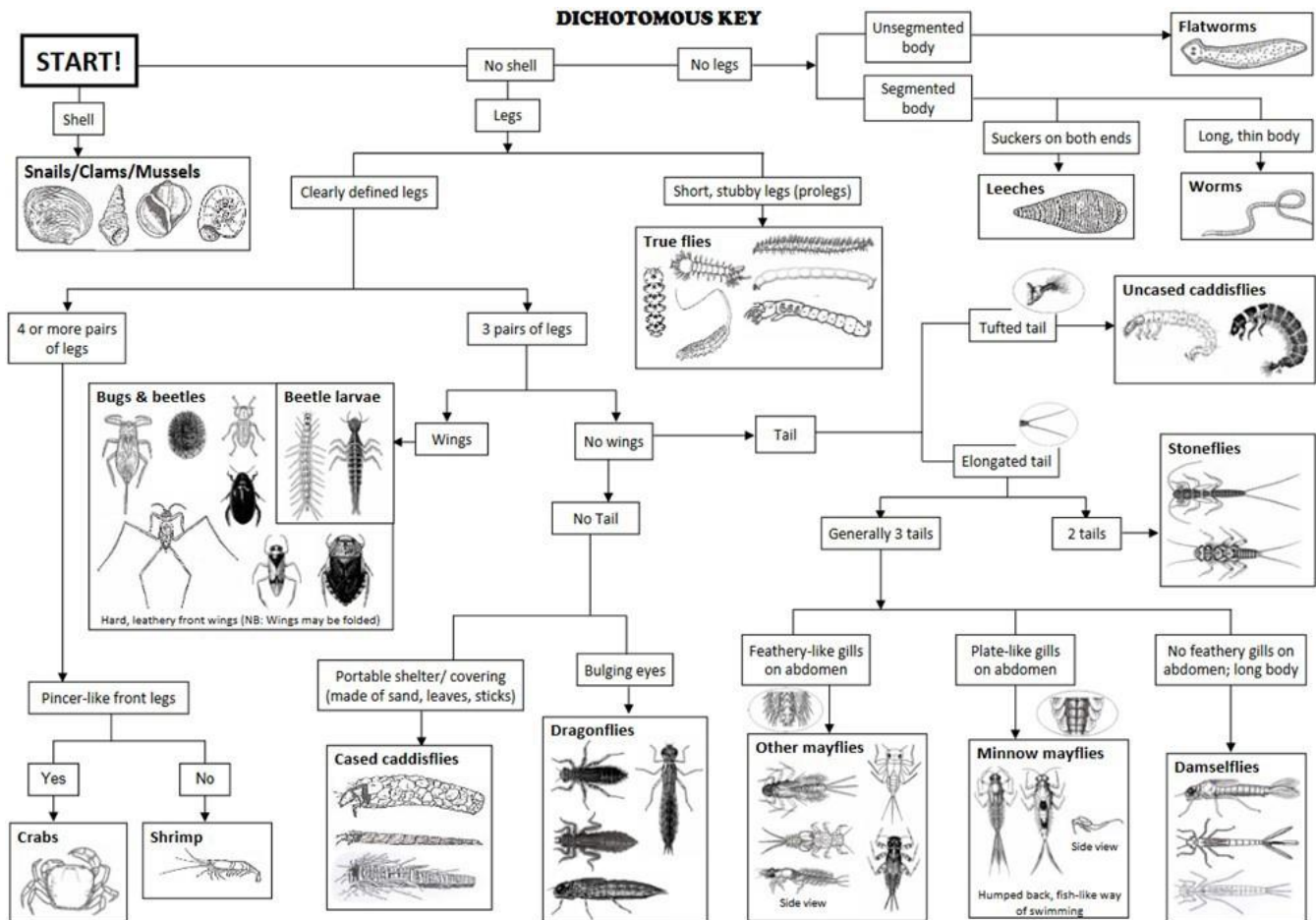
Figure 1 The miniSASS dichotomous key initially developed for miniSASS operators.

regarding morphological structural differences, were simplified for the purposes of a citizen scientist who perhaps has little experience with identifying aquatic macroinvertebrates being able to navigate the key.

An example of possible oversimplification is that to reach the 'Damselflies' group following the key, one would follow this key pathway: *Legs → clearly defined legs → three pairs of legs → no wings → tail → elongated tail → generally three tails → no feathery gills on abdomen*. These decisions are based on what is generally visible to the naked eye for the average damselfly specimen, and how those traits would be interpreted by the average user. However, technically the decision nodes for 'tail', 'elongated tail', 'generally three tails', and 'no feathery gills on abdomen' are morphologically incorrect and can be misleading. In fact, damselfly larvae do not technically have tails. Rather, the protrusions at the

posterior of their bodies are gills (that look like a tail to an inexperienced person). The gills are 'leaf' or 'paddle' shaped, and not 'feathery'.

An example of ambiguity inherent in the original key is in the classification pathway (though, again, this was done purposefully based on how lay citizen scientists would interpret what they were seeing) is that for the 'Bugs and beetles' grouping. In the pathway to arrive at 'Bugs and beetles', the second decision node requires the user to identify if the organisms have legs or not. The user should select that they do have clear legs. However, in the case of the *Psephenidae* (commonly known as water penny beetles) the legs are seldom visible. Consequently, the classification of *Psephenidae*, or of organisms with similar unclear morphological characteristics, becomes difficult and frustrating when using the naked eye. Most of the miniSASS

groups are highly diverse containing organisms with considerable morphological variation. Therefore, it becomes challenging to create single decision nodes that describe the morphological features of all the organisms within a group.

Considering these issues, a different approach to implementing and designing a new dichotomous key for miniSASS was undertaken to ensure the key presented in the mobile app is easy to use, simple and intuitive for the miniSASS operator to identify their specimens.

2.3. The digitally upgraded dichotomous key

Translating and transcribing the physical dichotomous key to use into digital format accessible via a mobile app required making large changes to the layout and operation of the key. Inherently, the changes increase the complexity of the key, so maintaining ease of use was imperative to ensure that the key still performed its core function of helping minimally trained citizen scientists identify aquatic macroinvertebrates to the miniSASS standard. Part of the need for intuitive use is the need for speed with identification, so that miniSASS surveys are efficient.

The first core design feature of the new key was that it would be based on a filtering system. For a filtering approach, a list of initial broad morphological characteristics relevant to each of the 13 miniSASS group classifications is provided. Some of the decision nodes in the original dichotomous key were reused, where appropriate (e.g., has a shell, defined legs, has a clear tail, or has a long thin body). However, numerous new criteria have been added increasing the number of morphological characteristics in the key, thereby encompassing most of the morphological variation within each of the groups. These new criteria include features such as having a rounded body, a relatively short tail, and/or paddle-shaped gills. A list of 22 morphological features is used in the digital key (Table 1). Many of the groups share similar criteria, but each group will be defined by either a single unique feature, or a unique combination of features.

When a miniSASS operator opens the key a list of all 22 feature filters is given, together with an image or images (i.e., real photographs, not drawings) illustrating an example of the typical appearance of the relevant feature (Figure 2). Additionally, a short description for each filter is available with an information icon next to the filter; selecting this information icon will bring up some extra information as well as an enlarged image of the typical appearance of the feature to help with identification.

To use the key, the operator needs to examine each aquatic macroinvertebrate they have sampled and, for each different specimen, individually go through to the list of features and select those which the organism has. Based on the selection, organisms that have the selected feature will appear at the top of the filter as potential identifications. Organisms not described by the selected feature will not be listed as options. As the operator progresses with the filter selecting more features that describe the specimen, the number of potential identifications listed at the top of the filter will reduce until only a single option remains. In this way, an operator does not need to select all the relevant features that describe the specimen. As they progress through the key, it is only important that the features which are unique identifiers end up being selected. Essentially, as more features are selected, the options for what the specimen could be will grow narrower until only a single identification option remains available based on the combination of features selected.

If an operator selects the filter for 'three pairs of legs', all the groups that contain organisms with three pairs of legs will be given in the list at the top of the filter, while those that do not possess three pairs of legs will not appear. Many groups have three pairs of legs, but this will rule out the 'Flatworms', 'Snails / clams / mussels', 'Crabs and shrimps', 'Trueflies', 'Leeches' and 'Worms' groups. If the user then also selects 'long thin body', only two groups are left that have a combination of 'three pairs of legs' and a 'long thin body' – the 'Damselflies' and 'Caddisflies' (Figure 3).

The remaining filters in the list that are not associated with 'Damselflies' or 'Caddisflies' groups are removed and only those that potentially distinguish these groups from each other remain. The operator can then continue to select features until only a single identification option remains. For example, if the user then selected 'feather-like gills', then only the 'Caddisflies' would have all the selected features leaving them as the only option for selection (Figure 4).

If a user is either unsure of the morphological feature they selected, or not convinced by the resulting identification options, they can select or deselect features from the filter list and compare identification options as they go. In comparison to the original key method, the number of decisions needed to classify an organism as belonging to the caddisfly group can potentially be reduced from seven necessary decision nodes down to just to three.

In some instances, a user can select the morphological feature that is unique to a certain group from the beginning if they can clearly observe it. For example, if a user observes short stubby legs present on an organism and they select that filter from the

Table 1 The 22 features used in the new mini stream assessment scoring system (miniSASS) dichotomous key filter system. For each of the 13 miniSASS groups, an 'x' is shown if they possess the feature. Each miniSASS group is defined by a unique combination of features.

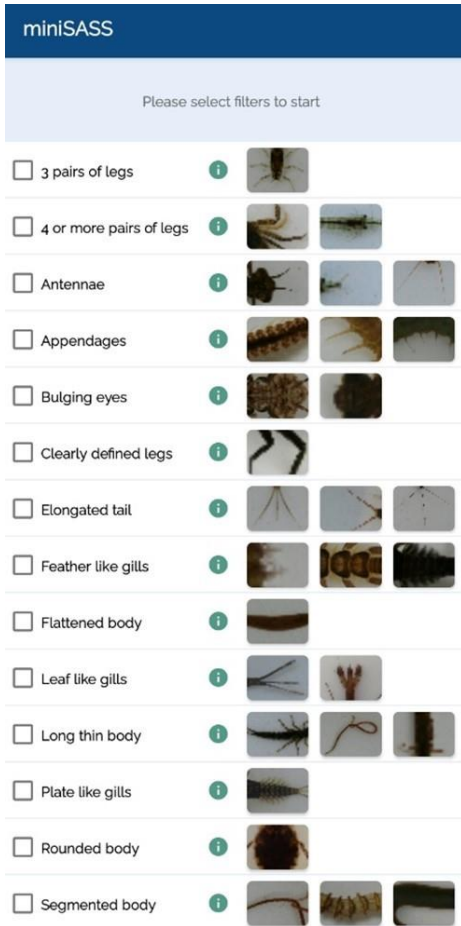| Group / Feature	Bugs and beetles	Caddis-flies	Crabs and shrimps	Damsel-flies	Dragon-flies	Flat-worms	Leeches	Minnow mayflies	Other mayflies	Snails, clams, and mussels	Stoneflies	Trueflies	Worms
Shell										x			
Shelter		x											
Clearly defined legs	x	x	x	x	x			x	x		x		
Segmented body							x					x	x
Long, thin body	x	x		x								x	x
Appendages	x	x										x	
Three pairs of legs	x	x		x	x			x	x		x		
Four or more pairs of legs			x										
Elongated tail								x	x		x		
Tufted tail		x											
Short tail	x	x											
Plate-like gills								x					
Feather-like gills	x	x							x		x		
Leaf-like gills				x									
Bulging eyes					x								
Stocky body	x				x								
Antennae	x		x	x	x			x	x		x		
Suckers at both ends							x						
Wing buds				x	x			x					
Flattened body						x							
Short, stubby legs												x	
Rounded body	x												

Figure 2. Fourteen of the 22 filters available at the first step of using the new mini stream assessment scoring system (miniSASS) dichotomous key as they appear within the miniSASS mobile application (app). Images illustrate an example of the typical appearance of each of the features, with information icons (i) providing options to view ancillary information about each of the features.
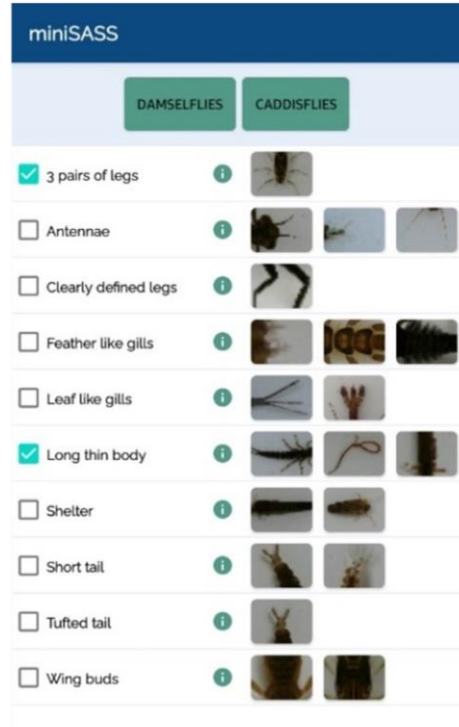

Figure 3. With both the '3 pairs of legs' and 'long thin body' filters selected, only two identification options – damselflies and caddisflies – remain. The features still listed are those that could be used to separate the two groups, while features that describe neither of those groups have been removed from the filter options. The mini stream assessment scoring system (miniSASS) operator will need to keep selecting features from the filter list which the specimen in question has until a unique combination describing only one possible miniSASS group remains. The image is displayed as a screenshot of how it appears in the miniSASS mobile application (app).
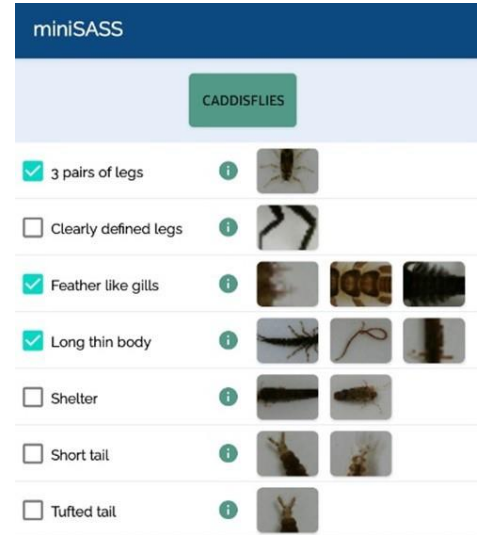

Figure 4. With the '3 pairs of legs', 'long thin body', and 'feather-like gills' features selected, the only possible identification that remains is the caddisflies group (of the 13 mini stream assessment scoring system (miniSASS) groups). Notably, the only features left that can still be selected all fit for caddisflies, but they need not all be selected to arrive at a unique identification. The image is displayed as a screenshot of how it appears in the miniSASS mobile application (app).

list, the only identification option available will be the 'Trueflies', given that that is the only group that has that feature. The same is true for a 'shell', which characterizes only the 'Snails / clams / mussels' group, or the 'rounded body' which characterizes only the 'Bugs and beetles' group.

3. Exploring the potential for upscaling the ML identification algorithm for use in SASS5

The use of ML for the identification and classification of macroinvertebrate groups used in miniSASS presents an

exciting integration of modern artificial intelligence (AI)

technology into ecology and biomonitoring. The ML identification model in miniSASS is used to classify organisms within one of 13 broad, Order-level groups. These groups contain considerable morphological diversity.

Therefore, being able to assign unique identifiers for the purposes of ML classification represents an important milestone in the utility of AI in ecology. However, ongoing development has highlighted that the use of ML to aid in the automatic verification of miniSASS survey scores, via auto- verifying identifications, still requires further refinement and development.

Taxonomic resolution presents a significant challenge for the identification and classification accuracy of an ML algorithm. The finer the taxonomic resolution, the more specific, unique morphological variation there is among different groups. In theory, this should make it easier to assign unique features to each specified group. In the case of coarser taxonomic resolution, there is less uniquely identifiable morphological variation between organisms since the groups will include an increasing number of increasingly dissimilar organisms, making them harder to all identify within the same group. Essentially, the more specific the group, and the finer the resolution, the easier it is to distinguish an individual as part of that group. A simple illustration of this would be to consider vehicles: it would be difficult to assign unique identifiers between vehicles if one was looking at a course resolution. Many different vehicles have four wheels, a windshield, a chassis, wing mirrors, four doors, etc. However, as the resolution gets finer and is based on make, model, year of production, and finally on license plate and engine number, it is easier to define different vehicles by a unique identifier.

The classification of organisms used in SASS5 is based on family level identification, a much finer resolution than that used in miniSASS. With the finer taxonomic resolution, the variation becomes more specific (with individuals at higher taxonomic resolution more alike and more specifically different from others). Therefore, classifying organisms into a specific family should be easier. However, practically, this is not always the case with developing ML identification models. The more specific the groupings, and the finer the nuances of unique identifiers, the greater the amount of training data that will be required to get the model to find, define, and consistently identify those unique features. A SASS5 assessment requires identification of specimens into one of 91 potential families of aquatic macroinvertebrates. Consequently, the number of images needed to train the ML identification algorithm is substantially larger than that required for classification into just 13 miniSASS groups.

In development of a deep neural network ML identification model, it is recommended that a minimum of 1000 images are used for training for each group. This results in roughly 91,000 images, as a minimum, for training an ML identification algorithm to be functional at SASS5 resolution. For greater accuracy, a 10-fold increase is recommended for retraining the algorithm, raising the required number of images to 910,000. As a result, the use of ML to identify and classify aquatic macroinvertebrates for the purposes of in SASS5 presents a real challenge simply because of the number of images needed to train and retrain the ML

identification algorithm to enable accurate classification and identification. However, it remains possible, especially if the number of images required decreases because of the higher taxonomic resolution. With images being collected by people nationwide for miniSASS assessments, it is plausible that the required number of images to train an ML identification algorithm for SASS5 may one day be captured.

References

Arndt, J.; Kirchner, J.S.; Jewell, K.S.; Schluesener, M.P.; Wick, A.; Ternes, T.A.; and Duester, L. 2022. Making waves: Time for chemical surface water quality monitoring to catch up with its technical potential. Water Research 213: 118168. https://doi.org/10.1016/j.watres.2022.118168

Bere, T. and Nyamupingidza, B.B. 2014. Use of biological monitoring tools beyond their country of origin: A case study of the South African Scoring System Version 5 (SASS5). Hydrobiologia 722(1): 223–32. https://doi.org/10.1007/s10750-013-1702-7

Bouchard Jr, R.W.; Huggins, D.; and Kriz, J. 2005. A review of the issues related to taxonomic resolution in biological monitoring of aquatic ecosystems with an emphasis on macroinvertebrates. Lawrence, KS, USA: Kansas Biological Survey. Available at https://biosurvey.ku.edu/sites/biosurvey/files/2023-01/KBSRept133_TaxResol.pdf (accessed 12/12/2023).

Buytaert, W.; Zulkafli, Z.; Grainger, S.; Acosta, L.; Alemie, T.C.; Bastiaensen, J.; De Bièvre, B.; Bhusal, J.; Clark, J.; Dewulf, A.; Foggin, M.; Hannah, D.M.; Hergarten, C.; Isaeva, A.; Karpouzoglou, T.; Pandeya, B.; Paudel, D.; Sharma, K.; Steenhuis, T.; Tilahun, S.; Van Hecken, G.; and Zhumanova, M. 2014. Citizen science in hydrology and water resources: Opportunities for knowledge generation, ecosystem service management, and sustainable development. Frontiers in Earth Science 2: 26. https://doi.org/10.3389/feart.2014.00026

Dickens, C.W.S. and Graham, P.M. 2002. The South African Scoring System (SASS) version 5 rapid bioassessment method for rivers. African Journal of Aquatic Science 27(1): 1–10. https://doi.org/10.2989/16085914.2002.9626569

Fourie, H.E.; Thirion, C.; and Weldon, C.W. 2014. Do SASS5 scores vary with season in the South African highveld? A case study on the Skeerpoort River, North West province, South Africa. African Journal of Aquatic Science 39(4): 369–76. https://doi.org/10.2989/16085914.2014.978256

Graham, P.M.; Dickens, C.W.S.; and Taylor, J. 2004. MiniSASS—A novel technique for community participation in river health monitoring and management. African Journal of Aquatic Science 29(1): 25–35. https://doi.org/10.2989/16085910409503789

Graham, P.M. and Taylor, J. (Eds.) 2018. Development of Citizen

Science Water Resource Monitoring Tools and Communities of Practice for South Africa, Africa and the World. Pretoria, South Africa: Water Research Commission (WRC) Report No. TT 763/18. Available at https://www.wrc.org.za/wp-content/uploads/mdocs/TT%20763%20web.pdf (accessed 12/12/2023).

Guareschi, S. and Wood, P.J. 2019. Taxonomic changes and non-native species: An overview of constraints and new challenges for macroinvertebrate-based indices calculation in river ecosystems. Science of the Total Environment 660: 40–46. https://doi.org/10.1016/j.scitotenv.2019.01.008

Hulbert, J.M.; Turner, S.C.; and Scott, S.L. 2019. Challenges and solutions to establishing and sustaining citizen science projects in South Africa. South African Journal of Science 115(7–8): 1–4. https://doi.org/10.17159/sajs.2019/5844

Jones, F.C. 2008. Taxonomic sufficiency: The influence of taxonomic resolution on freshwater bioassessments using benthic macroinvertebrates. Environmental Reviews 16(NA): 45–69. https://doi.org/10.1139/A07-010

Morse, J.C.; Bae, Y.J.; Munkhjargal, G.; Sangpradub, N.; Tanida, K.; Vshivkova, T.S.; Wang, B.; Yang, L.; and Yule, C.M. 2007. Freshwater biomonitoring with macroinvertebrates in East Asia. Frontiers in Ecology and the Environment 5(1): 33–42. https://doi.org/10.1890/1540-9295(2007)5[33:FBWMIE]2.0.CO;2

Ndatimana, G.; Nantege, D.; and Arimoro, F.O. 2023. A review of the application of the macroinvertebrate-based multimetric indices (MMIs) for water quality monitoring in lakes. Environmental Science and Pollution Research 30: 73098–115. https://doi.org/10.1007/s11356-023-27559-0

Odountan, O.H.; Bisthoven, L. de; Abou, Y.; and Eggermont, H. 2019. Biomonitoring of lakes using macroinvertebrates: Recommended indices and metrics for use in West Africa and developing countries. Hydrobiologia 826: 1–23. https://doi.org/10.1007/s10750-018-3745-2

Paisley, M.F.; Trigg, D.J.; and Walley, W.J. 2014. Revision of the biological monitoring working party (BMWP) score system: Derivation of present-only and abundance-related scores from field data. River Research and Applications 30(7): 887–904. https://doi.org/10.1002/rra.2686

Pattinson, N.B.; Koen, R.C.J.; Koen, F.J. 2022. Artificial intelligence-based biomonitoring of water quality. CGIAR Technical Report. Prepared in collaboration with GroundTruth and North-West University (NWU) as part of the CGIAR Initiative on Digital Innovation. Colombo, Sri Lanka. 32p. Available at https://www.iwmi.cgiar.org/Publications/Other/PDF/artificial_intelligence-based_biomonitoring_of_water_quality.pdf (accessed 12/12/2023).

Pattinson, N.B.; Taylor, J.; Dickens, C.W.S.; and Graham, P.M. 2023. Digital Innovation in Citizen Science Water Quality Monitoring in Developing Countries. Vol. 207. Colombo, Sri Lanka: International Water Management Institute (IWMI). 50p. In press.

Taylor, J.; Graham, P.M.; Louw, A.J.; Lepheana, A.T.; Madikizela, B.; Dickens, C.W.S.; Chapman, D. V; and Warner, S. 2022. Social change innovations, citizen science, miniSASS and the SDGs. Water Policy 24(5): 708–17. https://doi.org/10.2166/wp.2021.264

Thirion, C. 2007. Module E: Macroinvertebrate response assessment index in river ecoclassification. In River Ecoclassification Manual for Ecostatus Determination (Version 2). Pretoria, South Africa: Water Research Commission (WRC) Report No. TT 332/08. 43p. Available at https://www.wrc.org.za/wp-content/uploads/mdocs/TT%20332-CONSERVATION.pdf (accessed 12/12/2023).