RMMS: Species' Range Model Metadata Standards

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Biosketch: C.M. is a quantitative ecologist interested in forecasting biological responses to global change. He likes pina coladas and getting caught in the rain.

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1 Abstract

Aim: The geographic range and ecological niche of species are widely-used concepts in ecology, evolution, and conservation and many modeling approaches have been developed to quantitatify each. Niche and distribution modeling methods require a litany of design choices; differences among subdisciplines have created communication barriers that increase isolation of scientific advances. As a result, understanding and reproducing the work of others is difficult, if not impossible. It is often challenging to evaluate whether a model has been built appropriately for its intended application or subsequent reuse. Here we propose a standardized model metadata framework that enables researchers to understand and evaluate modeling decisions while making models fully citable and reproducible. Such reproducibility is critical for both scientific and policy reports, while international standardization enables better comparison between different scenarios and research groups.

Innovation: Range Modeling Metadata Standards (RMMS) address three challenges: they (i) are designed for convenience to encourage use, (ii) accommodate a wide variety of applications, and (iii) are extensible to allow the research community to steer it as needed. RMMS are based on a data dictionary that specifies a hierarchical structure to catalog different aspects of the range modeling process. The dictionary balances a constrained, minimalist vocabulary to improve standardization with flexibility for users modify and extend. To facilitate use, we have developed an R package, `rangeModelMetaData`, to build templates, automatically fill values from common modeling objects, check for inconsistencies with standards, and suggest values.

Main Conclusions: Range Modeling Metadata tools foster cross-disciplinary advances in biogeography, conservation, and allied disciplines by improving evaluation, model sharing,

model searching, comparisons, and reproducibility among studies. Our initially proposed standards here are designed to be modified and extended to evolve with research trends and needs.

2 Introduction

Species' geographic ranges and environmental niches are fundamental units of biogeography and among the most widely-used summaries in biology (Guisan & Thuiller, 2005; Jetz *et al.*, 2012). Correlative range models (i.e., species distribution models, environmental niche models, resource selection models, etc.) describe how occurrence or abundance varies in environmental and/or geographic space and are applied to biodiversity assessments and forecasts, conservation planning, niche evolution, invasion biology, and many other fields (Franklin, 2010; Peterson *et al.*, 2011; Guisan *et al.*, 2017). Many modeling approaches have been developed to quantitatively characterize ranges and environmental niches with different goals in each field, and user-friendly software has enabled many thousands of studies. However, differences in approaches and methodologies—-some based on different study foci and others on field-specific jargon—-have created barriers to communication and led to increasing isolation of scientific advances. For example, wildlife ecology has a literature on resource selection modeling that is rather distinct from environmental niche modeling in plant ecology, in spite of very similar data, concepts, and objectives (Warton & Aarts, 2013). Recent calls have been made to standardize range model metadata to enable reuse of models both generally (Borba & Correa, 2015; Costa *et al.*, 2018) and with the specific goal of estimating biodiversity patterns (Araújo *et al.*, 2019), but detailed metadata standards remain lacking. Here, we propose Range Modeling Metadata Standards (RMMS) that aim to improve communication, reproducibility, and reusability of published models.

2.1 Why do we need RMMS?

Range modeling is a highly varied field with little consensus and calls for greater standardization and transparency (Joppa *et al.*, 2013). Without standardized metadata that describe range models, it can be difficult to evaluate if a model has been built appropriately for its intended use or if it is suitable for reuse in subsequent studies. A number of studies have outlined clear connections between modeling decisions and resulting inferences (Merow *et al.*, 2014; Guillera-Arroita *et al.*, 2015; Guisan *et al.*, 2017), and advances in biological metadata have already standardized and connected primary biodiversity data (Wieczorek *et al.*, 2012; Guralnick *et al.*, 2017). By specifying standards, methodologies will become more immediately transparent for peers as researchers adopt a standard metadata vocabulary. Easy-to-use metadata will considerably simplify the reviewing process by automating the reporting of decisions, which can take considerable time for reviewers and help them better understand the methodological context of a study's insights. Metadata can also help relieve manuscripts from laborious methodological descriptions, increasing valuable space to focus on results.

Range models constitute valuable information products that have been recognized as key for developing an understanding of the status and trends in species distributions. They are vital to large biodiversity modelling projects such as Botanical Information and Ecology Network (BIEN; biendata.org) and Map of Life (MOL, mol.org) and synthetic conservation efforts such as defining Species Distribution Essential Biodiversity Variables (Pereira *et al.*, 2013; Jetz *et al.*, 2019). The large taxonomic scale of the range models in these efforts leverages standardized approaches to improve model reliability, but such mass production places an even stronger onus to report how models were produced. The potential inclusion of range models produced by the research community in these databases necessitates metadata that enables comparisons and integration. Making range model products easily citable via searchable metadata increases accessibility to other subdisciplines of biology and environmental science and provides credit for the researchers who developed the models. Standardization also helps connect related subdisciplines that have evolved their own language or best practices but may benefit from cross-pollination. Over time, adherence to metadata standards would support a catalog where researchers could search for modeling studies based on features of interest (e.g., data sources, model method and settings, reported evaluation metrics) which would otherwise likely be inaccessible from metadata on a published paper. Meta-analyses leveraging this resource might have applications ranging from community ecology to biogeography to methodological development.

Taken together, advancing standardized range model metadata will enable more reproducible, standardized, searchable, and citable science. As these standards are meant to grow with the field, they will benefit from engagement and improvements from the user community. After an initial phase of testing and validation, we hope that RMMS can become a completely community-driven enterprise without need for management by a given entity or our research team. These gains in scientific precision and communication are well-positioned to outweigh the effort required to report standardized metadata. Furthermore, our efforts will bring range modeling in line with other successful efforts in Reproducible Research Systems (Mesirov, 2010) in other domains in the life sciences (Goecks *et al.*, 2010).

To promote adoption of our proposed metadata standard, we have designed convenient and flexible tools for its implementation, including a user-friendly interface to enable researchers to provide such descriptions with minimal effort and errors. We provide an R package, `rangeModelMetadata`, that automatically completes many required fields and can be extended to automatically fill them from common modeling objects in R.

3 rangeModelMetadata (rmm) Format

The `rangeModelMetadata` (`rmm`) format that we propose is designed to be human-readable to accommodate more flexible specification of inputs, as well as ensure generality beyond specific software or present-day use cases. After sharing a minimum set of critical metadata, provision of additional information is optional. This flexibility gives researchers three advantages: (i) it is adaptable to new technologies (e.g., algorithms, applications), (ii) it will ensure relevance to a broad user base, and (iii) it permits customization as needed. The standards are comprehensive enough to provide guidance and clarity, but not onerous.

The basic unit of RMMS is a single study with a single model per taxon to reduce the burden on researchers, in contrast to building a metadata object for each species or model (although this is a custom option). This follows standards from the biosciences standards community to focus on the study or experiment (Taylor *et al.*, 2008). The structure of rmm objects correspond to eight top-level fields: authorship, studyObjective, data, dataPrep (data preparation), modelFit, prediction, evaluation, and code (Table 1). Within each of these top-level fields are subfields, which may contain further granular reporting. The named *values* assigned to unique combinations of *fields* (e.g., data:environment:extent) are termed *'entities'* (see the data dictionary in Table 1). Entities have values that are vectors of characters or numbers.

Our metadata dictionary includes the hierarchical structure of the metadata *entities*, provides standardized and suggested inputs, and defines all the content needed to produce an `rmm` object (Table 1; Appendix S1). Each row defines a single *entity* in an `rmm` object, classified by columns specifying the field hierarchy described above. Some *entities* with commonly-used settings have a constrained vocabulary to standardize *values* (noted in the *constrainedValues* column of the dictionary), while others may take on any value. To balance flexibility with standardization, many entities are partially constrained such that a standardized vocabulary is available for certain common values while user-defined values are also accepted. To add further flexibility, many fields have a :Notes entity (e.g. data:notes, dataPrep:notes, modelFit:notes, etc.) to allow authors to mention any additional high-level critical information. Formatted examples as well as descriptions of guidelines for user-defined values are also included in the dictionary. All values can be entered programmatically with our R package `rangeModelMetadata` or manually into a csv file (templates provided in Supplements S5 and S6).

4 Standards

The standards below provide background on the predefined *entities* and guidance on how to extend them to include user-specified options.

4.1 A Case Study

As an example for constructing an `rmm` object in the sections that follow, we built a simplified range model for *Bradypus variegatus*, the Brown-throated sloth, in South America. Specifically, we use Maxent (Phillips *et al.*, 2006) and dismo (Hijmans *et al.*, 2010) applied to occurrence data from GBIF (GBIF.org, 2019) and climate data from Worldclim (Fick & Hijmans, 2017). See supplement S4 for complete workflow. Various modeling decisions are described below in the context of constructing a metadata object. Notably, we begin with a study involving only a single species and describe how to extend this below in *Multispecies Studies.* The resulting rmm object is shown in Figure 2.

4.2 Authorship

The `authorship:` field provides information on citation, contact information, related studies using the models, and licensing/use restrictions associated with the models. Each `rmm` object is given a unique name in the format *Author_Year_Taxa_Model_fw*. We suggest the convention that *Author* be limited to surnames and that multiple authors be included via camel case (e.g., *MerowMaitnerOwensKassEnquistJetzGuralnick*). *Year* should include a four-digit year. *Taxa* can be specified at the author's' discretion and include common or scientific names at any appropriate taxonomic level (e.g., *Sloth, Bradypus, BradypusVariegatus*). *Model* should describe the algorithm used (multiple models can be specified when using ensemble models (Araújo & New, 2007; Thuiller *et al.*, 2009)) —-standardized model names can be viewed in the `modelFit:algorithm` field of the data dictionary. Finally, two random alphanumeric characters should be appended to the `rmm` name to prevent cases where ambiguity might arise. A complete example could take the form (Fig. 2): *MerowMaitnerOwensKassEnquistJetzGuralnick_2018_BradypusVariegatus_Maxent_b3.*

4.3 Study Objective

Entities under `studyObjective,` including `:purpose,` `:rangeType`, `:invasion`, `:transfer`, etc. provide authors with a text field to briefly describe the intended application of their study to set the context for modeling decisions specified in other fields. In our example study, the model it was fit in the northern part of South America, and transferred to the southern part in order to determine whether there is any potentially suitable habitat in a region where no records exist:

```
studyObjective:purpose='transfer'
studyObjective:rangeType='potential'
studyObjective:transfer='detect unoccupied suitable habitat'
```

4.4 Data

Information within the `data` field pertains to occurrence records (`data:occurrence)` and environmental data (`data:environment`) used to train or transfer models. The `:occurrence` field may contain taxon names (`:occurrence:taxaVector`), the type of occurrence data used (`:occurrence:occurrenceDataType;` e.g., presence-only, presence-absence, abundance), the temporal extent of the occurrence records (`:occurrence:yearMin,` `:occurrence:yearMax`), occurrence data sources (`:occurrence:sources`), and information on sample sizes. The `data:environment` field may contain information on the environmental variables used (`:environment:variableName`), the temporal extent of the environmental layers (`:environment:yearMin,` `:environment:yearMax`), and the source of the environmental data (`:environment:sources`). For example, occurrence information for our example includes (additional *entities* in Supplement S4):

```
data:occurrence:presenceSampleSize=290

data:occurrence:backgroundSampleSize=5084

data:occurrence:yearMin=1970

data:occurrence:yearMax=2000
```

4.5 Data Prep

Information within the `dataPrep` field details any changes, cleaning, or validation done to the data. Errors or inherent biases (i.e., spatial) in publicly available occurrence data are common (Serra-Diaz *et al.*, 2018) and may have serious consequences for modeling (Phillips *et al.*, 2009; Merow *et al.*, 2016). Common reasons for excluding coordinates include: coordinates not falling in the specified political division, coordinates reflecting non-native or cultivated occurrences, coordinates representing centroids of a political division, duplicated coordinates, or biased spatial clustering (Aiello-Lammens *et al.*, 2015; Robertson *et al.*, 2016; Maitner *et al.*, 2017; Serra-Diaz *et al.*, 2018). Valid points may also need to be removed if they constitute environmental outliers that may strongly bias a model (Soley-Guardia *et al.*, 2014).

Within the `dataPrep` field there are four subfields: `:errors`, `:biological`, `:environmental`, and `:geographic`. The `:errors` field contains information regarding any removal of duplicate (`:errors:duplicate`) or suspicious points (`:errors:questionablePointRemoval`). The `:geographic` field contains information related to geographic name standardization (`:geographic:geographicStandardization`) and occurrence point validations (`geographic:geographicOutlierRemoval, :geographic:centroidRemoval, :geographic:pointInPolygon`) on the basis of geopolitical regions as well as geographic outlier removal (`:geographic:geographicOutlierRemoval`). The biological field contains information related to taxonomic name standardization (:biological:taxonomicHarmonization) as well as the identification of records that are likely to represent introduced or cultivated species (:biological:nonNativeRemoval, :biological:cultivatedRemoval). The environmental field contains data related to changes made to the environmental layers used, as well as occurrence point exclusion on the basis of environmental data (environmental:environmentalOutlierRemoval).

In our simplified example, we removed records duplicated within cells (on the 10 km grid of the environmental layers) and thinned the occurrence data to reduce the effects of spatial autocorrelation:

```
dataPrep:biological:duplicateRemoval:rule='one observation per cell'
dataPrep:geographic:spatialThin:rule="20km used as minimum distance
        between points"
```

4.6 Model Fitting

The modelfit field has the largest variety of *entities* owing to the profusion of modeling algorithms and decisions applied in their use. A subfield specifies the algorithm name and can be user-defined to accommodate newly developed algorithms. In cases where ambiguity may exist about algorithm definitions, e.g., determining whether one should define modelFit:algorithm = ‘Poisson point process’ or ‘glm’ because the latter can be fit with GLM software, we leave this to the authors’ discretion and provide the modelFit:algorithmNotes entity if needed. It is worth remembering that the intention of rmm objects is to be human-readable and therefore subject to context and interpretation. ...Notes entities, such as modelFit:notes, allow users to describe this context to the desired level of detail. The `modelFit` field contains subfields for specifying data partitioning methods (e.g., *k*-fold cross-validation), specification of how covariates are treated (e.g., scaled, z-scores) and algorithm-specific settings. For Maxent modeling, we have specified comprehensive examples, while providing only minimal recommendations for other algorithms. We leave extensions to other algorithms for their expert users to recommend as part of our efforts to engage the research community in further development. For example, users can also specify their own custom *entities* to accommodate less common metadata. This flexibility ensures that our metadata framework is not so prescriptive that it excludes less-common modeling tools or those yet to be developed.

In our simplified example, we used Maxent via the ENMeval R package (Muscarella *et al.*, 2014) to compare different combinations of feature classes and different regularization parameters. Models were compared based on AUC evaluated on test data, obtained from spatial block cross-validation. As `rmm` objects are designed to handle a single model per species, we report the optimal model settings only and include information in the relevant `...Notes` entities on the model selection strategy. Had we used ensemble averaging over these candidate models, we would have reported the attributes of the ensemble and including attributes of the component models in the `...Notes` fields.

```
rmm$modelFit$partition$partitionRule='spatial block cross validation’
rmm$modelFit$maxent$featureSet='LQ'
rmm$modelFit$maxent$regularizationMultiplierSet=1
rmm$modelFit$maxent$samplingBiasRule='ignored'
rmm$modelFit$maxent$notes='ENMeval was used to compare models with L
    and LQ features, each using regularization multipliers of 1,2,3.
```

```
The best model was selected based on test AUC evaluated under
spatial block cross-validation.'
```

4.7 Prediction

The `prediction` field describes common attributes of a variety of possible output types, including the prediction in geographic space (optionally a single prediction or the mean of multiple models), predictions transferred in space or time, and prediction uncertainty. For each of these prediction types, users specify the units (e.g., binary presence/absence, abundance, absolute probability of occurrence, etc.), the maximum and minimum values, and notes associated with interpretation. For each prediction type (except uncertainty), users can optionally specify a threshold value or rule to convert continuous predictions to binary. Finally, text can be provided to describe rules for extrapolation, building ensembles of models, and other optional attributes of model reporting. In our example study, we make predictions using Maxent's 'raw' (or relative occurrence rate; Merow et al. 2013) values. Note the use of functions (raster::cellStats(); Hijmans et al. 2019) to fill in entities, where `p` is the prediction raster. Further, analogous entities related to transferring predictions to a new regions, are shown in Supplement S4 for brevity.

```
rmm$prediction$continuous$units="relative occurrence rate"
rmm$prediction$continuous$minVal=raster::cellStats(p,min)
rmm$prediction$continuous$maxVal=raster::cellStats(p,max)
rmm$prediction$extrapolation="clamping"
```

4.8 Evaluation

The `evaluation:` field stores a range of statistics used to quantify model training, testing or overall evaluation. This follows recommendations common in machine learning (Hastie *et al.*, 2009) for splitting data into three subsets before model building: training, testing, and evaluation. Training statistics are evaluated on the data used to fit, or train, the model. Testing statistics are calculated on data withheld from training and describe evaluation on test data to assess generality. Such testing statistics can be used for model selection or for weighting in model ensembles, and can help determine which model settings are optimal of those tested (answering the question 'of the models run, which is "best"?'). The evaluation data are independent of both training and testing data and provide a means to assess how well the selected/average model performs with out-of-sample prediction (answering the question 'how good is the best model?'). While we recommend data partitioning as the most robust option, we realize that many studies do not have sufficient data—- it is thus common to use testing data for evaluation. In this case, researchers should report their statistics as `testing`, and provide an `evaluation:notes` that these statistics were also used for evaluation. For training, testing, and evaluation a common set of names of standardized statistics are provided (e.g. AUC, TSS, etc.); users can also include their own statistics and cite them in `evaluation:references.` Notably, we have designed the `rmm` object structure to accommodate a single model per taxon; this model can either be the output of a single algorithm, or the summary (i.e. mean or median) of a single algorithm fit to subsets of the data (e.g. *k*-fold cross validation), or multiple models (e.g., an ensemble, as from the biomod2 R package (Thuiller et al)). In studies where multiple models are relevant to report for each species, a separate `rmm` object should be used for each model type.

In our example study, only AUC evaluated on test data was used to select optimal model settings. In general, it is better practice to examine multiple metrics. Note that we fill in values directly from those stored in an `ENMeval` object called `e`.

```
rmm$evaluation$trainingDataStats$AUC=e@results[i,]$trainAUC
rmm$evaluation$testingDataStats$AUC=e@results[i,]$avg.test.AUC
```

4.9 Code

The `code:` field stores obligate information about software references and versions as well as optional links to scripts hosted online. As `rmm` objects are designed to be human-readable, information that enables true reproducibility is stored in these scripts, e.g., hosted by journals in supplemental information or on Github. We recommend these files be free of constraints beyond those used by journals to avoid a prohibitive amount of work by authors which discourages sharing their code. As biologists continue to strive toward greater reproducibility, we hope standards do emerge, but this is beyond the current scope of our metadata standards. We do however offer entities for different types of code, which currently include `code:demoCodeLink` (for brief, reduced functionality examples), `code:vignetteCodeLink` (for commented, tutorial-styled code), and `code:fullCodeLink` (for a full reproduction of the analysis). These distinctions aim to help users better understand what to expect from the code and for authors to target different audiences needing different levels of detail. We recommend that `code:codeNotes` include information on which platforms the code has been tested. In our example study, we cite the relevant R packages with:

```
rmm=rmmAutofillPackageCitation(rmm=rmm,
          packages=c('rgbif','sp','raster','dismo','ENMeval'))
```

4.10 Vector-valued entities

Some entities are naturally defined as vectors so we adopt JSON formatting (www.json.org) to help clearly define named vector-valued entities. For example, when specifying the spatial extent of the modeling domain, it is common to use the minimum and maximum coordinates (i.e., bounding box). To specify these limits unambiguously with JSON, we use (from the example study): `[{"xmin":-125,"xmax":-32,"ymin":-56,"ymax":40}]`. (In JSON syntax, the 'string' describing the name of a quantity is in double quotations and its 'value' is given following a colon.) Vector-valued entities are apparent in a number of cases: `data:environment:minVal` and `:maxVal` indicate the extremes of each environmental layer in the analysis (e.g., `[{"bio1":289,"bio12":7682,"bio16":2458}]`. Even if users are not familiar with JSON, the `jsonlite` package (Ooms, 2014) provides convenient tools to convert an R `data.frame` to JSON text (see vignettes). A number of vector-valued entities already have names defined, but we expect that use cases will arise that require users to extend JSON formatting to other entities.

4.11 Multispecies Studies

Thus far we have focused on studies that have a single species; however RMMS are readily extended to include multiple species. As many model properties can (and arguably should) be specific to a particular species, we have also designed the metadata structure to accommodate multi-species studies through the use of a *taxonSpecific* column in metadata dictionary (Table 1). This column defines whether a given *entity* applies to all taxa in the study (e.g., `data:occurrence:dataType`), applies to each species separately by specifying a vector with a value for each species (e.g. `data:occurrence:presenceSampleSize`), or is a single value or vector with a value for each species (e.g., `data:occurrence:backgroundSampleSizeSet`). Hence the *taxonSpecific* column indicates whether or not a vector-valued *entity* describes different taxa (e.g., `data:environment:sources` may contain a vector of references to different sources and a value of *taxonSpecific*=no indicates that these sources apply generally and not to different taxa). Note that any entity with taxon-specific values can optionally be specified as `[{"species1":value1, "species2":value2}]`, but users can also choose the simpler multispecies vector formatting with `value1,value2`, etc.

In multispecies studies, *entities* can take single or multiple values and are associated with a vector of taxon names. Thus an *entity* may have a single value if it is constant for all study taxa, or a vector of values associated with their respective taxa. This framework can also be thought of as a table with columns for taxa and rows for *entities*. For example, a study containing two species would specify their names (using R syntax for convenience) as `data:occurrence:taxon=c('taxon1','taxon2')`, and all subsequent entities can be provided with values as vectors of length 2 when the value differs among species or length 1 when the value is the same among species (e.g., `data:occurrence:presenceSampleSize=c(24137, 4520)` and `data:occurrence:yearMax=2018`, respectively). Models of each taxon in a study are likely to have different properties, such as presence sample size, but may also have different model settings. Indeed, model evaluation and ecological reality of the response may be greatly improved by tuning parameters to individual datasets (Merow *et al.*, 2013, 2014; Muscarella *et al.*, 2014).

For simplicity in multispecies studies, users can specify unique values of an *entity* for each species as just described or a character string describing a methodological rule for choosing the value. Most model settings have ...`Set` and ...`Rule` entities that users can choose from. For example, when thresholding continuous predictions to make a binary map, `modelFit:prediction:thresholdSet=c(.003,.002)` could be used to indicate the specific threshold values or alternatively `modelFit:prediction:thresholdRule='5% training presence'` could be used to identify the rule to determine the thresholds applied to multiple taxa. In cases where multiple modeling algorithms are relevant, we recommend making a separate `rmm` object for each algorithm—-this is designed to keep `rmm` objects easily human-readable and avoid confusion about *entities* that might have similar inputs but different names/interpretations with different modeling approaches.

4.12 Common Use Cases

To help guide users through determining which *entities* to include, we define a suite of common *families* of *entities* in the metadata dictionary that may be relevant for a given study. As a baseline, the *base family* defines the minimum set of entities used to define a typical model. Certain *entities* are obligate, such as those relating to data sources, while others are recommended as typically sufficient to meet research community standards, and yet others are entirely optional. Researchers can modularly combine the *base family* with other *families* to represent different workflows that most closely match their study type as a template (examples in Table 1). *Entities* can then be added or removed as seen fit (except for obligate *entities*, which can be left empty but not deleted so that the decision to omit them is readily apparent).

Some *entities* are conditionally obligate: e.g., if any *entities* in the optional field `prediction:transfer:environment1` (defining the environmental conditions, perhaps for some data set on future conditions for model transfer) are non-NULL, related *entities* must have non-NULL values (`:yearMin, :yearMax, :resolution, :extent, :sources`). Hence someone modeling the future extinction risk of a species with Maxent could combine the families *obligate, dataPrep, maxent* (*entities* associated with the Maxent modeling algorithm), and *transferEnv1* (entities associated with environmental conditions where a model is projected) as a starting point for their metadata template.

5 rangeModelMetadata R Package

Although our RMMS framework is software-agnostic, we simplify the process of building a metadata list by providing an R package, `rangeModelMetadata`, which provides a number of user-friendly tools that define, print, autofill, query, and check `rmm` S3 objects. It begins by defining the *families* of *entities* relevant to the study to generate an empty template. These templates are defined as lists of lists which capture the natural hierarchical structure of our metadata documentation scheme. As shown in Figure 1, this structure allows users to get or set values of particular *entities* using the format `field1$field2$field3$entity` (e.g. `model$algorithmSettings$maxent$featureSet,` or `output$prediction$units` in the case where only the first two fields are relevant. To enable flexibility for analysis outside of R, we provide tools to export `rmm` objects as csv files.

The `rangeModelMetadata` package provides a number of convenience features. `rmmPrintFull()` displays only non-null entities while `rmmPrintEmpty()` displays only null entities to help determine missing information. These can further be parsed into obligate and optional entities. To reduce errors and simplify information entry, we provide a number of `rmmAutoFill...()` functions that capture relevant information from commonly used R objects during modeling. For example, in the simplest case, one can provide a `raster::stack` of environmental input layers or model predictions to automatically fill in associated metadata entities. Similar functionality exists for citations, occurrence data, and `ENMeval` (Muscarella *et al.*, 2014) objects. These functions also provide useful examples for other package developers to write `rmmAutofill...()` functions to connect to new packages. For further refining inputs, `rmmSuggests()` has predefined options for input entities and their values.

We provide a number of automated checks to help researchers detect potential issues (e.g., misspellings) and ensure some level of standardization with a number of `rmmCheck...()` functions. Checking standards are drawn directly from terms in the data dictionary and hence update automatically with any changes. Multiple checks are available, including those for standardized fields (`rmmCheckNames`), standardized entities (`rmmCheckValues`), missing fields (`rmmCheckMissingNames`) and empty entities (`rmmCheckEmpty`). Each check function returns information on names that are (1) matched exactly to standardized values, (2) names of partial matches to standardized values, and (3) unmatched names. This enables users to see what changes might be relevant while allowing them the flexibility to ignore the suggestions and include their own custom names or values. Checks for empty entities can be split into obligate, recommended, and optional entities to help users determine missing information. For a final check of all entities in an `rmm` object, we provide the `rmmCheckFinalize()` function that runs all the `rmmCheck...()` functions together.

The `rangeModelMetadata` package include a number of other facilities. The base R function `str()` can print an `rmm` object to different field depths. `rmmToCSV`() exports the `rmm` object into a 'flat' csv format that is readable by other software platforms and more human-readable. Finally, users can also specify their own custom entities to accommodate metadata for less-common or currently undeveloped tools, e.g.,

```
modelFit:algorithm:algorithmSettings:`userDefinedEntity`=x
```

where `` `userDefinedEntity` `` is a name provided by the user and `x` is its value.

6 Discussion

We propose a comprehensive framework for recording metadata on range models that enhances transparency, reproducibility, and sharing. To reduce the burden on researchers to provide this information, we have developed an R package with a variety of convenience functions to fill, suggest, and check metadata objects efficiently. We anticipate that these advances will enable better comparisons between studies and synthesis across disciplines, improved models based on the ability to readily check for best practices, and improved citability and sharing of knowledge products.

Our decision to make `rmm` objects extensible, rather than tightly constrained, reflects our goal of prioritizing convenience to researchers, but involves some tradeoffs. A rigidly-structured object with strictly predefined entities and values for those entities would ensure standardization, prevent errors due to typos, and generally be more easily searchable. However, as the field of range modeling is always growing, an exhaustively prescriptive metadata framework would be impractical to maintain and would likely involve such a lengthy manual that it would inhibit use.

Hence we have elected to implement a more lightweight and flexible framework with fewer entities that can be more readily adapted to any range modeling workflow. It remains the responsibility of the researchers, editors, and data providers to curate the text in these entities to ensure clarity and precision.

To enable an evolving data dictionary we will maintain it on Github so that contributions and suggestions are readily tracked, discussed, and incorporated. We ultimately plan to follow Github vocabulary management processes similar to those used by the Darwin Core maintenance group (see https://github.com/tdwg/dwc). We will serve as an initial governance board to moderate proposed changes but welcome others to join our team, particularly those with different expertise. Facilitating community-moderated evolution of the data dictionary will be the subject of future work and will depend critically on the reception and responses to the currently proposed framework. We aim for RMMS to be a fully open source and community driven enterprise.

RMMS has the potential to improve the review process for manuscripts using range models. Journals may choose to define their own families of standards for particular applications or to adopt those we propose. These standards (and convenience functions like `rmmCheckFinalize()`) will make it easier for authors checking model details before journal submission and for journal reviewers/editors checking the compliance and completeness of submitted `rmm` objects. To allow a broader user base to easily evaluate `rmm` objects, we have developed a web-based graphical interface (with the R package shiny; (Chang *et al.*, 2017)) that enable users to upload an `rmm` object either as a CSV or RDS (R's data format for a single object) file and check for missing fields or standardization issues Figure 3). It can be accessed within R using the two commands:

```
library(rangeModelMetadata)
rmmCheckShiny()
```

Because Shiny applications are built over the top of R, this allows us to use the exact R code that console users would use to check `rmm` objects. The code used for checking and the results can readily be exported so that editors can share these results with authors without ambiguity. Finally, the application includes options to submit multiple `rmm` objects to report differences among them for comparing with previous studies.

Defining community standards can support reporting and help encourage best-practice approaches to science. Suboptimal methodologies will become more immediately transparent and requests for metadata information will encourage researchers to conduct more comprehensive analyses and supply information that is vital for their peers to understand, evaluate, and use their work. (Araújo *et al.*, 2019) recently proposed a set of best practices and reporting standards for the use of SDMs in biodiversity models; our metadata standards and tools reflect these same ideals. For example, best practices can be established by defining a family of the entities required for biodiversity assessments (e.g., a new `biodiversity` family). By proposing standardized values associated with acceptable practices for the biodiversity use case, best practices can be clearly defined (e.g., to characterize the quality of predictor variables proposed by (Araújo *et al.*, 2019)).

Community standards mean that both smaller scale efforts or larger taxon-region specific projects that produce range models can do so in a way that supports community efforts and assures that catalogs across independent efforts can be developed. Any downstream uses will benefit from the transparency enabled by the standards which should enhance the rigor and credibility of range models for, e.g., conservation application for more applied outcomes. Similar to how standards such as Darwin Core or Humboldt Core are facilitating the combination of point and inventory data of often vastly different origins (Wieczorek *et al.*, 2012; Guralnick *et al.*, 2017) in support of aggregators such as the Global Biodiversity Information Facility (GBIF), we hope that RMMS and its future evolution will set the stage for a more programmatic synthesis of range models and their products. For example, in Map of Life, which is integrating biodiversity information to develop a range of species distribution resources and both produces and consumes range models, RMMS opens up the opportunity for a more informed visual and quantitative comparison and eventually integration of range models produced by different groups. Thus the standards open the door for contributed range models from taxon experts to enable their aggregation and integration in support of advancing the biodiversity knowledge base broadly.

As RMMS evolve and grow, we will facilitate other software developers to link their work easily to `rangeModelMetadata` and enable `rmm` objects to be largely autofilled based on the output of other R packages. For example, in complex cases involving more comprehensive range modeling workflows such as *Wallace* (Kass *et al.*, 2018), an R-based ecological modeling software, or those used by BIEN and MOL, filling in `rmm` object entities can be built into the workflow. In *Wallace* an additional top level *field*, `wallace:`, is added to store additional information that can be used to reproduce a session. Other workflows may similarly benefit from reading in settings from `rmm` objects to automatically select parameters, in which case `rmm` objects would serve as automatic lab notebooks to reproduce analyses. This next stage of integration with other software tools will serve as way to further refine and maintain the data dictionary while engaging key range modeling teams in the process.

The range model metadata standards that we propose provide a number of tools to clarify and streamline reporting, sharing, evaluating and searching range models. We consider this the beginning of a community process rather than its endpoint, and the standards are therefore software agnostic, extensible and readily updated. If further engagement, adoption, and advancement by others is successful, the proposed standards hold long-term benefits for the larger community and the impact of their work.

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8 Data Accessibility Statement

All code is maintained on Github (https://github.com/cmerow/rangeModelMetadata) and also served on CRAN (http://cran.us.r-project.org/).

9 Tables

Table 1. An example of entries in the `rmm` metadata dictionary. The full dictionary is available in Supplement SS1. *Fields* specify the hierarchy of the metadata object while *entities* define the quantity of interest. *Entities* are assigned *values* as shown in the examples (example values are separated by semicolons). *Families* specify collections of related entities used for generating templates and checking for conditionally obligate entities. The examples column shows a variety of appropriate values which might be relevant in different studies.

field1	field2	field3	entity	family	examples
authorship			rmmName	base	MerowMaitnerOwensKassEnquistGuralnick_2018_Acer_Maxent_b3
authorship			license	base	CC; CC BY; CC BY-SA; CC BY-ND; CC BY-NC; CC BY-NC-SA; CC BY-NC-ND
studyObjective			purpose	base	projection
studyObjective			rangeType	base	potential; realized
studyObjective			invasion	base	native; invasive; naturalized; colonized
data	occurrence		taxon	base	Acer rubrum; Nasua_nasua;
data	occurrence		dataType	base	presence only; presence-absence; abundance
data	occurrence		occurrenceType	NULL	breeding; wintering; migratory; resident
data	occurrence		yearMin	base	1900
data	occurrence		yearMax	base	2000
data	occurrence		presenceSampleSize	occurrence, po, pa	87
data	occurrence		backgroundSampleSizeSet	occurrence, po	1000
data	environment		variableNames	base	bio1, bio4, bio12, bio15
data	environment		minVal	transferEnv2	[{”bio1”:-273,”bio12”:0,”bio15”:0,”bio2”:9}]
data	environment		maxVal	transferEnv2	[{”bio1”:292,”bio12”:10017,”bio15”:246,”bio2”:212}]
data	environment		yearMin	base	1970
data	environment		yearMax	base	2000
data	environment		extentSet	base	[{”xmin”:-5582581.9734,”xmax”:5367418.0266,”ymin”:-7389365.067,”ymax”:7410634.933}]
modelFit			algorithm	base	generalized linear model; generalized additive model; boosted regression trees; maxent; bioclim; Poisson point process; range bagging; all biomod2 models;
modelFit	maxent		featureSet	maxent	L; LQ; LQP; LQPT; LQPTH; H; HT
modelFit	maxent		featureRule	maxent	L for <50 presences; LQ for >= 50 presences
modelFit	maxent		regularizationMultiplierSet	maxent	1, 1.5, 2, 2.5, 3
modelFit	maxent		regularizationRule	maxent	Chosen based on 5-fold cross validation on a grid of regularization multipliers from [0;10]
modelFit	maxent		convergenceThresholdSet	maxent	1.00E-05
modelFit	maxent		samplingBiasRule	maxent	target group; offset; none;
modelFit	maxent		samplingBiasNotes	maxent	NULL
prediction	transfer	environment1	units	transferEnv1	absolute probability; relative occurrence rate; presence/absence
prediction	transfer	environment1	minVal	transferEnv1	0.001
prediction	transfer	environment1	maxVal	transferEnv1	0.97
prediction	transfer	environment1	thresholdSet	transferEnv1	0.34
prediction	transfer	environment1	thresholdRule	transferEnv1	5% quantile of training presences
prediction	transfer	environment1	extrapolation	base	clamping; extrapolate function
evaluation	trainingDataStats		AUC	binaryClassification	0.923
evaluation	testingDataStats		AUC	binaryClassification	0.923
evaluation	evaluationDataStats		AUC	binaryClassification	0.923
code	software		platform	base	@Manual{title = {R: A Language and Environment for Statistical Computing},author = {{R Core Team}},organization = {R Foundation for Statistical Computing},address = {Vienna, Aus-

10 Figures

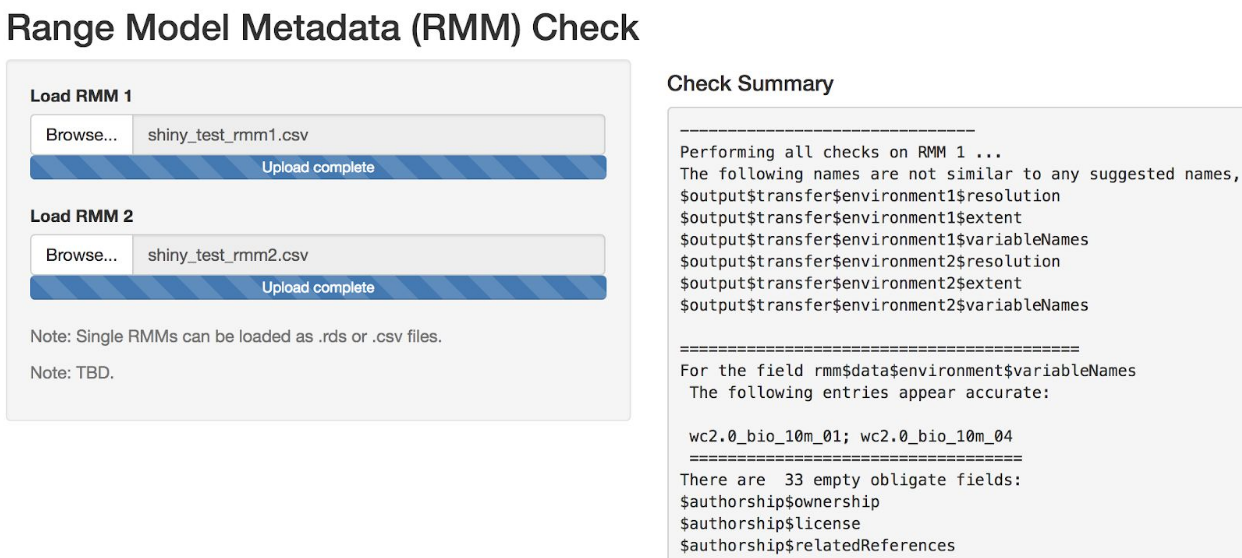
Figure 1. An example rmm object template generated in R. Note the hierarchical list structure. This example includes only the entities that are considered fundamental for use with every range model. Top level fields are indicated with bold.

```
> rmm1=rmmTemplate(family=c('base'))
> str(rmm1,2)
List of 8
 $ authorship    :List of 9
  ..$ rmmName        : NULL
  ..$ names          : NULL
  ..$ ownership      : NULL
  ..$ license        : NULL
  ..$ contact        : NULL
  ..$ relatedReferences: NULL
  ..$ authorNotes      : NULL
  ..$ miscNotes        : NULL
  ..$ doi              : NULL
 $ studyObjective :List of 4
  ..$ purpose  : NULL
  ..$ rangeType: NULL
  ..$ invasion : NULL
  ..$ transfer : NULL
 $ data          :List of 4
  ..$ occurrence :List of 6
  ..$ environment:List of 9
  ..$ observation:List of 3
  ..$ dataNotes  : NULL
 $ dataPrep      :List of 1
  ..$ dataPrepNotes: NULL
 $ modelFit      :List of 9
  ..$ algorithm        : NULL
  ..$ algorithmCitation : NULL
```

Figure 2. An example rmm object with values, based on the example from the main text. Top level fields are indicated with bold. Note that some output has been omitted from the figure for space, indicated by *truncated.*

```
$ authorship    :List of 6
      [truncated]
$ studyObjective:List of 3
 ..$ purpose  : chr "transfer"
 ..$ rangeType: chr "potential"
 ..$ transfer : chr "detect unoccupied suitable habitat"
$ data          :List of 4
 ..$ occurrence :List of 7
 .. ..$ dataType              : chr "presence only"
 .. ..$ yearMin               : num 1970
 .. ..$ yearMax               : num 2000
 .. ..$ sources               :List of 16
      [truncated]
 .. ..$ backgroundSampleSizeSet: int 5359
 .. ..$ presenceSampleSize     : int 122
 .. ..$ backgroundSampleSize   : int 5359
 ..$ environment:List of 7
      [truncated]
 ..$ dataNotes  : chr "WorldClim data accessed through dismo v1.1-4"
 ..$ transfer   :List of 1
 .. ..$ environment1:List of 6
      [truncated]
$ dataPrep      :List of 3
 ..$ geographic   :List of 1
 .. ..$ spatialThin:List of 1
 .. .. ..$ rule: chr "20km used as minimum distance between points"
 ..$ biological   :List of 1
 .. ..$ duplicateRemoval:List of 1
 .. .. ..$ rule: chr "one observation per cell"
$ modelFit      :List of 5
 ..$ algorithm         : chr "Maxent 3.3.3k via dismo 1.1.4"
 ..$ selectionRules    : chr "highest mean test AUC"
 ..$ finalModelSettings: Factor w/ 6 levels "L_1","L_2","L_3",..: 4
 ..$ partition         :List of 5
 .. ..$ partitionSet         : chr "spatial blocks"
 .. ..$ partitionRule        : chr "block cross validation: partitions occurrence
                    localities by finding the latitude "| __truncated__
 .. ..$ notes                : chr "background points also partitioned"
 .. ..$ occurrenceSubsampling: chr "k-fold cross validation"
 .. ..$ numberFolds          : int 4
 ..$ maxent            :List of 5
 .. ..$ featureSet                 : chr "LQ"
 .. ..$ regularizationMultiplierSet: num 1
 .. ..$ samplingBiasRule           : chr "ignored"
 .. ..$ notes                : chr "ENMeval was used to compare models with
                    L and LQ features, each using  "| __truncated__
 .. ..$ numberParameters           : num 13
$ prediction    :List of 3
 ..$ extrapolation: chr "clamping"
      [truncated]
 ..$ continuous   :List of 3
 .. ..$ units : chr "relative occurrence rate"
 .. ..$ minVal: num 1.19e-12
 .. ..$ maxVal: num 0.0164
$ evaluation    :List of 1
 ..$ testingDataStats :List of 3
 .. ..$ AUC         : num 0.802
 .. ..$ omissionRate: num [1:2] 0.0501 0.2207
 .. ..$ notes       : chr "omission rate thresholds are 1) minimum training
      presence, 2) 10% training presence"
$ code          :List of 2
 ..$ software        : chr "@Manual{\n  title = {R: A Language and
       Environment for Statistical Computing},\n  "| __truncated__
 ..$ vignetteCodeLink: chr "https://github.com/cmerow/"| __truncated__
```

Figure 2. A screenshot of the web-based Shiny app that enables checking and comparing `rmm` objects without writing code. The Check Summary continues on to report on a number of other comparisons, omitted here for the sake of space.



11 Supplementary Materials

S1. Metadata dictionary. Current version of the metadata dictionary. This currently exists as a google sheet and is served on Github (https://github.com/cmerow/rangeModelMetadata/blob/master/inst/extdata/dataDictionary.csv) to enable updating and this static version is distributed with `rangeModelMetaData` package. Download the most recent version of the `rangeModelMetaData` package from CRAN for any updates.

S2. Function directory for `rangeModelMetaData` package. This is distributed as a vignette with the package. Download the most recent version of the `rangeModelMetaData` package from CRAN for any updates.

S3. `rangeModelMetadata` vignette. This is distributed as a vignette with the R package. Download the most recent version of the `rangeModelMetaData` package from CRAN for any updates.

S4. A complete example workflow. This includes building a range model and building a rangeModelMetadata object. This follows the example in the main text and Figure 1, and is distributed as a vignette with the R package. Download the most recent version of the `rangeModelMetaData` package from CRAN for any updates.

S5. Full CSV template. A complete template of all entities, as a csv, for users who prefer to enter values manually.

S6. Minimal CSV template. A template of base entities (minimum criteria) as a csv for users who prefer to enter values manually.