

iDADwgl - an R package for open-system uranium-thorium dating

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Abstract

For several decades, uranium-thorium (U-Th) dating has allowed geochronologists to precisely date geological materials, providing invaluable geochronological constraints on Quaternary processes. Open-system dating of bones and teeth has also provided ages of human and faunal remains of archaeological significance.

To facilitate access of open-system U-Th dating to the broad scientific community, here we provide an R package, named *iDADwgl*, that implements the Diffusion-Adsorption-Decay model of Sambridge et al. (2012). Description of input and output parameters is given, as well as a guide for running the model. The package can be used three different ways: (i) as a web application, (ii) through your browser or (iii) in R studio. Examples of application of the model are also provided, showing that it yields ages within error of previously published values.

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1 Introduction

2 Open-system uranium-thorium (U-Th) dating of teeth and bones, while chal-
3 lenging, has revolutionised our ability to provide reliable chronology for humans
4 and fauna (Eggins et al. 2005; Grün et al. 2014; Sambridge, Grün, and Eggins
5 2012). Thus, this approach has significantly improved our understanding of hu-
6 man evolution (e.g. Dirks et al. 2017; Sutikna et al. 2016). Uranium-thorium
7 dating is based on the premise that a material takes up U but no Th, so all the
8 ^{230}Th in the sample comes from decay of ^{238}U . If detrital Th is included to the
9 sample, a correction must be included to account for the fraction of ^{230}Th which
10 is detrital and not derived from ^{238}U decay. Another requirement is that there
11 is no gain or loss of ^{230}Th , ^{234}U or ^{238}U after formation of the material. While it
12 is often the case for many geological samples such as corals or speleothems, this
13 requirement is rarely met for teeth and bone (although enamel can sometimes be
14 quite impervious to isotope gain or loss). Thus, for teeth and bone, U-Th dating
15 requires to take into account open system behaviour. The diffusion-adsorption-
16 decay (DAD) model developed by Sambridge et al. (2012) was instrumental to
17 implement successfully open-system U-Th dating. It allows for advective and
18 diffusive transport of uranium and thorium isotopes, while include synchronous
19 radioactive decay. The software implementation was written in Fortran and is
20 available as a Java GUI (<http://www.earth.org.au/codes/iDaD/>). In this arti-
21 cle, we propose a R package which implements the model of Sambridge et al.
22 (2012).

23 The motivation for providing this model as an R package is to increase
24 the transparency, reproducibility, and flexibility of the analytical workflow for
25 computing U-Th ages. Currently it is difficult to include the Java GUI in a
26 fully scripted data analysis so the method for computing the DAD model is not
27 highly transparent. This can obscure steps where key decisions are made that
28 are important for others to see to verify the reliability of the analysis. Enabling
29 a scripted workflow for computational analysis of geoscience data is important
30 for improving the reproducibility of results. Reproducibility refers the ability to
31 recreate the results or retest the hypotheses leading to a scientific claim, either
32 by rerunning the same code used by the original authors, or by writing new
33 code. High rates of irreproducibility of research results have been estimated
34 in several fields and disciplines (Medical Sciences 2015; Freedman, Cockburn,
35 and Simcoe 2015; Institute 2013; Ioannidis 2005; Collaboration and others 2015;
36 Camerer et al. 2018, 2016). Consequently, the transparency, openness, and
37 reproducibility of results and methods are receiving increased attention, and
38 the norms of research in many fields are changing (Nosek et al. 2015; Miguel et
39 al. 2014; Marwick 2016).

40 There is strong interest in open, transparent, and reusable research in the
41 geoscience community (Gil et al. 2016) and substantial progress toward open
42 data has been made in the geosciences with the widespread use of data services
43 of NASA, USGS, NOAA and community-built data portals such as OneGeol-
44 ogy, EarthChem, RRUFF, PANGAEA, PaleoBioDB, and others (Kattge, Díaz,
45 and Wirth 2014; Ma 2018). However, the use of open source software such

as R (Pebesma, Nüst, and Bivand 2012), and sharing of scripted data analysis workflows with research publications is not yet widespread (Hutton et al. 2016). With this R package our goal is to make scripted and reproducible data analysis easy for open-system uranium-thorium dating. This will improve the transparency of geochronology research, and provide a more credible and robust foundation for scientific advancement (Hutton et al. 2016).

To enable re-use of our materials and improve reproducibility and transparency, all the results and visualisations in this paper can be reproduced using the RMarkdown vignette document included with the iDADwgl package. We have archived these files at <http://doi.org/10.17605/OSF.IO/D5P7S> to ensure long-term accessibility. Our code is released under the MIT licence, our data as CC-0, and our figures as CC-BY, to enable maximum re-use (for more details, see Marwick 2016).

Methods

Data required for the DAD model are ($^{230}\text{Th}/^{238}\text{U}$) and ($^{234}\text{U}/^{238}\text{U}$) activity ratios collected along a transect perpendicular to the surface of the tooth or bone (brackets denote activity ratios throughout this article). Sampling for analysis can be done by micro-drilling or laser ablation. If the former, aliquots are then dissolved, followed by separation of U and Th using ion exchange chromatography. This is more time consuming (at least one week of work) than laser ablation, where the material sampled by the laser is directly sent to the mass spectrometer.

While laser ablation also offers a better spatial resolution than micro-drilling, the precision of the data is inferior because of the much smaller amount of material sampled. Uranium and thorium isotope ratios are then analysed by multi-collector inductively-coupled plasma mass spectrometry. A plasma ionise all U and Th atoms, their isotopes are separated through a magnetic field and each collected in a different collector. If using laser ablation, it is best to have two ion counters so ^{230}Th and ^{234}U can be collected simultaneously.

The distance of each analysis location from the inner and outer surfaces of the bones, for instance, needs to be recorded. One surface is given a coordinate of 1 and the other one -1, thus coordinates of analyses take values in between (Figure 1).



Figure 1: Modern human femur (132A/LB/27D/03) from Liang Bua, Flores, Indonesia. Two analysis transects can be seen. For a given transect, the outer and inner surface of the bone are given 1 and -1 reference coordinates, and the position of each analysis is calculated accordingly. Modified from Sutikna et al. (2016)

79 Working with the package

80 We provide three methods for using this package to suit different levels
 81 of familiarity with the R programming language. The simplest way to use the
 82 package is our web application (Figure 2). Using the web application requires no
 83 familiarity with R. To use the web application you upload a CSV file, then click
 84 through a series of tabs to inspect the data, adjust the model parameters, run
 85 the model, and inspect the output. The interface is mouse-driven and requires
 86 no programming. In the web application you upload the data file on the *Load*
 87 *the data* tab, set parameters from the *Set model parameters* tab, run the model
 88 by clicking the button *Run Simulation* on the same tab, and observe the results
 89 on the *Visualise the model* and *Inspect the model* tabs. You can change the
 90 parameters and re-run the model by click the button *Run Simulation*. Once
 91 done, close the window.

92 The second way to use the package is with Binder, a browser-based instance
 93 of R and RStudio that includes our package ready to work with. Binder is a
 94 server technology that turns computational material, such as an R package, into
 95 interactive computational environments in the cloud. Using Binder requires a
 96 novice level of familiarity with R, for example to use the code in this paper and
 97 adapt it to work with a different CSV file. Because Binder provides a complete
 98 R environment, custom R code can be written during a Binder instance to
 99 further explore the model's output in the browser. These two methods, the
 100 web application and Binder, do not require any software to be downloaded and

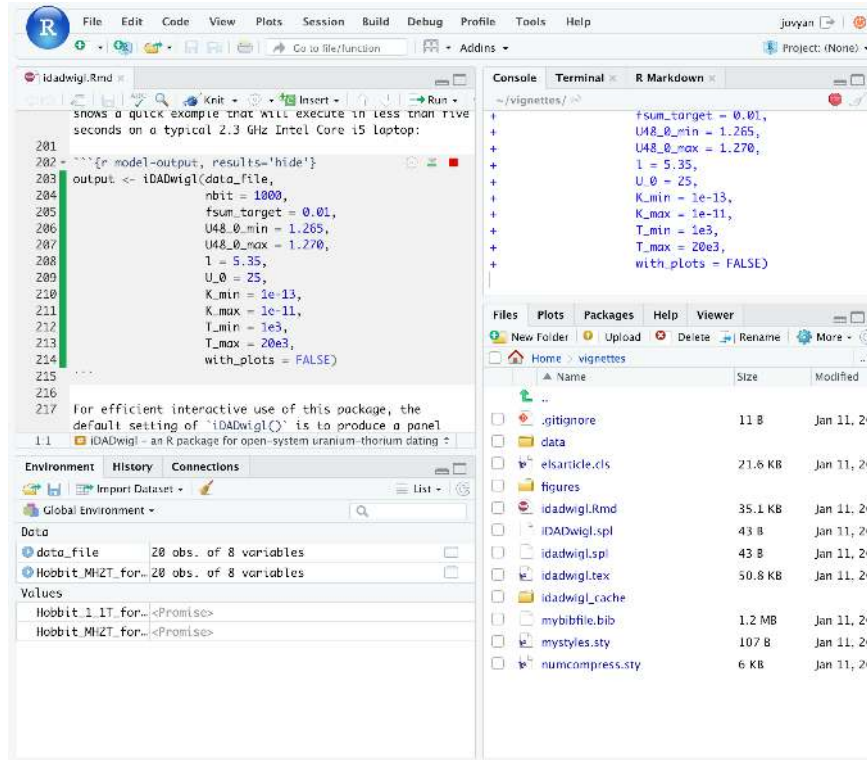


Figure 3: Screenshot of Binder running R and RStudio in a web browser window.

installed on your computer, all computation occurs in the browser. The web app and Binder are suitable for getting a quick start on working with the package, but they require a connection to the internet, and they have limited memory and compute time available per instance.

The third method is to download and install the package locally to your computer, and work with it in your local installation of R and RStudio. This method requires some familiarity with R, but gives the most flexibility when working with the model because you are not limited by the memory and compute time of the cloud services. Our recommendation is to use Binder or a local installation of `iDADwgl` because then you can save an R script file that includes the name of the input file, the specific parameters used to generate the model output, and any downstream processing and visualisation. This script file and the CSV file can then be archived in a data repository to ensure long-term accessibility for other researchers.

Installing and attaching the package

First you will need to download and install R, and we also recommend downloading and installing RStudio. To run the model, start RStudio and install the

118 package from GitHub. There are many ways to do this, one simple method is
119 shown in the line below. This only needs to be done once per computer.

```
source("https://install-github.me/tonydoss/iDADwig1")
```

120 For routine data analysis, R scripts need to contain the following line to
121 attach the package to the current working environment. This line needs to be
122 run at the start of each analysis:

```
# attach the package  
library(iDADwig1)
```

123 Alternatively, the model can be run from your browser without installing R
124 or RStudio with this link.

125 Input data format

126 The key function of our package, `iDADwigl()` requires a data frame (a form
127 of table in R) with the following column names:

- 128 • `iDAD.position`
- 129 • `U234_U238_CORR`
- 130 • `U234_U238_CORR_Int2SE`
- 131 • `iDAD.position.1`
- 132 • `Th230_U238_CORR`
- 133 • `Th230_U238_CORR_Int2SE`
- 134 • `U_ppm`
- 135 • `U_ppm_Int2SE`

136 To help with preparing data for input into our function, we have included
137 two examples of input files. Inspecting the included data sets will be helpful for
138 understanding how to prepare new data to prepare for use with this package.
139 After attaching the package, we can access the built-in datasets with the `data()`
140 function, like this:

```
# access the data included in the iDADwigl package  
data("Hobbit_1_1T_for_iDAD")  
data("Hobbit_MH2T_for_iDAD")
```

141 This will make the built-in data available in the R environment to inspect
142 and explore how to use the `iDADwigl()` function.

143 To use new data with this package, we need to import a CSV or Excel file
144 with the U-Th data into the R environment using a generic function such as
145 `read.csv` or `read_excel` from the `readxl` package (Wickham and Bryan 2018).
146 The code chunk below shows how to read one of the CSV files included in the
147 package into the R environment. This is a good method to use if you supply
148 your own CSV file to use with `iDADwigl()`. In this case we assume that the
149 working directory contains a directory called `data` and our CSV file is in this
150 `data` directory:

```
# read in one of the example CSV files included in the package  
data_file <-  
read.csv('data/Hobbit_MH2T_for_iDAD.csv')
```


Table 1 shows the data contained in the `Hobbit_MH2T_for_iDAD.csv` file included in the package

iDAD.position	U234_U238_CORR	U234_U238_CORR_Int2SE	iDAD.position.1	Th230_U238_CORR	Th230_U238_CORR_Int2SE	U_ppm	U_ppm_Int2SE
-0.956	1.270	0.004	-0.956	0.073	0.002	12.3	0.6
-0.857	1.273	0.004	-0.857	0.073	0.002	12.7	0.6
-0.758	1.265	0.004	-0.758	0.076	0.002	12.5	0.6
-0.659	1.267	0.005	-0.659	0.077	0.002	14.2	0.7
-0.560	1.269	0.003	-0.560	0.072	0.002	19.8	1.0
-0.461	1.266	0.003	-0.461	0.077	0.002	18.0	0.9
-0.361	1.267	0.003	-0.361	0.082	0.002	20.0	1.0
-0.262	1.276	0.002	-0.262	0.079	0.001	27.2	1.4
-0.163	1.266	0.002	-0.163	0.075	0.001	26.7	1.3
-0.064	1.277	0.002	-0.064	0.073	0.001	0.3	0.0
0.035	1.271	0.002	0.035	0.078	0.002	33.9	1.7
0.134	1.264	0.002	0.134	0.067	0.001	37.7	1.9
0.233	1.266	0.003	0.233	0.071	0.001	30.7	1.5
0.332	1.265	0.002	0.332	0.077	0.002	25.2	1.3
0.431	1.266	0.003	0.431	0.083	0.001	28.9	1.4
0.530	1.268	0.003	0.530	0.086	0.002	29.0	1.4
0.629	1.264	0.003	0.629	0.082	0.002	27.5	1.4
0.728	1.263	0.002	0.728	0.070	0.001	30.1	1.5
0.827	1.266	0.005	0.827	0.095	0.002	19.6	1.0
0.926	1.263	0.003	0.926	0.096	0.002	14.8	0.7

Table 1: Data contained in the example CSV file `Hobbit_MH2T_for_iDAD.csv` included in the package

The columns `iDAD.position`, `U234_U238_CORR`, `U234_U238_CORR_Int2SE`, `Th230_U238_CORR` and `Th230_U238_CORR_Int2SE` must be present in the input data frame with these exact names for the model to function. The `iDADwig1()` function will check if the input data frame has these columns, and will stop with an error message if it does not find these columns. The `names()` function can be used to update column names of a data frame to ensure they match the names that the model function requires. The order of the columns in the data frame is not important.

161 The `iDAD.position` column corresponds to the coordinates of the ($^{234}\text{U}/^{238}\text{U}$)
 162 analyses, which as indicated above take values between -1 and 1 (Figure 1). The
 163 second `iDAD.position.1` column is used if the coordinates of the ($^{230}\text{Th}/^{238}\text{U}$)
 164 analyses are different from those of the ($^{234}\text{U}/^{238}\text{U}$) analyses.
 165 Columns `U234_U238_CORR` and `U234_U238_CORR_Int2SE` are the ($^{234}\text{U}/^{238}\text{U}$)
 166 activity ratios and their 2σ errors. Columns `Th230_U238_CORR` and `Th230_U238_CORR_Int2SE`
 167 are the ($^{230}\text{Th}/^{238}\text{U}$) activity ratios and their 2σ errors.
 168 Columns `U_ppm` and `U_ppm_Int2SE` are the calculated uranium concentra-
 169 tions (in ppm) and their 2σ errors. Uranium concentrations are not necessary
 170 for the model but needed to display the U concentration profile in a figure.

171 Details of the input parameters

172 Our key function, `iDADwigl()` has several arguments that need to be set
 173 before we can get meaningful results.

174 `nbit` is the number of iterations. For the first run, set to 1.

175 `fsum_target` is the sum of the squared differences between the calculated
 176 and observed activity ratios. Give it a low value to start with (e.g. 0.01). If
 177 script takes too long, try a higher value for `fsum_target`.

178 `U48_0_min` and `U48_0_max` are the minimum and maximum values allowed
 179 for the ($^{234}\text{U}/^{238}\text{U}$) activity ratio at the surface of the sample. Since ($^{234}\text{U}/^{238}\text{U}$)
 180 does not vary greatly over the time period generally studied, the values mea-
 181 sured near the surface of the sample can be used as a guide. These values
 182 can be adjusted if the model fit to the data is not optimal. For `Hobbit_1-1T`
 183 they are taken to be 1.360 and 1.375, and for `Hobbit_MH2T`, 1.265 and 1.270,
 184 respectively.

185 `l` is the thickness of the sample in centimeters. For `Hobbit_1-1T` it is 3.5
 186 cm, for `Hobbit_MH2T` it is 5.35 cm

187 `U_0` is the uranium concentration at the surface in ppm. This value does
 188 not significantly affect the model results and values from analyses near either
 189 surface of the sample can be used as a guide. For `Hobbit_1-1T` it is taken to
 190 be 15 ppm; for `Hobbit_MH2T`, 25 ppm.

191 `K_min` and `K_max` are the minimum and maximum values allowed for the
 192 uranium diffusion coefficient (in cm^2/s). Values between 10^{-13} and 10^{-11} cm^2/s
 193 are generally appropriate.

194 `T_min` and `T_max` are the minimum and maximum values for the age of the
 195 specimen (yr). If there is no estimated knowledge of the sample age, the range
 196 of values can be 1,000 to 500,000 yr and adjusted later. For `Hobbit_1-1T`,
 197 in the final model run, they are taken to be 50,000 and 100,000 yr, and for
 198 `Hobbit_MH2T`, 1,000 and 20,000 yr, respectively.

199 After setting the U480 maximum and minimum values, run the function and
 200 adjust these min and max values by looking at the calculated `U48_0_final`,
 201 `K_final`, and `T_final`. Adjust `T_min` and `T_max` using first estimates of the
 202 age. As you iterate, increase the `nbit` value to reduce the error.

203 How to run the model

204 Attach the package as shown above and then run `iDADwigl()`, specifying
205 the input data frame and the input parameters as described above. The code
206 block below shows a quick example that will execute in less than five seconds
207 on a typical 2.3 GHz Intel Core i5 laptop:

```
output <- iDADwigl(data_file,  
  nbit = 1000,  
  fsum_target = 0.01,  
  U48_0_min = 1.265,  
  U48_0_max = 1.270,  
  l = 5.35,  
  U_0 = 25,  
  K_min = 1e-13,  
  K_max = 1e-11,  
  T_min = 1e3,  
  T_max = 20e3,  
  with_plots = FALSE)
```

208 For efficient interactive use of this package, the default setting of `iDADwigl()`
209 is to produce a panel plot as seen in Figure 4(Figure 4. The setting `with_plots`
210 `= FALSE` prevents plots from being generated which is more useful when the
211 function is part of a longer sequence of code. The function runs faster when not
212 producing pots, which is helpful when replicating many runs.

213 When run on the R console, this function will print a confirmation that the
214 input data frame has the required columns, and print the resulting age value
215 with an error reported as the 67% and 33% quantiles, for instance:

```
216 All required columns are present in the input data  
217 [1] "Age: 7 +0.6/-0.7 ka"
```

218 The model computes a Monte Carlo simulation where age of the sample,
219 U diffusion coefficient and ($^{234}\text{U}/^{238}\text{U}$) ratio at the surface of the sample are
220 taken randomly within the range of values allowed. Results are only kept if the
221 calculated sum of the squared differences between the calculated and observed
222 activity ratios is less than the value set in `fsum_target`. If this is the case,
223 the calculated ratios and the set of solutions for age of the sample, U diffusion
224 coefficient and ($^{234}\text{U}/^{238}\text{U}$) ratio at the surface of the sample are saved. The
225 model stops once the number of sets of solutions reaches `nbit`.

226 The final calculated age `T_final` (in yr), U diffusion coefficient `K_final` (in
227 cm^2/s) and ($^{234}\text{U}/^{238}\text{U}$) ratio at the surface of the sample `U48_0_final` are the
228 set of solutions where the solution age is the closest to the median age of the
229 population of solutions. The uncertainty on each output paramter is calculated
230 as the 67% and 33% quantiles of the population of solution sets.

231 In a typical analysis we will explore the model fit by first running the model
232 with a single iteration `nbit` and a small value for `fsum_target`, and then chang-
233 ing the range of allowed values for the ($^{234}\text{U}/^{238}\text{U}$) ratio at the surface and the
234 age of the sample. Once we obtain a satisfying fit (by visual inspection of the
235 produced figures), we would increase `nbit` to a higher value (e.g. 1000) and run
236 the model one last time. See below for an example of analysis.

237 *Inspecting the model's output*

238 `T_final`, `K_final` and `U48_0_final` are included in the model's output,
 239 along with their uncertainties. The function also includes a one-row data frame
 240 summarising the age:

Age (ka)	Age 67% quantile (ka)	Age 33% quantile (ka)	U234_ U238_0	U234_ U238_0 67% quantile	U234_ U238_0 33% quantile
6.96	0.63	0.66	1.2678	0.0022	0.0028

Table 2: Summary table of the computed age and error values

241 The last item in the output is a copy of the input data with two additional
 242 columns, the calculated activity ratios, ($^{234}\text{U}/^{238}\text{U}$) and ($^{230}\text{Th}/^{238}\text{U}$), for each
 243 measurement location on the sample.

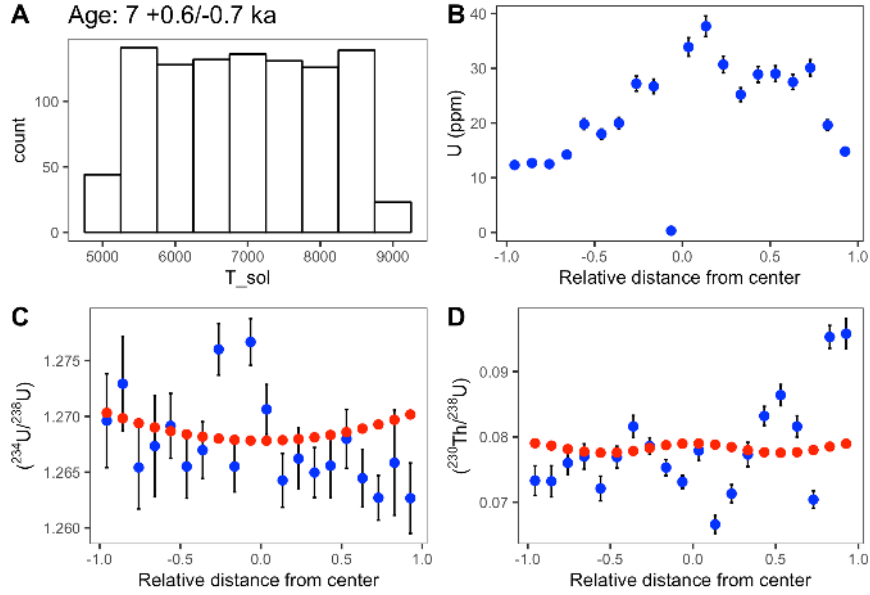


Figure 4: Example of the visualisations produced by the `iDADwig1()` function, using the demonstration run described above. A: Histogram of the solution ages, B: Uranium concentration profile for transect 2 of modern human femur 132A/LB/27D/03. C: Calculated (red) and observed (blue) $^{234}\text{U}/^{238}\text{U}$ activity ratios for transect 2 of modern human femur 132A/LB/27D/03. D: Calculated (red) and observed (blue) $^{230}\text{Th}/^{238}\text{U}$ activity ratios for transect 2 of modern human femur 132A/LB/27D/03.

Visualising the model's output

`iDADwig1()` returns several figures useful for visualisation of the model results along with the data:

1. a histogram of the solution ages (Figure 4 A)
2. the U concentrations in the sample as a function of the relative distance from the center (Figure 4 B)
3. the measured (in blue) and modelled (in red) $^{234}\text{U}/^{238}\text{U}$ activity ratios as a function of the relative distance from the center (Figure 4 C), and
4. the measured (in blue) and modelled (in red) $^{230}\text{Th}/^{238}\text{U}$ activity ratios as a function of the relative distance from the center (Figure 4 D).

iDAD.position	U234_U238_CORR	U234_U238_CORR_Int2SE	iDAD.position.1	Th230_U238_CORR	Th230_U238_CORR_Int2SE	U_ppm	U_ppm_Int2SE	U234_U238_CALC	Th230_U238_CALC
-0.956	1.270	0.004	-0.956	0.073	0.002	12.3	0.6	1.270	0.079
-0.857	1.273	0.004	-0.857	0.073	0.002	12.7	0.6	1.270	0.079
-0.758	1.265	0.004	-0.758	0.076	0.002	12.5	0.6	1.269	0.078
-0.659	1.267	0.005	-0.659	0.077	0.002	14.2	0.7	1.269	0.078
-0.560	1.269	0.003	-0.560	0.072	0.002	19.8	1.0	1.269	0.078
-0.461	1.266	0.003	-0.461	0.077	0.002	18.0	0.9	1.268	0.078
-0.361	1.267	0.003	-0.361	0.082	0.002	20.0	1.0	1.268	0.078
-0.262	1.276	0.002	-0.262	0.079	0.001	27.2	1.4	1.268	0.078
-0.163	1.266	0.002	-0.163	0.075	0.001	26.7	1.3	1.268	0.079
-0.064	1.277	0.002	-0.064	0.073	0.001	0.3	0.0	1.268	0.079
0.035	1.271	0.002	0.035	0.078	0.002	33.9	1.7	1.268	0.079
0.134	1.264	0.002	0.134	0.067	0.001	37.7	1.9	1.268	0.079
0.233	1.266	0.003	0.233	0.071	0.001	30.7	1.5	1.268	0.078
0.332	1.265	0.002	0.332	0.077	0.002	25.2	1.3	1.268	0.078
0.431	1.266	0.003	0.431	0.083	0.001	28.9	1.4	1.268	0.078
0.530	1.268	0.003	0.530	0.086	0.002	29.0	1.4	1.269	0.078
0.629	1.264	0.003	0.629	0.082	0.002	27.5	1.4	1.269	0.078
0.728	1.263	0.002	0.728	0.070	0.001	30.1	1.5	1.269	0.078
0.827	1.266	0.005	0.827	0.095	0.002	19.6	1.0	1.270	0.079
0.926	1.263	0.003	0.926	0.096	0.002	14.8	0.7	1.270	0.079

Table 3: Example of output table including the input data described above, and two new columns

254 **Case study of two ages from Sutikna et al. 2016**

255 The package includes two sample data sets derived from Sutikna et al.
 256 (2016) : “Hobbit_MH2T_for_iDAD.csv” is data from transect 2 for mod-
 257 ern human femur 132A/LB/27D/03 (shown above in Table 1). “Hobbit_1-
 258 1T_for_iDAD.csv” is data from transect 1 for *Homo floresiensis* ulna LB1/52
 259 (Table 4). For the latter, six analyses were removed from the set as in Sutikna
 260 et al. (2016).

iDAD_position	U234_U238_CORR	U234_U238_CORR_Int2SE	iDAD_position.1	Th230_U238_CORR	Th230_U238_CORR_Int2SE	U_ppm	U_ppm_Int2SE
-0.143	1.369	0.002	-0.143	0.699	0.006	32.0	1.6
0.165	1.370	0.002	0.165	0.733	0.008	41.1	2.1
0.319	1.364	0.002	0.319	0.672	0.006	35.8	1.8
0.472	1.362	0.003	0.472	0.636	0.006	27.6	1.4
0.626	1.365	0.003	0.626	0.641	0.006	31.0	1.6
0.780	1.374	0.003	0.780	0.712	0.005	27.9	1.4

Table 4: Data contained in the example CSV file Hobbit_11T_for_iDAD.csv included in the package

261 *Age of the modern human remains from Sutikna et al. 2016*

262 For transect 2 of 132A/LB/27D/03, Sutikna et al. (2016) reported an age
 263 of 7.4 ± 0.5 ka (thousand years before 2014). With iDADwigl, we first run
 264 the model with `nbit = 1`, `fsum_target = 0.05`, `U48_0_min` and `U48_0_max`
 265 `= 1.25` and `1.3`, respectively, `l = 5.35` cm, `U_0 = 25` ppm, `K_min` and `K_max`
 266 `= 10^{-13}` and `10^{-11}` cm²/s, respectively, `T_min` and `T_max = 10^3` and `500×10^3`
 267 yr, respectively. `U48_0_min` and `U48_0_max` are determined by considering the
 268 measured (²³⁴U/²³⁸U) values near the surfaces of the sample. `T_min` and `T_max`
 269 values were chosen such that no a priori knowledge of the age biases the results.

270 With this first run, we obtain an age of 6.3 ka. There is no calculated error
 271 on the age since there is only one iteration. The calculated (²³⁴U/²³⁸U) and
 272 (²³⁰Th/²³⁸U) ratios can be quite different from observed values (Figure 6). For
 273 the (²³⁴U/²³⁸U), it makes sense to thus use a narrower range for `U48_0_min` and
 274 `U48_0_max`. Higher calculated (²³⁰Th/²³⁸U) ratios compared to observed values
 275 suggests that the calculated age is too old (since this ratio increases with age),

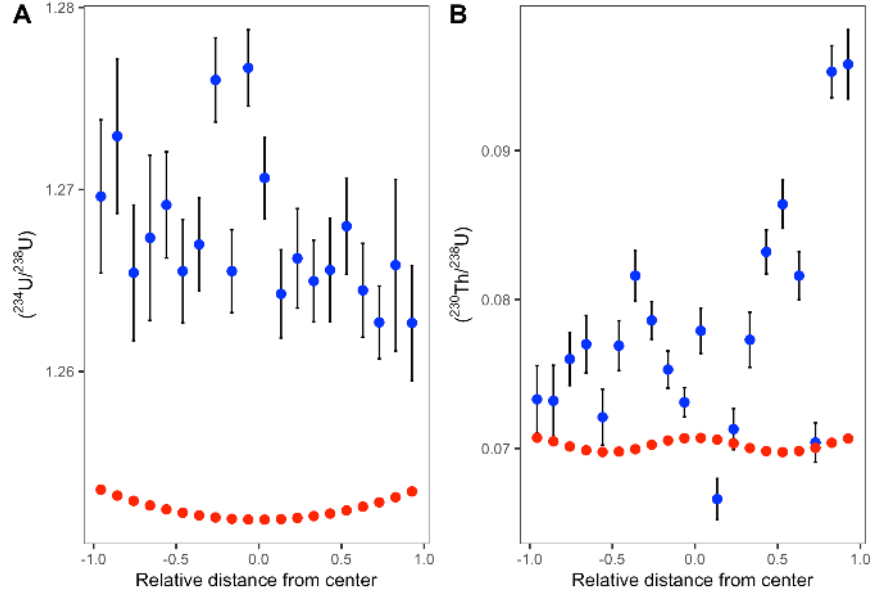


Figure 5: Results from the model's first run with the modern human femur. A: Calculated (red) and observed (blue) $(^{234}\text{U}/^{238}\text{U})$ activity ratios for transect 2 of modern human femur 132A/LB/27D/03. B: Calculated (red) and observed (blue) $(^{230}\text{Th}/^{238}\text{U})$ activity ratios for transect 2 of modern human femur 132A/LB/27D/03.

276 and the opposite if the calculated $(^{230}\text{Th}/^{238}\text{U})$ ratios are too low. Thus, we
 277 should adjust T_{mix} and/or T_{max} accordingly.

278 Since the first run suggests a Holocene age for the sample, the measured
 279 $(^{234}\text{U}/^{238}\text{U})$ at the surfaces must be similar to the calculated values, thus the
 280 chosen values for the range above. Once $U48_0_min$, $U48_0_min$, T_{min} and
 281 T_{max} parameters have been adjusted, the model is run again. `fsum_target`
 282 can also be decreased to 0.01 in order to get a better fit and error, but it is at
 283 the expense of computing time. This operation is repeated until a satisfying
 284 fit is obtained (by visual inspection of the figures). Finally, the model is run
 285 once more, increasing the number of iterations to 1000 (or more). Following
 286 this method, we obtain an age of $6.4 \pm 1.1/-1.1$ ka (Figure 6).

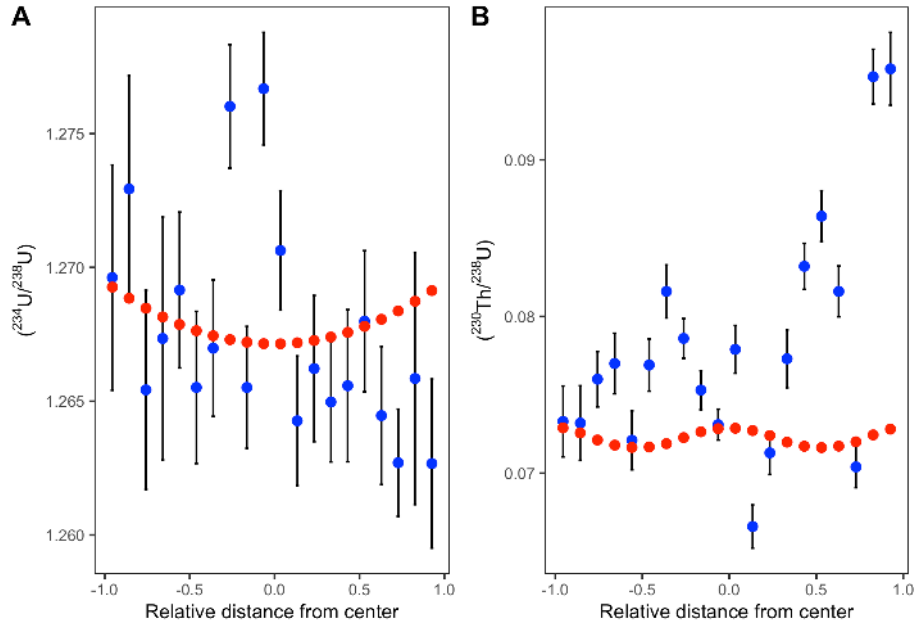


Figure 6: Results from the model's second run with the modern human femur. A: Calculated (red) and observed (blue) ($^{234}\text{U}/^{238}\text{U}$) activity ratios for transect 2 of modern human femur 132A/LB/27D/03. B: Calculated (red) and observed (blue) ($^{230}\text{Th}/^{238}\text{U}$) activity ratios for transect 2 of modern human femur 132A/LB/27D/03.

287 *Age of the Homo floresiensis remains from Sutikna et al. 2016*

288 For transect 1 of LB1/52, Sutikna et al. (2016) reported an age of 79.0
289 ± 3.7 ka. With iDADwigl, using data in the file `Hobbit_1-1T_for_iDAD.csv`
290 provided in the package, and following the same method as above, we obtain
291 an age of $75.5 +0.9/-1$ ka (Figure 7).

292 Note that results and errors will vary slightly for each run since populations
293 are solution sets are randomly generated.

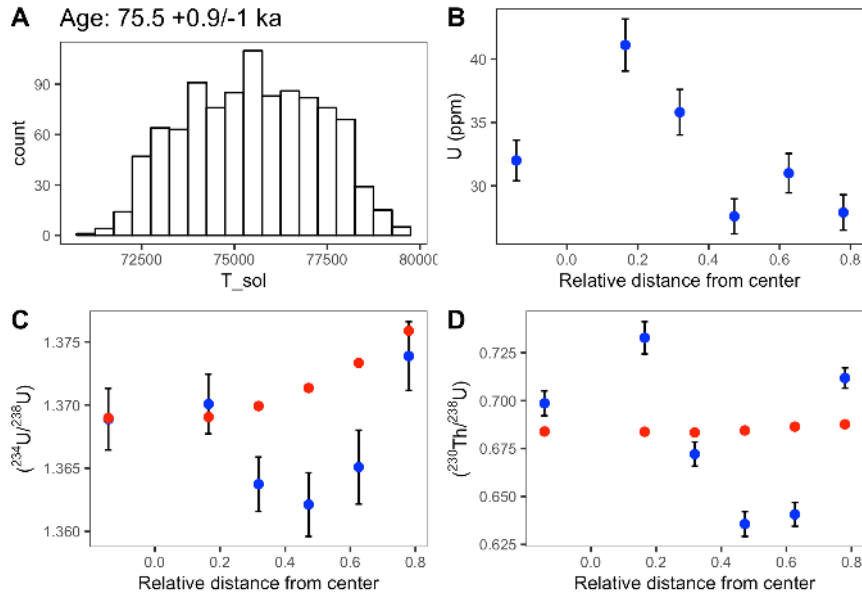


Figure 7: Results from running the model with *Homo floresiensis* ulna LB1/52 data from Sutikna et al. (2016). A: Histogram of the solution ages, B: Uranium concentration profile for transect 1 of *Homo floresiensis* ulna LB1/52. C: Calculated (red) and observed (blue) ($^{234}\text{U}/^{238}\text{U}$) activity ratios for transect 1 of *Homo floresiensis* ulna LB1/52. D: Calculated (red) and observed (blue) ($^{230}\text{Th}/^{238}\text{U}$) activity ratios for transect 1 of *Homo floresiensis* ulna LB1/52.

Conclusions

In this paper we have described `iDADwig1`, an open source R package for computation of open-system U-Th ages. This helps to enable transparency, reproducibility, and flexibility of the analytical workflow for computing U-Th ages. The examples above show that results from our model are within error of previously published ages.

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Colophon

This report was generated on 2019-01-11 07:53:36 using the following computational environment and dependencies:

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# which R packages and versions?
devtools::session_info()
```

```
## - Session info -----
## setting value
## version R version 3.5.1 (2018-07-02)
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## system  x86_64, darwin15.6.0
## ui      X11
## language (EN)
## collate C
## ctype   en_US.UTF-8
## tz      America/Los_Angeles
## date    2019-01-11
##
## - Packages -----
## ! package * version      date      lib
## assertthat 0.2.0      2017-04-11 [1]
## backports  1.1.3      2018-12-14 [1]
## bookdown    0.9        2018-12-21 [1]
## callr       3.1.1      2018-12-21 [1]
## cli         1.0.1      2018-09-25 [1]
## colorspace  1.3-2      2016-12-14 [1]
## commonmark  1.7        2018-12-01 [1]
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## crayon      1.3.4      2018-12-18 [1]
## desc        1.2.0      2018-05-01 [1]
## devtools    2.0.1      2018-10-26 [1]
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## dplyr        * 0.7.99.9000 2018-12-25 [1]
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## labeling    0.3        2014-08-23 [1]
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## Github (hadley/xml2@de9781d)
## CRAN (R 3.5.0)
## CRAN (R 3.5.0)
##
## [1] /Library/Frameworks/R.framework/Versions/3.5/Resources/library
##
## P -- Loaded and on-disk path mismatch.

```

The current Git commit details are:

```
git2r::repository(here::here())
```

```
## Local:    master /Users/bmarwick/Desktop/iDADwigl
## Remote:   master @ origin (https://github.com/benmarwick/iDADwigl.git)
## Head:     [032e542] 2019-01-11: so we can make the PDF in binder
```