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TURBO2: A MATLAB simulation to study the effects of bioturbation on paleoceanographic time series

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ABSTRACT

Bioturbation (or benthic mixing) causes significant distortions in marine stable isotope signals and other palaeoceanographic records. Although the influence of bioturbation on these records is well known it has rarely been dealt systematically. The MATLAB program called TURBO2 can be used to simulate the effect of bioturbation on individual sediment particles. It can therefore be used to model the distortion of all physical, chemical, and biological signals in deep-sea sediments, such as Mg/Ca ratios and UK37-based sea-surface temperature (SST) variations. In particular, it can be used to study the distortions in paleoceanographic records that are based on individual sediment particles, such as SST records based on foraminifera assemblages. Furthermore, TURBO2 provides a tool to study the effect of benthic mixing of isotope signals such as ^{14}C, $\delta^{18}O$, and $\delta^{13}C$, measured in a stratigraphic carrier such as foraminifera shells.

1. Introduction

Bioturbation (or benthic mixing) causes significant distortions in the stable isotope records preserved in deep-sea sediments (Fig. 1) (Berger and Heath, 1968; Peng et al., 1977, 1979; Schiffelbein, 1984, 1985; Trauth, 1998a; Anderson, 2001; Leuschner et al., 2002; Charbit et al., 2002; Löwemark and Grootes, 2004; Löwemark et al., 2008; Hughes et al., 2009). The process of bioturbation has previously been quantified, in particular with regard to the thickness of the mixed layer in deep-sea sediments and the overall mixing intensity in the uppermost layers of the sedimentary column (e.g. Peng et al., 1979; Erlenkeuser, 1980; Berger and Killingley, 1982; Thomson et al., 1993, 1995, 2000; Trauth et al., 1997; Henderson et al., 1999; Smith and Rabouille, 2002; Teal et al., 2010; Heard et al., 2008). Attempts have also been made to deconvolve the effects of bioturbation, for instance by removing the resulting noise in isotope records (e.g. Trauth, 1998b), or the effects of amplitude reduction and phase shifts (Ruddiman et al., 1976; Berger et al., 1977; Bard et al., 1987), sometimes even being able to take into account variations in mixing intensity through time (Trauth, 1995). The process of benthic mixing has also been modeled in many ways to predict its influence on different time scales, as a diffusion process (Berger and Heath, 1968; Shull, 2001), a frequency-domain process (Schiffelbein, 1985), a Markov-chain type single particle process (Foster, 1985; Trauth, 1998a), or a mixed diffusion-single particle process (Boudreau et al., 2001; Choi et al., 2002). Some authors have identified the particular importance of time-dependent variations in mixing intensity in their models (Trauth, 1998a; Charbit et al., 2002). Others have focused on the size dependency of the bioturbation process, for instance to explain age differences between different sized foraminifera shells (Erlenkeuser, 1980; Shull and Yasuda, 2001; Bard, 2007).

The TURBO bioturbation algorithm published in 1998 (Trauth, 1998a) can be used to simulate the effects of benthic mixing on individual sediment particles such as foraminifera tests. The advantage of this model is that it allows users of the program to study the effect of bioturbation on isotopic signals such as ^{14}C, $\delta^{18}O$, and $\delta^{13}C$ from stratigraphic carriers such as foraminifera. It is also able to simulate the effect that a small sample size (i.e. a small number of foraminifera tests with isotopic measurements) has on the noise level of an isotope record. Most studies have only measured 5 benthic or 20–40 planktonic foraminifera tests to obtain a stable isotope record (e.g. Boyle, 1984; Schiffelbein and Hills, 1984; Trauth, 1998b). Replicate or duplicate measurements, made to determine the accuracy of the isotope measurements from deep-sea cores, are rare (Killingley et al., 1981; Schiffelbein and Hills, 1984; Trauth, 1995, 1998b). The disadvantage of TURBO, however, is that it was written in *FORTRAN77*. This programming language is very inefficient in daily use compared to increasingly popular numerical computer programming languages such as the open-source freeware *Python* (http://python.org), or commercial

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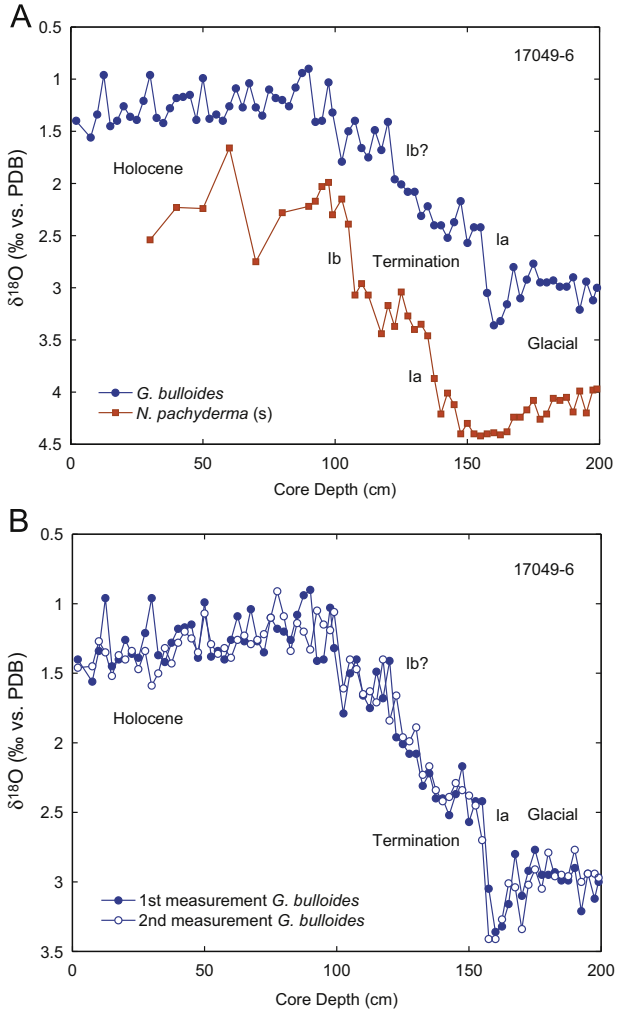

Fig. 1. (A) Real $\delta^{18}O$ oxygen isotope record for planktonic foraminifera species *G. bulloides* (blue circles) and *N. pachyderma* (sinistral) (red squares) in deep-sea core 17049-6 (Rockall Plateau, east Atlantic, 55.26N 26.73W, 3331 m water depth). (B) Duplicate record of oxygen isotope measurements on *G. bulloides* from the same core. Stable isotope analyses were performed on multi-shell samples of 20 tests each. Sedimentation rates were around 10 cm kyr^{-1} during the Holocene and around 6 cm kyr^{-1} during the glacial period (Jung, 1996). Sampling interval is 2.5 cm, corresponding to 250 yr during the Holocene and 240 yr during the glacial period. The thickness of the homogeneous mixed layer is around 11 cm for the Holocene and around 14 cm for the glacial period, using the equation by Trauth et al. (1997) to reconstruct the mixing depth on the basis of organic carbon flux at the seafloor. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

software packages such as *Mathematica* by Wolfram Research (http://wolfram.com) and *MATLAB* by The MathWorks Inc. (http://mathworks.com).

During the last few years MATLAB has become an increasingly popular tool in earth sciences. It has been used for finite element modeling, for processing seismic data, for analyzing satellite imagery, and for generating digital elevation models from satellite data (e.g. Trauth, 2010; Trauth and Sillmann, 2012). MATLAB has therefore been chosen as an appropriate programming language for a complete rewrite of TURBO, to be known as *TURBO2*. TURBO2 provides a tool for time-variant bioturbation modeling of signal carriers, such as foraminifera carrying an isotope signal. The TURBO2 MATLAB program consists of only ~50 lines of computer code; the script to import the synthetic data to be mixed, to run TURBO2, and to display the results consists of another ~50 lines of MATLAB code. In contrast, the original FORTRAN77 TURBO program consisted of ~900 lines of code, not including any algorithm for the graphical display of results.

2. Simulation algorithm

The classic way to describe benthic mixing or bioturbation on the deep-sea floor is to postulate a mixed layer of a specific thickness (typically between 0 and 20 cm, global average about 8 cm), resting on top of a sediment pile that is not influenced by benthic activity (e.g. Peng et al., 1979; Berger and Killingley, 1982; Thomson et al., 1993, 1995, 2000; Trauth et al., 1997; Henderson et al., 1999; Teal et al., 2010; Heard et al., 2008) (Fig. 2). Berger and Heath (1968) suggest instantaneous mixing within such a layer and many studies on the distribution of high-resolution ^{14}C data series in box core profiles have shown that this model describes the process of bioturbation in the deep-sea sediments sufficiently accurately, at least on radiocarbon time scales (Peng et al., 1979; Berger and Killingley, 1982; Broecker et al., 1991; Trauth et al., 1997). In contrast, the distribution of short-lived radionuclides such as ^{210}Pb (half-life=22.3 yr) is more sensitive to the mixing rate and these radionuclides therefore require models with finite mixing rates within the mixed layer to simulate bioturbation (e.g. Nozaki et al., 1977; DeMaster and Cochran, 1982; Cochran, 1985; Trauth, 1998b; Henderson et al., 1999).

The mixed layer model with instantaneous mixing has been used as a basis for developing TURBO2. Although the MATLAB program produces statistically very similar results to the FORTRAN77 routine called TURBO (Trauth, 1998a), the code has been completely rewritten to take full advantage of the available library of ready-to-use routines that come with MATLAB, such as random number generators and rich graphics functions with which to display the results. TURBO uses a transition matrix to control the rearrangement of sediment grains in a simulated vertical section of sediment, in order to simulate biogenic mixing. The user must provide appropriate sedimentation-control parameters and a set of transition matrices in order to be able to run a simulation. The reason for using the transition matrices is to be able to run the simulation with down-core variations in mixing intensities, using

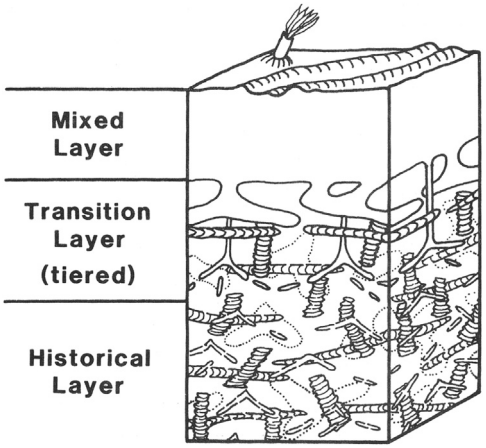

Fig. 2. Generalized burrow stratigraphy in oxygenated pelagic sediments according to Savrda et al. (1991) and Savrda (1992). The surface mixed layer (typically 5–10 cm thick) represents an interval of rapid and complete biogenic homogenization. The transition layer, a zone of heterogeneous mixing that extends to subsurface depths of 20–35 cm, is characterized by burrows produced by organisms that live or feed at greater depths in the substrate (i.e. below the mixed layer). With continued sediment accretion and associated upward migration of the mixed and transition layers, sediment passes out of the actively bioturbated zone into a historical layer, in which no new disruptive burrowing takes place.
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a mixing model for short-lived radionuclides. TURBO has, to my knowledge, rarely been used for this purpose and the TURBO2 MATLAB program therefore does not use the transition matrix approach to model the effect of bioturbation on radiocarbon time scales. Instead it simulates homogeneous mixing, with mixing depths that vary along the length of the core.

The TURBO2 code contained in the MATLAB function `turbo2` is explained below, followed by the script `turbo2script` for running the simulation. Both can be downloaded from the webpage of the journal. The code in `turbo2` starts with the `function` statement, introducing a MATLAB function with input and output variables:

```
function [oriabu,bioabu,oriiso,bioiso]=...
turbo2(abu,iso,mxl,numb)
```

The input variables for `turbo2` are the record of the abundance `abu` of a signal carrier (such as a foraminifera species), its isotope signature `iso`, the mixed layer thickness `mxl` through time (or down core), and a single value `numb` defining the number of foraminifera tests that are to be picked and have their isotope values measured. While there is only one foraminifera species in the input of `turbo2` (called *Species 1* and identified by the number 1 in the algorithm), the program creates a second foraminifera species (called *Species 2*) which has an abundance variation complementary to that of *Species 1*, such that the sum of both abundances is constant.

The first few lines of the code define the size of the array representing the uppermost layers of a virtual sedimentary column, consisting of tests of foraminifera from *Species 1* and *Species 2*. The number of rows in the array (`nrows`) corresponds to the number of rows in `abu` or `iso` plus the maximum thickness of the mixed layer in `mxl` and a number of extra layers defined by the user (zero in our example). The number of columns in the array (`ncols`) corresponds to the maximum number of foraminifera tests in `abu` plus a number of extra particles defined by the user (50 in our example). Including these extra particles ensures that there are at least this number of *Species 2* particles available.

```
nrows=max(mxl)+0;
ncols=max(abu)+50;
```

Using the values for `nrows` and `ncols` we create an initial sedimentary column of foraminifera tests in `sedabu` and their corresponding isotope values in `sediso`. For simplicity, the elements in these two arrays (`sedabu` and `sediso`) are all `NaN`s, which stands for *not a number* and is the "no-data" identifier in MATLAB.

```
sedabu=NaN(nrows,ncols);
sediso=NaN(nrows,ncols);
```

Before we start the actual mixing loop, we can introduce a `waitbar` that displays the progress of the mixing algorithm. The `waitbar` first needs to be initialized outside the loop:

```
h=waitbar(0,'Mixing Process ...');
```

The mixing `for` loop includes the sedimentation of a new layer `i` on top of the initial sediment column `sedabu`, with a thickness equal to the sum of `max(mxl)` and the extra layers defined by the user. We first create a random permutation `rncols` of the integers between `1` and `ncols`. Then we add a new layer `sedabu` of twos (for *Species 2*) and replace the first original `1` to `abu` carriers with ones (for *Species 1*). We then mix the two species types horizontally within the new layer using the uniformly distributed random numbers in `rncols`. We also create a new layer of isotope values in `sediso` but in this case no horizontal mixing is required as both species have the same isotope values. This is therefore just a layer of identical isotope values in `iso`. The additional `for` loop within the first `for` loop represents the actual mixing process using the series of mixed layer thicknesses in `mxl`. We again need to first create a random permutation `z` of the integers between `1` and `mxl(i)`, and then distribute the foraminifera tests in `sedabu` within the mixed layer. The isotope values in `sediso` are then also mixed with the same random permutation `z`. The interim results of the mixing are stored in the interim variables `ns` for the tests and `ni` for the isotopes, the bioturbated sediment column is now `sedabu` and the bioturbated isotope value column is now `sediso`. We can clear some superfluous variables after the sedimentation and mixing loop.

```
for i=1:length(abu)
    waitbar(i/length(abu))
    rncols=randperm(ncols);
    sedabu(size(sedabu,1)+1,1:ncols) =...
        2*ones(1,ncols);
    sedabu(size(sedabu,1),1:abu(i)) =...
        ones(1,abu(i));
    sedabu(size(sedabu,1),:) =...
        sedabu(size(sedabu,1),rncols);
    sediso(size(sediso,1)+1,1:ncols) =...
        iso(i)*ones(1,ncols);
    for j=1: ncols
        z=randperm(mxl(i));
        ns(1:mxl(i),j)=...
        sedabu(size(sedabu,1)-mxl(i)+...
        1:size(sedabu,1),j);
        sedabu(size(sedabu,1)-mxl(i)+...
        1:size(sedabu,1),j)=ns(z,j);
        ni(1:mxl(i),j)=...
        sediso(size(sediso,1)-mxl(i)+...
        1:size(sediso,1),j);
        sediso(size(sediso,1)-mxl(i)+...
        1:size(sediso,1),j)=ni(z,j);
    end
end
clear ns ni i j mxl z
```

We next correct the `sedabu` and `sediso` series for the actual length of the series, i.e. we remove the initial pile of sediment with a thickness of `max(mxl)` plus the extra layers defined by the user, which is zero in our example.

```
sedabu=sedabu(nrows+1:end,:);
sediso=sediso(nrows+1:end,:);
```

We now calculate the abundances of *Species 1* and *Species 2* in each layer. The original abundance of *Species 1* before mixing was `abu` and of *Species 2* was `ncols-abu`. These original abundances are stored in the first and second columns of `oriabu`. The bioturbated abundances of *Species 1* and *2* in each layer are calculated by counting the ones and twos along the rows of `sedabu`. The bioturbated abundances of *Species 1* and *2* are stored in the first and second columns of `bioabu`:

```
oriabu(:,1)=abu;
oriabu(:,2)=ncols-abu;
bioabu(:,1)=sum(sedabu==1,2);
bioabu(:,2)=sum(sedabu==2,2);
```

We now calculate the isotope values from *Species 1* and *Species 2* for each layer. The original isotope signature of both *Species 1* and *2* is `iso`. The original (identical) isotope values from *Species 1* and *2* are stored in the first and second columns of `oriiso`. To calculate the bioturbated isotope values from *Species 1* and *2* for each layer we first create two copies of `bioiso`: `bioiso1` and

bioiso2. We then mask those particles that are not ones in bioiso1, and those that are not twos in bioiso2.

```
oriiso(:,1)=iso;
oriiso(:,2)=iso;
bioiso1=sediso;
bioiso2=sediso;
bioiso1(sedabu~=1)=NaN;
bioiso2(sedabu~=2)=NaN;
```

We then create two arrays of NaNs, biopart1 and biopart2, with the same size as bioiso1 and bioiso2. In the next set of commands the elements of these NaN arrays are replaced by the non-NaN elements of bioiso1 and bioiso2. We then reorganize the rows of the array to start each row with a non-NaN element. Hence in bioiso1 the ones are distributed randomly within rows, whereas in biopart1 the ones occur in the first 1:abu columns of the array and the remaining ncols-abu are all NaNs.

```
biopart1=NaN(size(bioiso1));
biopart2=NaN(size(bioiso2));
for i=1:length(abu)
    biopart1(i,1:bioabu(i,1))=...
        bioiso1(i,isnan(bioiso1(i,:))==0);
    biopart2(i,1:bioabu(i,2))=...
        bioiso2(i,isnan(bioiso2(i,:))==0);
end
```

We then reduce the number of columns in biopart1 and biopart2 to the numb carriers to be picked and measured. We next calculate the isotope values by averaging the numb values in biopart1 and biopart2. In a real isotope study, some layers may not contain numb particles to be measured, depending on the choice of the total number of particles ncols and the abundances abu of *Species 1*. This information is, however, contained in bioabu and will be included later in one of the graphics. The bioturbated isotope values from *Species 1* and *2* are stored in the first and second columns of bioiso. Finally, both bioabu and bioiso are flipped upside down because otherwise the sediment column in the turbo2 output grows downward instead of upward.

```
biopart1=biopart1(:,1:numb);
biopart2=biopart2(:,1:numb);
for i=1:length(abu)
    bioiso(i,1)=nanmean(biopart1(i,:));
    bioiso(i,2)=nanmean(biopart2(i,:));
end
oriabu=flipud(oriabu);
oriiso=flipud(oriiso);
bioabu=flipud(bioabu);
bioiso=flipud(bioiso);
```

The first pair of output variables from turbo2 is the two-column array bioabu containing the bioturbated version of oriabu, i.e. the mixed abundances of *Species 1* and *2* using the mixing depths through time (or down core) contained in mxl. The second pair of output variables, oriiso and bioiso, contain the original and the bioturbated isotope records from *Species 1* and *Species 2*, respectively.

3. Running the algorithm

To run the turbo2 bioturbation simulation we need some input data and a script. The MATLAB code turbo2 and a script turbo2script.m with which to run the simulation are provided online. The package of MATLAB files also includes several example input files to simulate homogeneous mixing of an individual layer, an impulse function, a step function, and oxygen isotope records from glacial terminations. These input data can be saved in an ASCII text file such as turbo2input_termination.txt. The rows of the data array correspond to sediment layers 1 cm thick. The first column contains the age of the sediment. Note that the array starts with the oldest layer, which is deposited first. In our example, the age (in calendar kyr BP) decreases linearly with time, i.e. by 0.2 kyr every centimeter corresponding to a sedimentation rate of 5 cm kyr^{-1}. The second column contains the mixed layer thickness in centimeters; in the example the mixed layer thickness is constant at 10 cm. The third column contains the abundance of *Species 1*. The fourth column contains the isotope signal from *Species 1* (in our example oxygen isotope values are in ‰ vs. PDB).

```
47.60    10   217  3.21
47.40    10   252  3.36
47.20    10   261  3.48
cont'd
```

We first clear the workspace, the figure, and the Command Window, and then load the data from the file turbo2_input.txt, which we store in the variable data.

```
clear, clc, clf
data=load('turbo2_input.txt');
```

We then define the input variables for turbo2. The variable age corresponds to the age of the sediment and to the first column of the data array. The mixed layer thickness mxl, the abundance abu, and the isotope values iso are stored in the second, third, and fourth columns of data. The variable lngth, which corresponds to the length of the input series, will later be used for displaying the data.

```
age  = data(:,1);
mxl  = data(:,2);
abu  = data(:,3);
iso  = data(:,4);
lngth = length(data(:,1));
```

We now define the number numb of signal carriers (or foraminifera tests) to be picked and measured. Typical values of numb are 5 benthic or 20–40 planktonic foraminifera. In our example we use 20 for numb.

```
numb=20;
```

We can now run the function turbo2 with the input variables defined above.

```
[oriabu,bioabu,oriiso,bioiso]=...
       turbo2(abu,iso,mxl,numb);
```

The results can be displayed in various graphics. In the first example the abundances of the two species *Species 1* and *2* and their isotope values, before and after bioturbation, are displayed in four subplots. In each of the subplots the original abundances and isotope values are depicted as black curves. The bioturbated records from *Species 1* are in blue and those from *Species 2* in red. The horizontal green line shows the number of foraminifera tests to be measured (numb), which assists in identifying samples with abundances lower than numb. All graphics have vertical and horizontal grids, which are displayed using grid. The *y*-axis of the isotope graphics is reversed following the convention for paleoceanographic stable isotope records. We first define the variables mxltext, which is a character string containing the mean mixed layer depth, and numbtext, which is the number of foraminifera tests to be measured.

```
mxltext=num2str(mean(mxl));
numbtxt=num2str(numb,2);

subplot(2,2,1)
```

```
plot(1:lngth,oriabu(:,1),'k'), hold on
plot(1:lngth,bioabu(:,1),'b')
plot(1:lngth,numb*ones(lngth),'g')
set(gca,'XGrid','On','YGrid','On')
title('Abundance of Carrier 1')
subplot(2,2,2)
plot(1:lngth,oriabu(:,2),'k'), hold on
plot(1:lngth,bioabu(:,2),'r')
plot(1:lngth,numb*ones(lngth),'g')
set(gca,'XGrid','On','YGrid','On')
title('Abundance of Carrier 2')
subplot(2,2,3)
plot(1:lngth,oriiso(:,1),'k'), hold on
plot(1:lngth,bioiso(:,1),'b')
set(gca,'YDir','Reverse','XGrid','On',...
       'YGrid','On')
title('Isotopes of Carrier 1')
subplot(2,2,4)
plot(1:lngth,oriiso(:,2),'k'), hold on
plot(1:lngth,bioiso(:,2),'r')
set(gca,'YDir','Reverse','XGrid','On',...
       'YGrid','On')
title('Isotopes of Carrier 2')
```

The graphics can be saved into a TIFF file `turbo2_fig1_8cm_20-carriers.tiff` containing the information on the average mixing depth `mxltext` and the number of foraminifera tests to be measured `numbtext`.

```
printfilename=...
       ['turbo2_fig1_',mxltext,'cm_',...
       numbtxt,'carriers.tiff'];
print('-dtiff',printfilename)
```

An alternative way of plotting the results is to use a graphics that includes the original isotope record (in black) and the bioturbated isotope record from *Species 1* and *2* (in blue and red respectively, as in the previous figures) to show the offset between the two isotope curves. The title of the graphics contains the information of the average mixed layer thickness `mxltext` and the number of foraminifera tests `numbtext`.

```
figure, hold on
plot(1:lngth,oriiso(:,1),'k')
plot(1:lngth,bioiso(:,1),'b')
plot(1:lngth,bioiso(:,2),'r')
set(gca,'YDir','Reverse','XGrid','On',...
       'YGrid','On','Box','On')
titletxt=['Isotopes of Carriers 1+2,',...
       mxltext,'cm Mixed Layer,',...
       numbtxt,'Carriers'];
title(titletxt)
legend('Original Isotopes',...
       'carriers 1','carriers 2')
```

The graphics can again be saved into a TIFF file `turbo2_fig2_8cm_20carriers.tiff` containing the information on the average mixing depth `mxltext` and the number of foraminifera tests to be measured `numbtext`.

```
printfilename=...
       ['turbo2_fig2_',mxltext,'cm_',...
       numbtxt,'carriers.tiff'];
print('-dtiff',printfilename)
```

The MATLAB function `print` also has the capability to save the graphics in a variety of other formats. As an example, the above code can be adjusted to export the graphics as an EPS file, so that it can be further manipulated in vector graphics software.

4. Examples

4.1. Example 1: simple example of homogeneous mixing

The first simulation demonstrates the sedimentation and bioturbation of a single layer at the sediment–water interface. This simulation (as well as all other simulations described below) does not require any modification of the `turbo2` algorithm or the script, except for a slightly different input file. The file `turbo2input_homogenousmixing.txt` comprises only a single line:

```
0.00   3   5   1.23
```

Mixing occurs to depth of 3 cm below the surface. A total of 5 foraminifera tests are deposited with an isotope signature of 1.23‰ vs. PDB. In `turbo2` we modify the lines in which the number of rows and columns are defined. In this example we add five extra layers to the initial `max(mxl)`-thick sediment package. The algorithm therefore creates an initial sediment package of 5 cm+3 cm=8 cm thickness. The number of columns, i.e. the total number of foraminifera tests, is `max(abu)`, i.e. no extra tests are added to the sediment layers.

```
nrows=max(mxl)+5;
ncols=max(abu)+0;
```

Two lines of code can be used after `close(h)` in `turbo2` to display the distribution of ones and their corresponding isotope values within the 3 cm thick mixed layer. The arrays of the sediment package and isotope values need to be flipped upside down because during the sedimentation process the array grows downward whereas in reality sediment is deposited at the top.

```
flipud(sedabu(1:8,1:5))
flipud(sediso(1:8,1:5))
```

When running the script `turbo2script` the function `turbo2` then yields the following output in the MATLAB Command Window:

```
NaN   NaN     1   NaN   NaN
  1   NaN   NaN     1     1
NaN     1   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
NaN   NaN   NaN   NaN   NaN
```

Here the ones can be seen to be successfully distributed within the uppermost 3 cm of the sediment column. The second array `sedis` represents the isotope values of the particles marked by ones in the `sedabu` array. Note that the isotope values occur in the same positions as the ones in the `sedabu` array.

```
  NaN   NaN  1.23   NaN   NaN
 1.23   NaN   NaN  1.23  1.23
  NaN  1.23   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
  NaN   NaN   NaN   NaN   NaN
```

Running the same simulation with a larger number of particles, e.g. 1000 foraminifera tests,

```
0.00   3    1000    0.00
```

results in ~333 particles per layer (i.e. one-third of the total within each of the three layers) in the uppermost 3 cm of the sedimentary column, as can be seen by typing

```
bioabu
```

after the prompt in the Command Window. The same simulation can easily be repeated with different values in the input file for the mixed layer thickness:

```
0.00   5    1000    0.00
```

and the corresponding results obtained, i.e. ones and their corresponding isotope values distributed over the uppermost five layers of the sedimentary column, and a total number of ~200 particles after mixing. This first simulation proves the validity of the algorithm for successful modeling of bioturbation in the homogeneous mixing example.

4.2. Example 2: mixing of an impulse sequence

The classic way to describe (or even to determine) the mixing intensity in a layer below the sediment–water interface is from the distribution of sediment particles that had been deposited in a single event. Examples are volcanic ash layers or microtectites (e.g. Ruddiman et al., 1980), which derive from an event that can be described, in a mathematical sense, as a very short pulse with an infinite amplitude in the continuous case (*Dirac delta function*). In the discrete case, and this is the case in our example, the impulse sequence is zero everywhere except for at a single location, where it is one (*Kronecker delta* or *unit impulse series*). The impulse response function (or sequence in a discrete case), and in particular its Fourier Transform, contains all necessary information concerning the changes in amplitude and phase of a stratigraphic signal going through a benthic mixing process.

When an impulse goes through a benthic mixing process we obtain the impulse response sequence of the bioturbation system. We create a file `turbo2input_impulsesequence.txt` with zero abundance everywhere except for a single layer that has an abundance of 1000 foraminifera tests (or any other type of sediment particle, such as ash particles or microtectites). We are not interested in the isotope values but in the abundance distribution of the signal carriers or foraminifera tests, but the algorithm requires some input for the isotopes.

```
(cont'd)
  0.00    5       0    0.00
  0.00    5       0    0.00
  0.00    5    1000    0.00
  0.00    5       0    0.00
  0.00    5       0    0.00
(cont'd)
```

Running `turbo2` with a constant mixing depth of 5 cm nicely demonstrates the dispersal of the sediment particles over a large depth interval. The highest concentration of ~200 particles occurs at the base of the mixed layer, i.e. 5 cm below their original location, and above that peak the abundance decreases exponentially reaching numbers of 2–5 particles at around 15 cm above the original position of the pulse layer. Since sediment particles (or foraminifera tests) can move both downward and upward, one can easily imagine that an individual signal carrier could move from the base of the mixed layer to a sediment layer 20 cm above its original position. The next examples demonstrate the influence of this effect on climate transitions recorded in a sediment core.

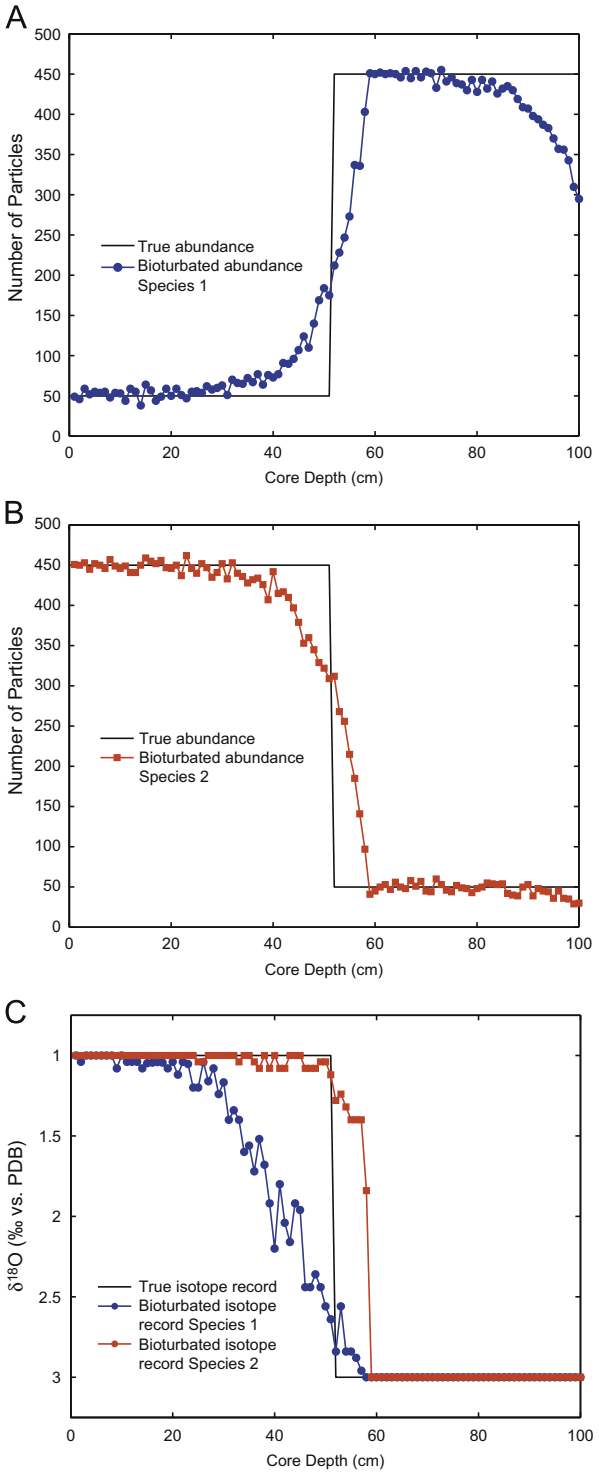

Fig. 3. Graphs of outputs produced from a `turbo2` sample run. Impact of a bioturbating community homogenizing the top 8 cm of sediment on an abrupt change in the abundance of a foraminifera species in the middle of a sequence, from 450 individuals below the change to 50 individuals above. The isotope values change simultaneously from 3.00‰ to 1.00‰. The result demonstrates the phase difference of around 20 cm between the isotope records of the two species, both of which experienced the same change in climate during deposition of the sediment layer at 50 cm depth, which can result in dramatic uncertainties when developing oxygen isotope stratigraphies for such deep sea cores.

4.3. Example 3: mixing of a step sequence

An understanding of the influence of benthic mixing on important climate transitions, such as glacial terminations in the high latitudes (i.e. a change from a cold climate to a warm climate) or changes in humidity within the tropics (e.g. a change from a dry climate to a wet climate) can be obtained from analysis of a step function (or sequence) (Fig. 3). Our input file `turbo2input_-stepsequence.txt` has an abrupt change in the abundance of a foraminifera species in the middle of the sequence, from 450 individuals below the transition to 50 individuals above. The isotope values also change simultaneously from 3.00‰ to 1.00‰.

```
(cont'd)
0.00    8    450    3.00
0.00    8    450    3.00
0.00    8    450    3.00
0.00    8    50     1.00
0.00    8    50     1.00
0.00    8    50     1.00
(cont'd)
```

The mixed layer thickness is constant at 8 cm. We allow the `turbo2` algorithm to work with 50 additional particles but add more than `mxl` extra sediment layers,

```
nrows=max(mxl)+0;
ncols=max(abu)+50;
```

and define `numb=20` particles to be measured in the `turbo2-script` script in order to obtain a good isotope record. As a result, the change in climate at 50 cm caused a change from heavy isotopes (3.00‰) to light isotopes (1.00‰). If these isotopes are stable oxygen isotopes, the change in climate could be interpreted as a shift from a cold climate to a warm climate, while the abundance of *Species 1* is reduced, suggesting that the species may prefer cold temperatures, whereas the abundance of *Species 2* reacts in the opposite way. Note that the results may show some edge effects at the base of the sequence due to the occurrence of a third species marked by `NaN`s, the initial pile of sediments described in the algorithm section.

The result of this simulation nicely demonstrates the up-core smearing of the distribution of the cold species (*Species 1*) and the down-core time-lag in the warm species (*Species 2*) to the base of the mixed layer (8 cm) (Fig. 3A and B). The consequences of these displacements is illustrated in the isotope graphics. The original shift in climate, documented by the change from heavy (3.00‰) to light (1.00‰) isotope values, occurs at 50 cm depth, whereas the cold species (*Species 1*) already documents this shift at ~60 cm depth; the isotope record from the warm species (*Species 2*), however, shows a broad transition band between ~60 and ~20 cm core depth (Fig. 3C). The phase difference of more than ~20 cm between the isotope records from the two species, which both experienced the same change in climate during deposition of the sediment layer (at 50 cm depth), can result in dramatic uncertainties when developing an oxygen isotope stratigraphy for this type of deep sea core.

4.4. Example 4: mixing of glacial terminations

The most realistic, but also the most complicated example is the mixing of an isotope signal across a glacial termination (Fig. 4). Here we use the synthetic data originally published in Trauth (1998a), but interpolated over an evenly spaced depth axis with 1 cm intervals. This isotope curve shows all the characteristic features of Termination I (the end of the last glacial period, further subdivided into Termination Ia and Termination Ib), as described by Bard et al. (1987), Broecker et al. (1988), and Jansen and Veum (1990). The same $\delta^{18}O$ signal has been recorded by both hypothetical subpolar (warm) planktonic foraminifera (*Species 1*) and polar (cold) planktonic foraminifera (*Species 2*), but with different down-core

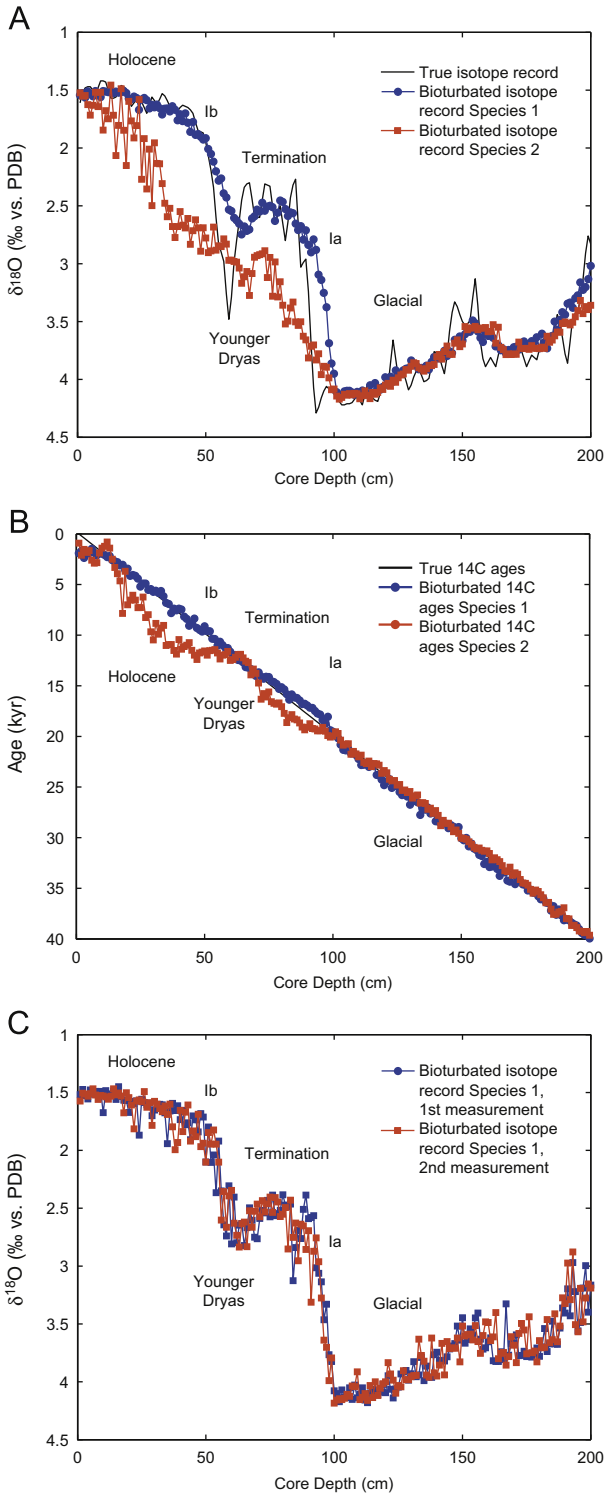

Fig. 4. Graphs of outputs produced from a `turbo2` sample run. (A) Impact of a bioturbating community homogenizing the top 10 cm of sediment on a synthetic $\delta^{18}O$ signal recorded by 50 shells each from synthetic subpolar (blue circles), and polar (red squares) planktonic foraminifera species. (B) Impact of bioturbating community on ^{14}C ages from synthetic subpolar and polar planktonic foraminifera species. (C) Impact of bioturbating community on duplicate measurement from 5 foraminifera tests. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

abundances. This sample run simulates an active, infaunal bioturbating community that instantaneously homogenizes the top 10 cm of sediment. The sedimentation rate is constant at 5 cm kyr^{-1}. Each sedimentation event deposits a 1 cm thick layer of new sediment that is mixed with older sediment during the subsequent bioturbation event. Each combined sedimentation and bioturbation event therefore represents a discrete time interval of 200 years. The input file `turbo2input_termination.txt` looks like this:

```
238   47.60   10   217   3.21
237   47.40   10   252   3.36
236   47.20   10   261   3.48
235   47.00   10   222   3.60
234   46.80   10   182   3.66
233   46.60   10   185   3.58
232   46.40   10   193   3.50
cont'd
```

We again allow the algorithm `turbo2` to work with 50 additional particles but this time we do not add more than `mxl` extra sediment layers,

```
nrows=max(mxl)+0;
ncols=max(abu)+50;
```

The number of measured foraminifera tests is `numb=50`. The bioturbated isotopic records show remarkable discrepancies in both amplitude and phase at around the time of the termination (Fig. 4A). The $\delta^{18}O$ record from the polar species lags the record from the subpolar species by 20 Fcm in Termination Ia and by almost 40 cm in Termination Ib. In the case of the subpolar species, the stratigraphic location of the $\delta^{18}O$ maximum, which is related to the Younger Dryas Event (YD, 11.6 calendar kyr BP) is well defined. The maximum, however, occurs at 62 cm depth, i.e. 3 cm above its original position at 59 cm depth. The bioturbated $\delta^{18}O$ value during the YD is ~2.8–2.9‰, i.e. ~0.6–0.7‰ lower than the original $\delta^{18}O$ value of 3.5‰. The stratigraphic position of the YD recorded by the polar species is unclear. The mixed abundance curves for this species suggest that this climatic event is probably recorded at 65 cm depth, rather than at 59 cm. The original isotope value is again reduced, in this case by ~0.3‰.We next simulate the impact of bioturbation on accelerator mass spectrometry (AMS) ^{14}C ages. To do this we use the same input file as before and the same settings for `nrows` and `ncols`, but run `turbo2` with `age` as the input for the isotope values.

```
[oriabu,bioabu,oriiso,bioiso]=...
       turbo2(abu,age,mxl,numb);
```

As the results show, the actual age for the beginning of Termination Ia (18.3 kyr BP) is increased by 1.3 kyr in the case of the subpolar species (Fig. 4B). This stratigraphic event has been shifted downward by ~8 cm in the core. The position of Termination Ia in the case of the polar species is unclear. A first shift toward light $\delta^{18}O$ values can be observed at 100 cm core depth but the attached AMS ^{14}C age of 19.8 kyr is too high. The AMS ^{14}C ages recorded for the $\delta^{18}O$ maximum of the YD from the subpolar species (13.0 kyr) and the polar species (12.6 kyr), are both too old compared to the correct value of 11.6 kyr (according to Winn et al., 1991). The age–depth relationship plotted in Fig. 4B shows the distorted AMS ^{14}C stratigraphy of the two signal carriers. The ages from both species mostly exceed the correct values. The maximum discrepancy compared to the original value is 9.0 kyr at 32 cm core depth, and the average discrepancy is 0.6 kyr.

The simulation illustrates how large uncertainties arise from signal distortion due to bioturbation. Within the 50 cm length of the termination core section, offsets of 20–40 cm occur between two the planktonic foraminifera species. The age discrepancies between the two foraminifera species, which originally recorded the same isotope signal, are of the order of the entire duration of the YD. These observations are in general agreement with the results from real data from deep-sea cores (Trauth, 1995; Jung, 1996). The discrepancies cannot be attributed to measurement errors alone but result from a combined effect of bioturbation, low sedimentation rates and limited sample size (e.g. Hutson, 1980; Schiffelbein, 1985; Bard et al., 1987; Trauth, 1995). The effects of bioturbation result in great uncertainties in stratigraphic correlation of deep-sea cores and paleoclimatic interpretations from paleoceanographic records. Additional consequences are miscalculations of sedimentation rates and consequent miscalculations of the accumulation rates of geochemical, paleontological, and mineralogical components.

Various authors have dealt with the possibility of deconvolving (unmixing) bioturbated deep-sea records (e.g. Ruddiman et al., 1976; Berger et al., 1977; Schiffelbein, 1985; Bard et al., 1987; Trauth, 1995; Trauth et al., 1997). However, the high sensitivity of deconvolution techniques to high-frequency noise results in a severe amplification of errors (Schiffelbein, 1985). In our next simulation we demonstrate the effect that a mixed layer thickness of 10 cm and a small sample size (`numb=5`) have on the reliability of an isotope record. We run the program `turbo2` twice with the same input variables but creating two sets of output variables each, for the isotope values and foraminifera abundances.

```
[oriabu1,bioabu1,oriiso1,bioiso1]=...
       turbo2(abu,iso,mxl,numb);
[oriabu2,bioabu2,oriiso2,bioiso2]=...
       turbo2(abu,iso,mxl,numb);
```

The output from the second run shows large discrepancies clearly demonstrating the great uncertainties in the interpretation of high-frequency climate variations from isotope records (Fig. 4C). Here we display the duplicate isotope record from *Species 2* as an example.

```
figure, hold on
plot(1:lngth,oriiso1(:,2),'k')
plot(1:lngth,bioiso1(:,2),'b')
plot(1:lngth,bioiso2(:,2),'r')
set(gca,'YDir','Reverse','XGrid','On',...
       'YGrid','On','Box','On')
titletxt=['Isotopes of Carriers 1+2, ',...
       mxltext, 'cm Mixed Layer, ',...
       numbtxt,'Carriers'];
title(titletxt)
legend('Original Isotopes',...
       'carriers 1','carriers 2')
```

Whereas the larger variations such as those due to glacial–interglacial shifts are nicely confirmed, the smaller ones are corrupted by noise. The `turbo2` program yields two different isotope records since the pseudorandom number generator in `randperm` was not set to its default values by using `rng('default')` at the beginning of the `turbo2` code. We can add this command when working with `turbo2` if we indeed wish to reproduce the same isotope and abundance records in each experiment. Using five tests is a standard sample size for $\delta^{18}O$ measurements on benthic foraminifera (Schiffelbein and Hills, 1984). The associated noise-free bioturbated record for the estimation of the residual noise variance is calculated by convolving the noise-free record with the impulse-response function of benthic mixing down to 10 cm depth (Hutson, 1980; Trauth, 1995). The average noise variance of the duplicate records is 3%, which is of the same order as actual $\delta^{18}O$ records (Schiffelbein and Hills, 1984; Trauth, 1995). The signal-to-noise ratio of duplicate time-series can, however, be automatically improved using adaptive filtering techniques before time-variable deconvolving the $\delta^{18}O$ records (Trauth, 1995, 1998b; Trauth et al., 1997).

The last simulation demonstrates time-dependent mixing intensities due to changes in benthic ecology (Trauth, 1998a; Charbit et al., 2002). Such a temporal change in mixing intensity can be simulated by varying the value of `mxl` in the input file `turbo2input_variablemixing.txt`. In this file the mixing depth increases gradually by 2 cm every 20 layers, starting with 0 cm (no bioturbation) at the bottom of the core and reaching 8 cm at the top. The number of measured foraminifera tests is `numb=50`. The simulation results clearly demonstrate the increasing offsets between the two records from *Species 1* and *Species 2*, as well as the upward increase in noise levels in both sets of records. A time-variable mixing intensity requires a time-variable deconvolution technique in either the time or the frequency domain. An example of such a deconvolution technique has been presented in a previous publication (Trauth, 1995). A duplicate isotope record is first adaptively filtered using an adaptive noise canceller published by Trauth (1998b). The filtered time series is then divided into segments, each overlapping by one sample. The overlapping segments are then Fourier transformed and divided by the Fourier transformed impulse response sequence of the bioturbation process. In order to avoid the typical edge effects of a Fourier transform an alternative method can be used to perform the deconvolution that uses a Wavelet transform instead of a Fourier transform. The impulse response sequence used to deconvolve the sample at a particular depth in the core depends on the mixed layer thickness at this depth. The mixed layer thickness *MXL* can be calculated using the equation

$$MXL = -0.36 + 2.01 \times FC$$

from Trauth et al. (1997), where *FC* corresponds to the organic carbon flux to the sea floor at the time of deposition of that particular layer. The thickness *MXL* of the bioturbated zone therefore increases by approximately 2 cm if the food supply *FC* increases by 1 g C m^{-2} yr^{-1}, at least within a range of *FC*=1–6 g C m^{-2} yr^{-1}. The combination of bioturbation modeling, adaptive filtering, and time variant deconvolution effectively removes signal distortions due to benthic mixing.

5. Conclusions

The TURBO2 MATLAB program can be used to simulate the effects of bioturbation on paleoceanographic signals such as those from stable isotopes and radiocarbon ages, measured in a stratigraphic carrier such as foraminifera. In this simulation bioturbation is treated as a time-varying process responding to changing ecological conditions at the water–sediment interface. It therefore allows paleoceanographers to recognize signal distortions that are introduced by bioturbation in combination with low sedimentation rates and small sample sizes of foraminifera shells used for isotope measurements. The `turbo2` MATLAB code, the script to run the simulations (`turbo2script`), and the example files discussed within this paper are all available for download from the server of this journal.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.cageo.2013.05.003.

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