Turbo2: First experiments with changes in abundance and isotopic signal

Dominik Hülse

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1 TURBO2: Very brief model description and experiment setup

1.1 The model:

TURBO2 simulates the effect of bioturbation on single sediment particles (Trauth, 2013). It is a mixed layer model with instantaneous, homogenous mixing (Fig. 1). The mixing depths can vary along the length of the core. TURBO2 simulates signal distortions of isotopic signals from stratigraphic carriers (e.g. forams). It can help to recognize distortions and uncertainties caused by bioturbation in combination with low sedimentation rates and low sample sizes of foraminifera shells used for isotope measurements.

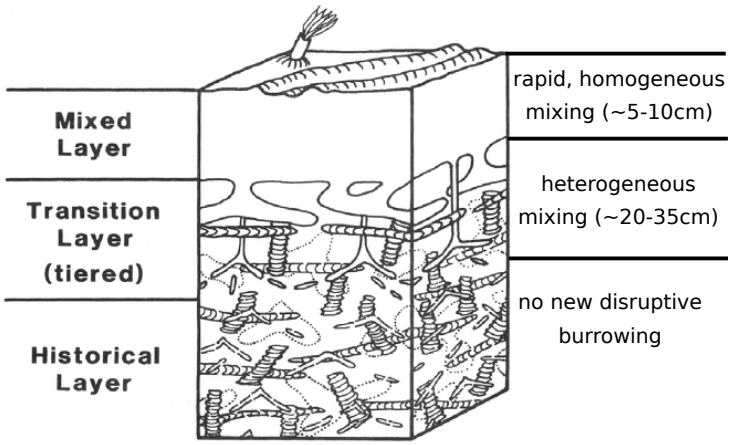

Figure 1: Copied from Trauth (2013): Generalized burrow stratigraphy in oxygenated pelagic sediments according to Savrda et al. (1991) and Savrda (1992). The surface mixed layer (typically 5–10 cm thick) represents an interval of rapid and complete biogenic homogenization. The transition layer, a zone 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. Reprinted without permission of C.V. Svarda.

1.2 Experiments:

In the first set of experiments we simulate the influence of different bioturbation depths (2cm, 5cm, 10cm, 20cm) on abundance and isotopic signals of 2 species. The real abundance and the isotopic signal are covaried (e.g. impulse- or stepchange for abundance and isotopic signal at the same time). About 500 total particles (species 1 + 2) are modeled in each layer. After mixing, 20 of each foram species are picked in each layer and their

isotope values are measured.

In the second set of experiments only the isotopic signal in the forams is changed (same magnitude in both species). Again about 500 total particles are modeled in each layer (now always 350 of species 1 and 150 of species 2). After mixing, in order to examine the uncertainties caused by low sample sizes, either 20 or 5 of each foram species are picked in each layer and their isotope values are measured. Bioturbation depths of 5cm, 10cm and 20cm are used.

TODO: How many mixing experiments? And then mean profile is taken!

2 Results

2.1 Experiments: Covary abundance and isotope signal

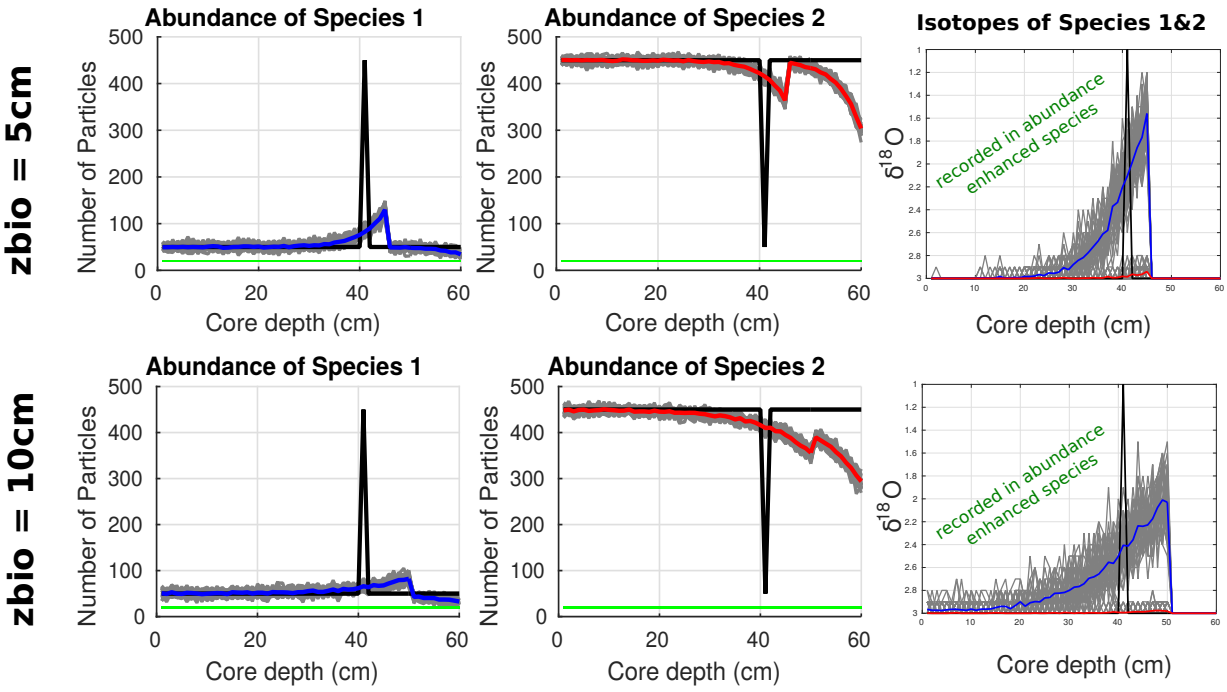

Figure 2: Example: point event + with background abundance

2.2 Experiments: Only change isotope signal - fixed abundance

Only the isotopic signal in the forams is changed (same magnitude in both species). Again about 500 total particles are modeled in each layer (now always 350 of species 1 and 150 of species 2). After mixing, in order to examine the uncertainties caused by low sample sizes, either 20 or 5 of each foram species are picked in each layer and their isotope values are measured. Bioturbation depths of 5cm, 10cm and 20cm are used.

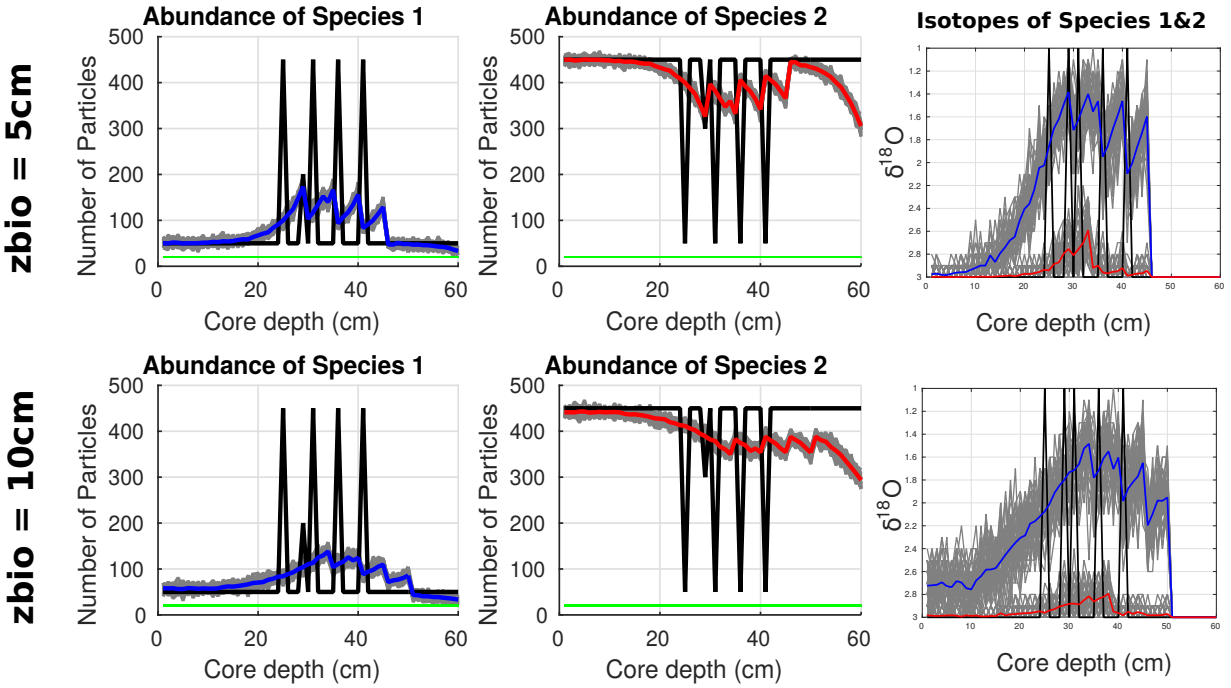

Figure 3: Example: 5 point event + with background abundance

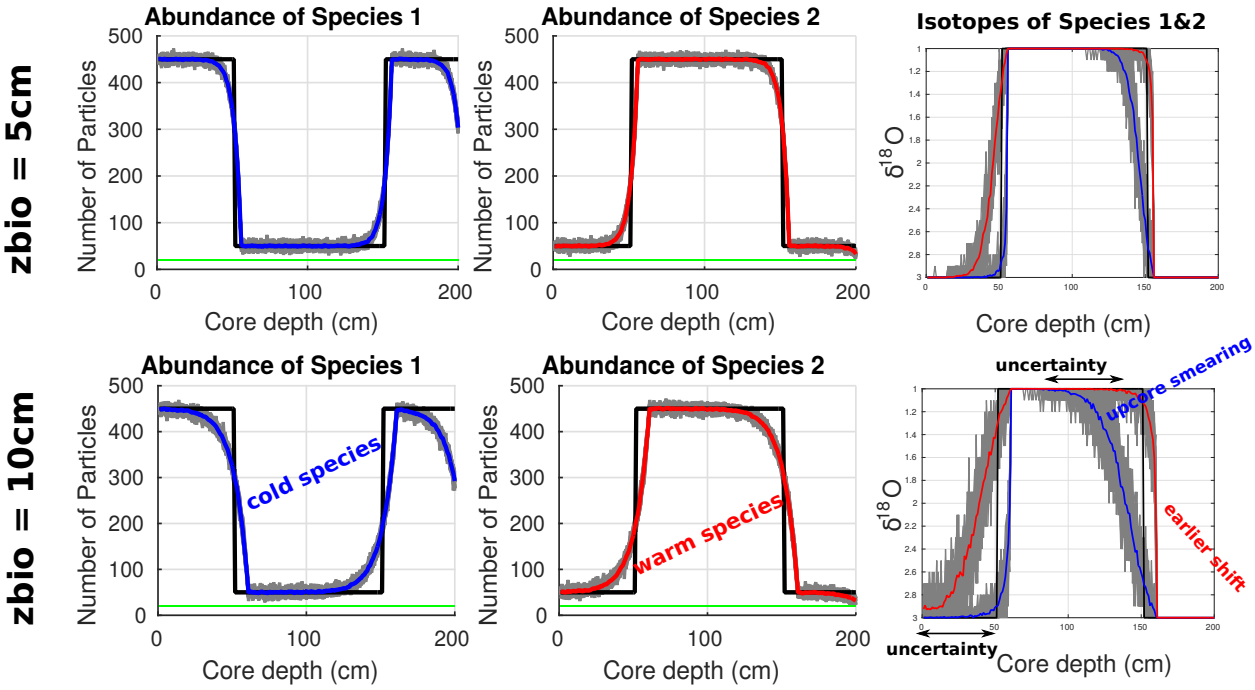

Figure 4: Example: Step change.

References

Trauth, M. H. (2013). TURBO2: A MATLAB simulation to study the effects of bioturbation on paleoceanographic time series. *Computers & Geosciences*, 61:1–10.

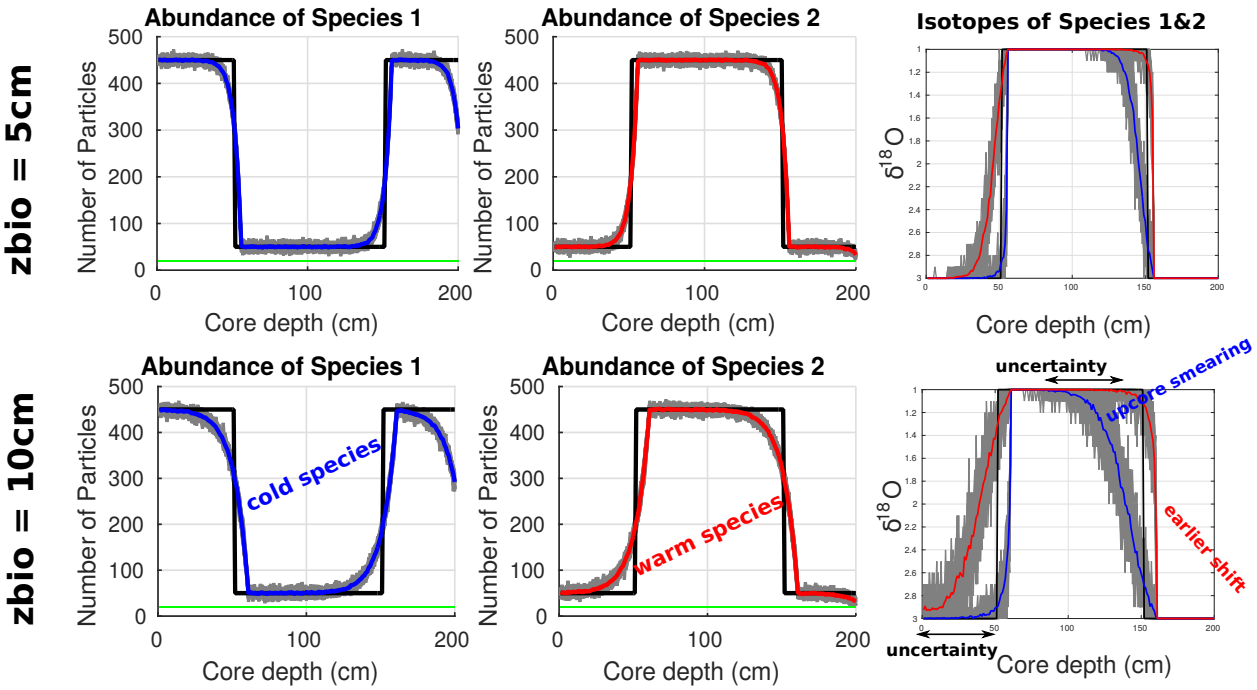

Figure 5: Example: Step change.

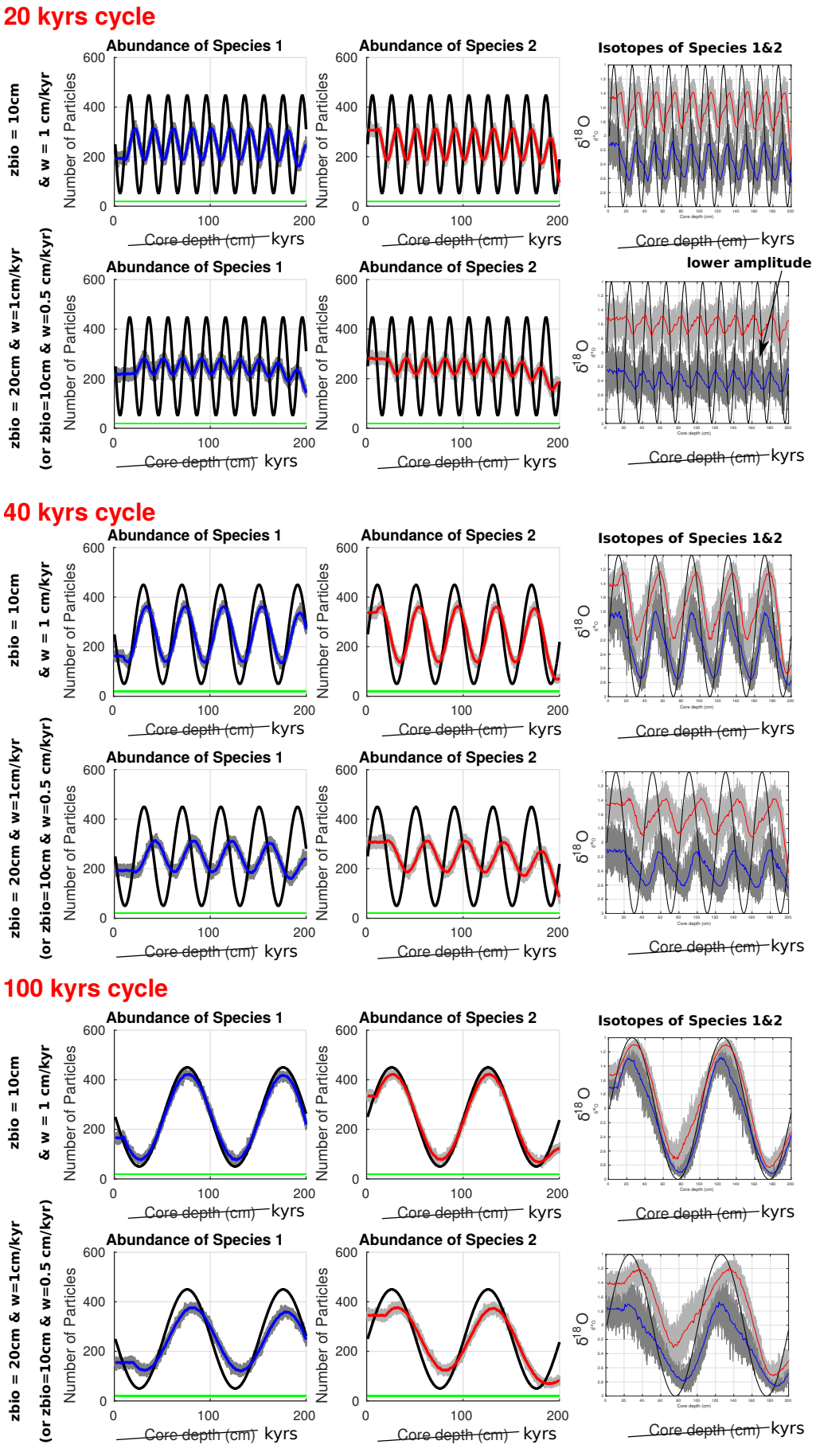

Figure 6: Example: Sine waves.

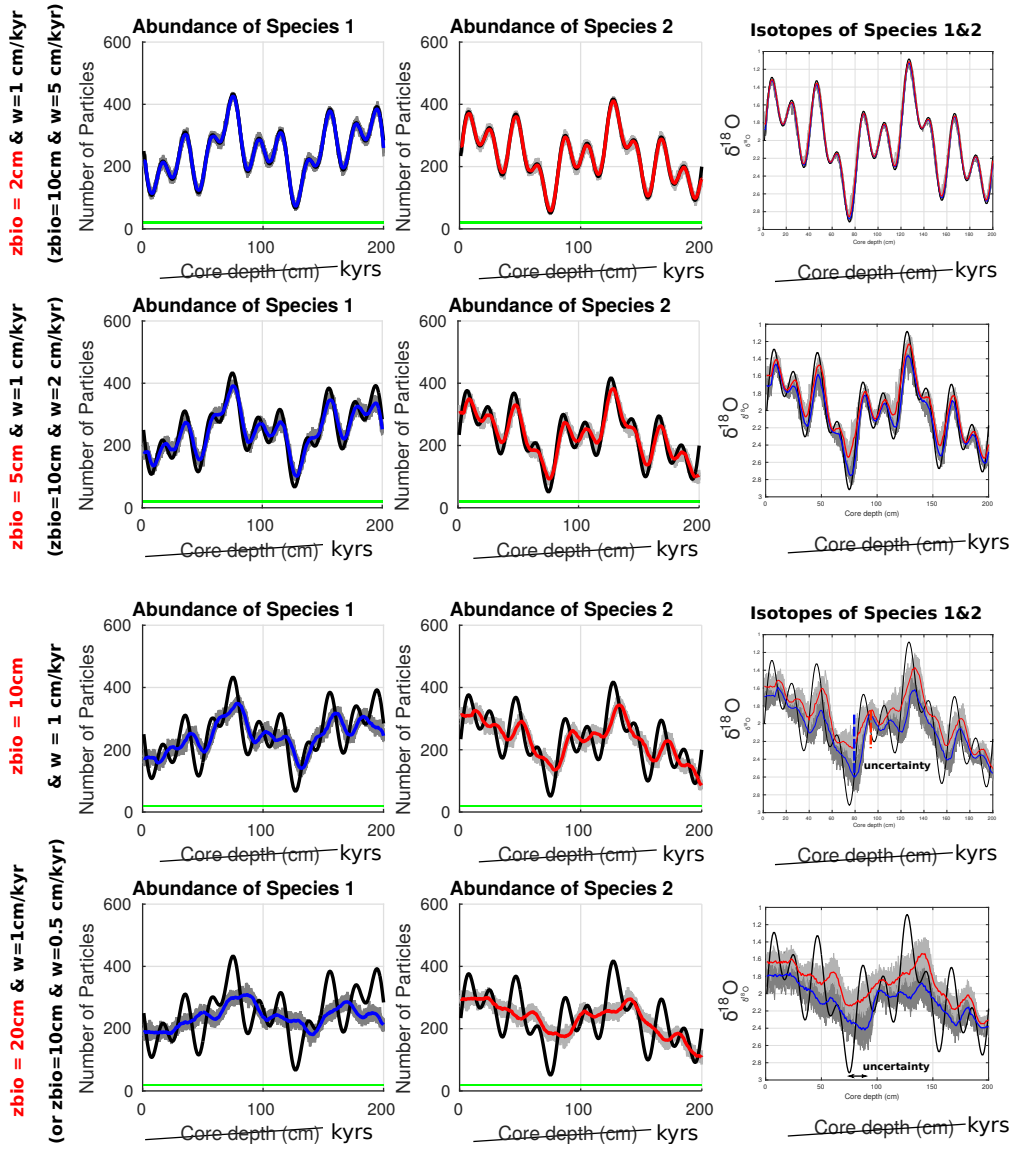

Figure 7: Example: All cycles combined with $z_{bio} \in \{2, 5, 10, 20\}$cm.

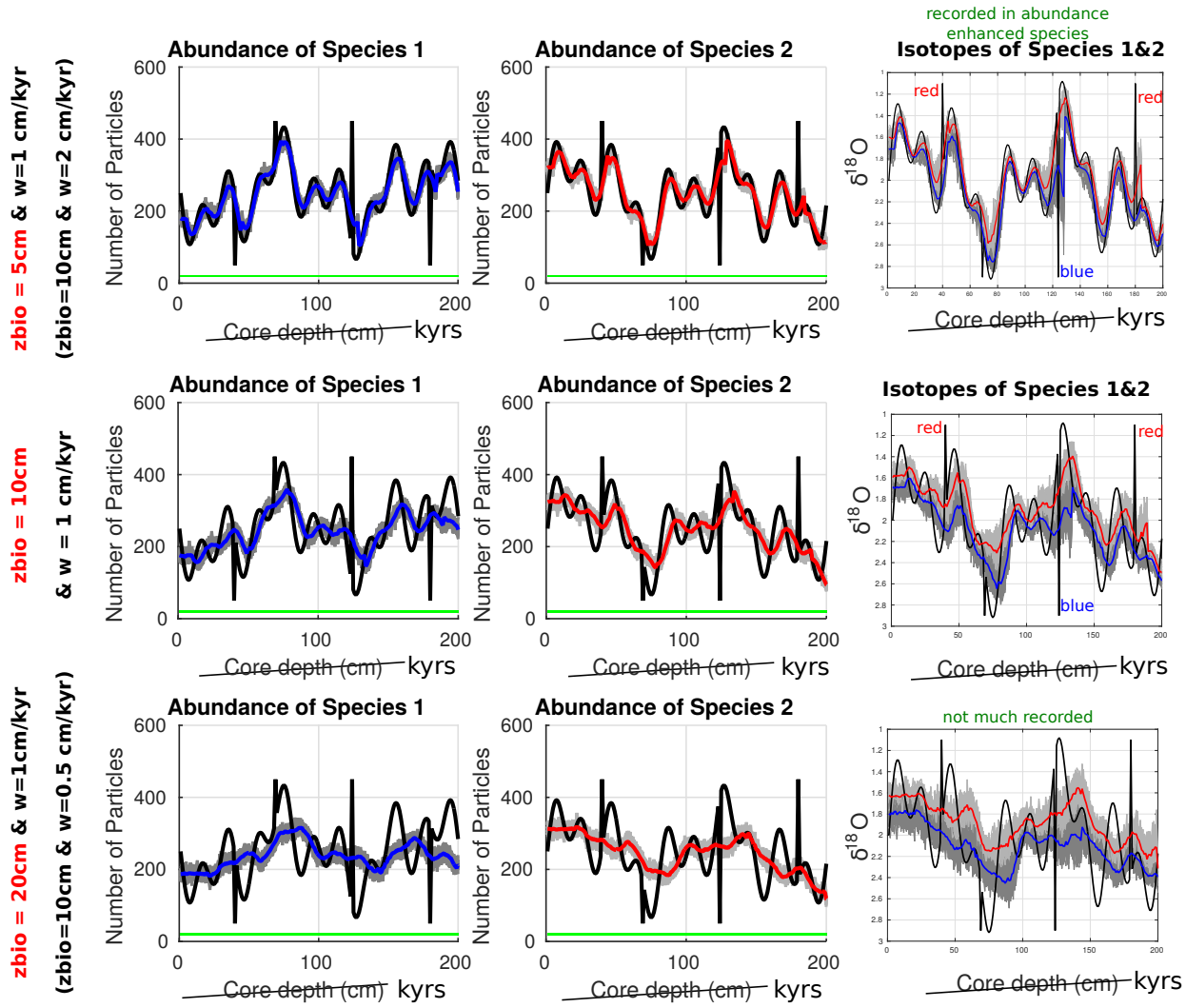

Figure 8: Example: Point event - all cycles combined with $z_{bio} \in \{5, 10, 20\}$cm.

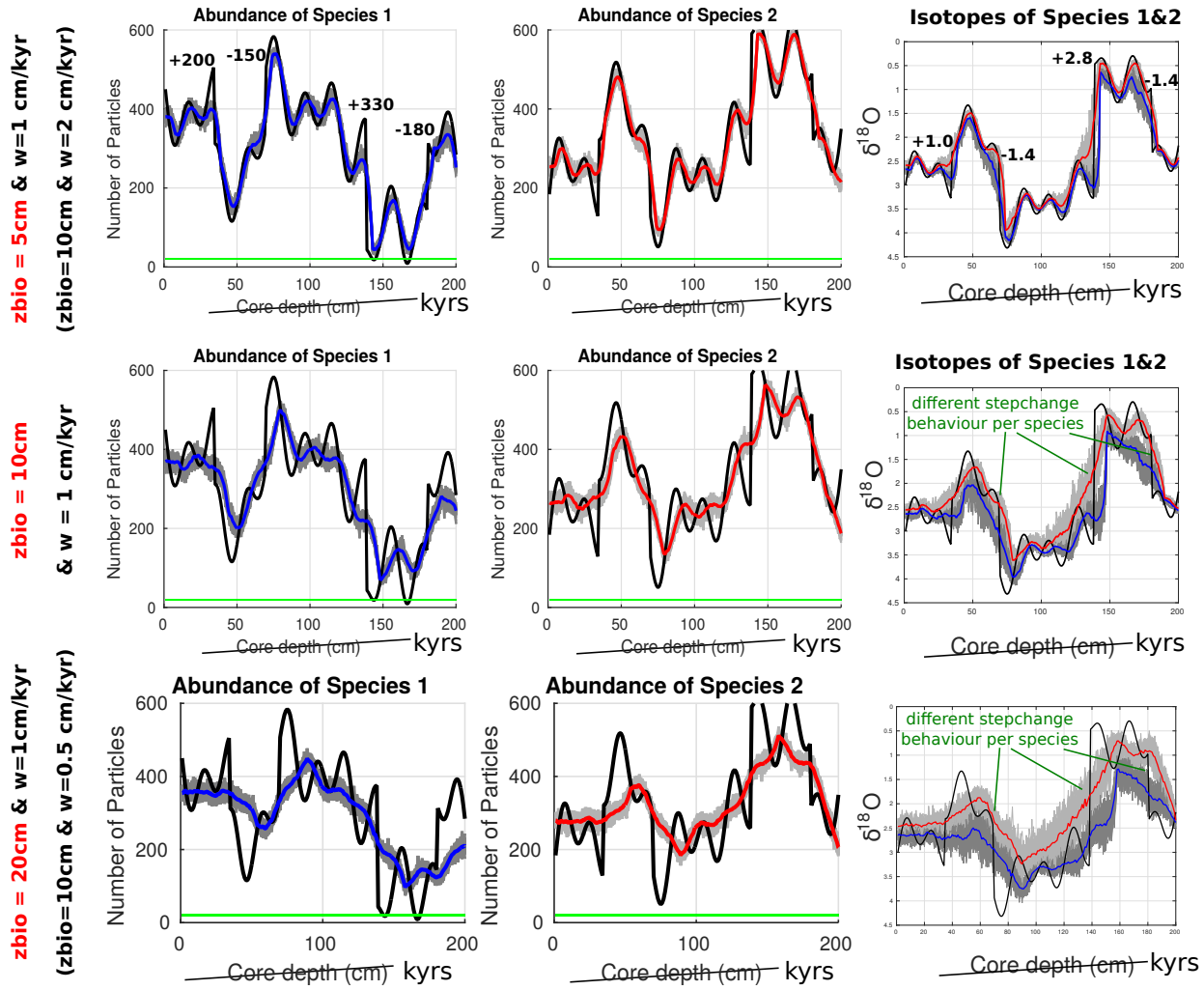

Figure 9: Example: Step changes - all cycles combined with $z_{bio} \in \{5, 10, 20\}$cm.

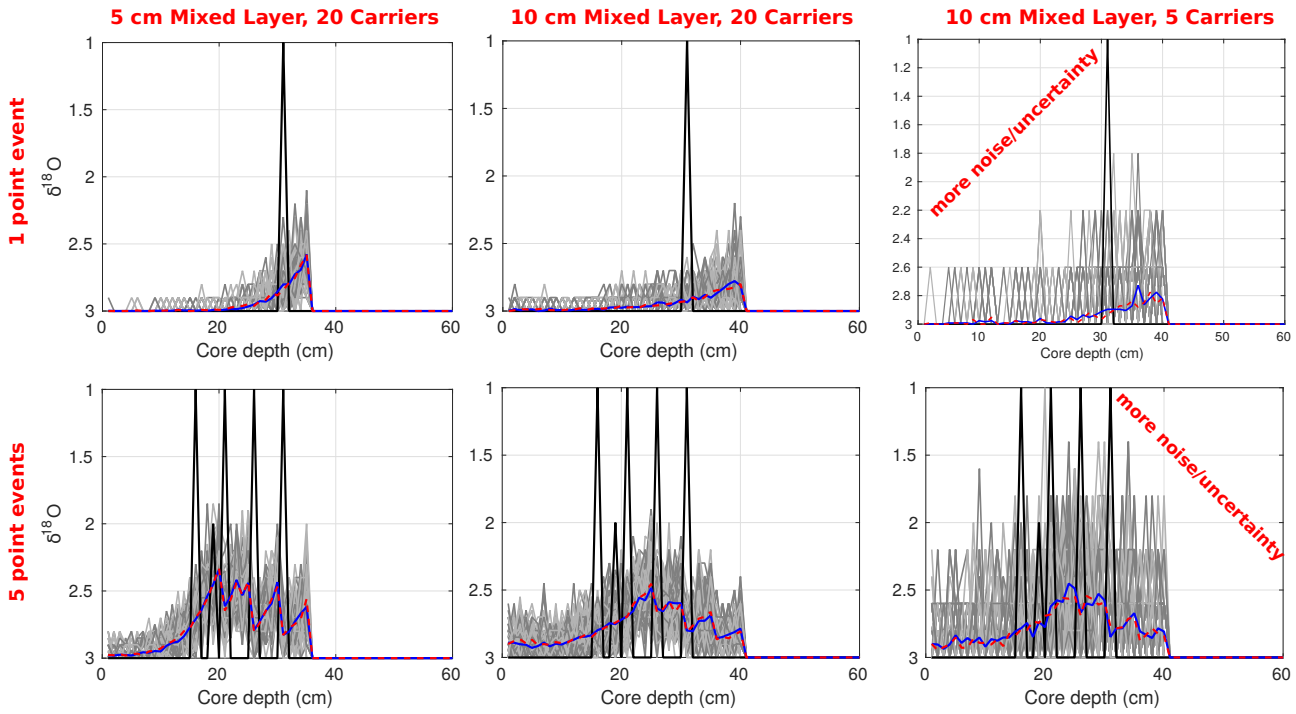

Figure 10: Example: Step changes - all cycles combined with $z_{bio} \in \{5, 10\}$cm and sample size of 20 and 5.

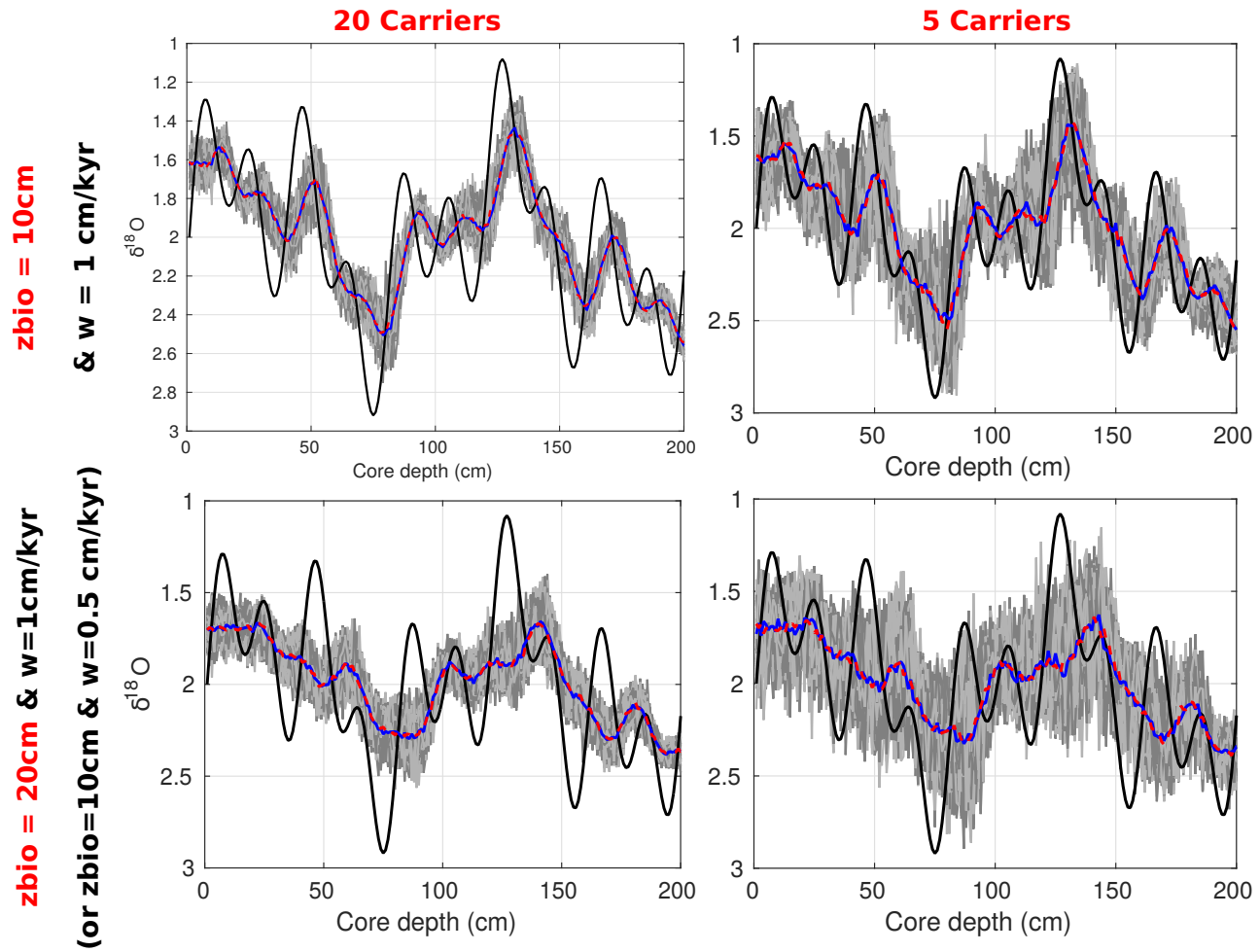

Figure 11: Example: All cycles combined with $z_{bio} \in \{10, 20\}$cm and sample size of 20 and 5.

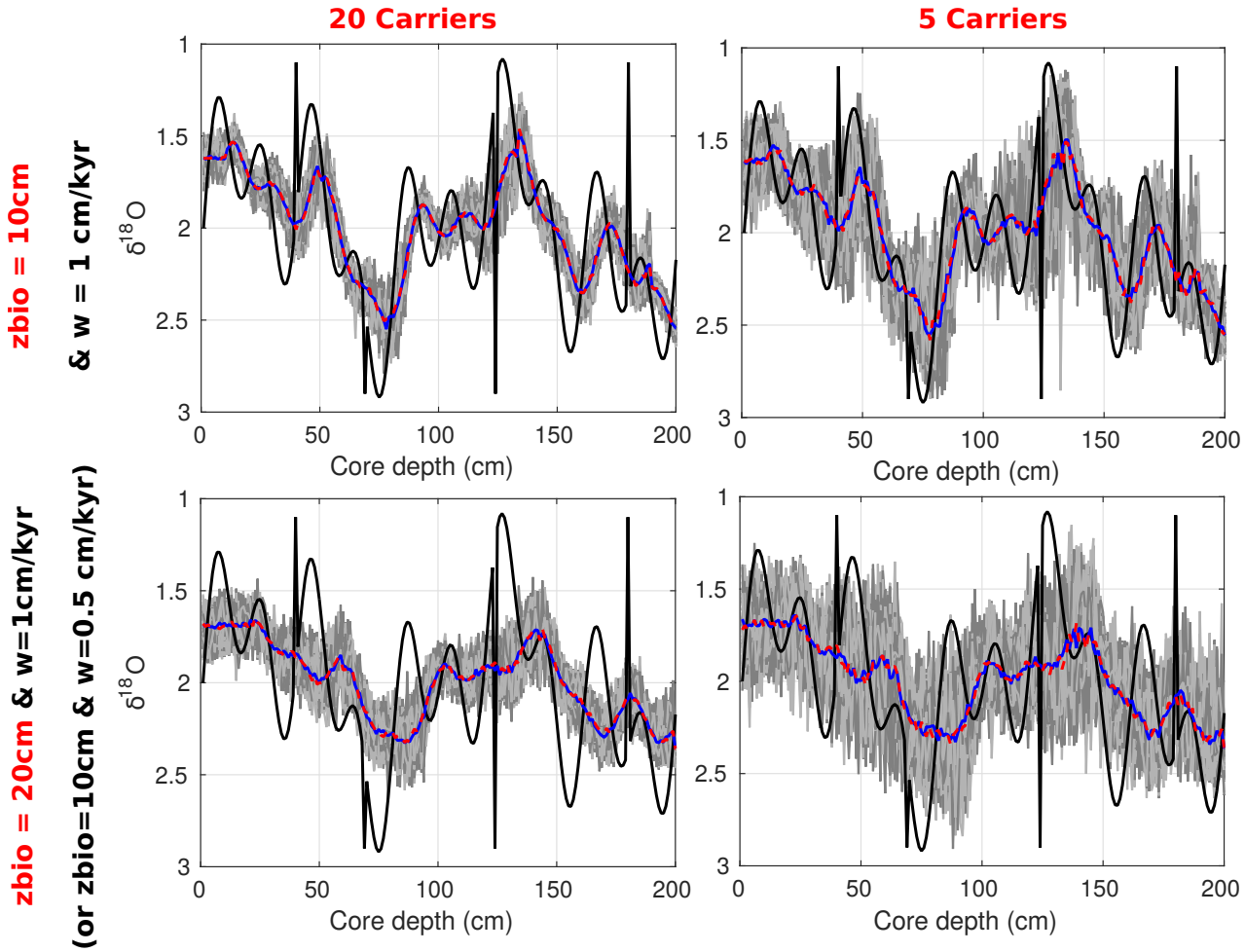

Figure 12: Example: Point events - all cycles combined with $z_{bio} \in \{10, 20\}$cm and sample size of 20 and 5.

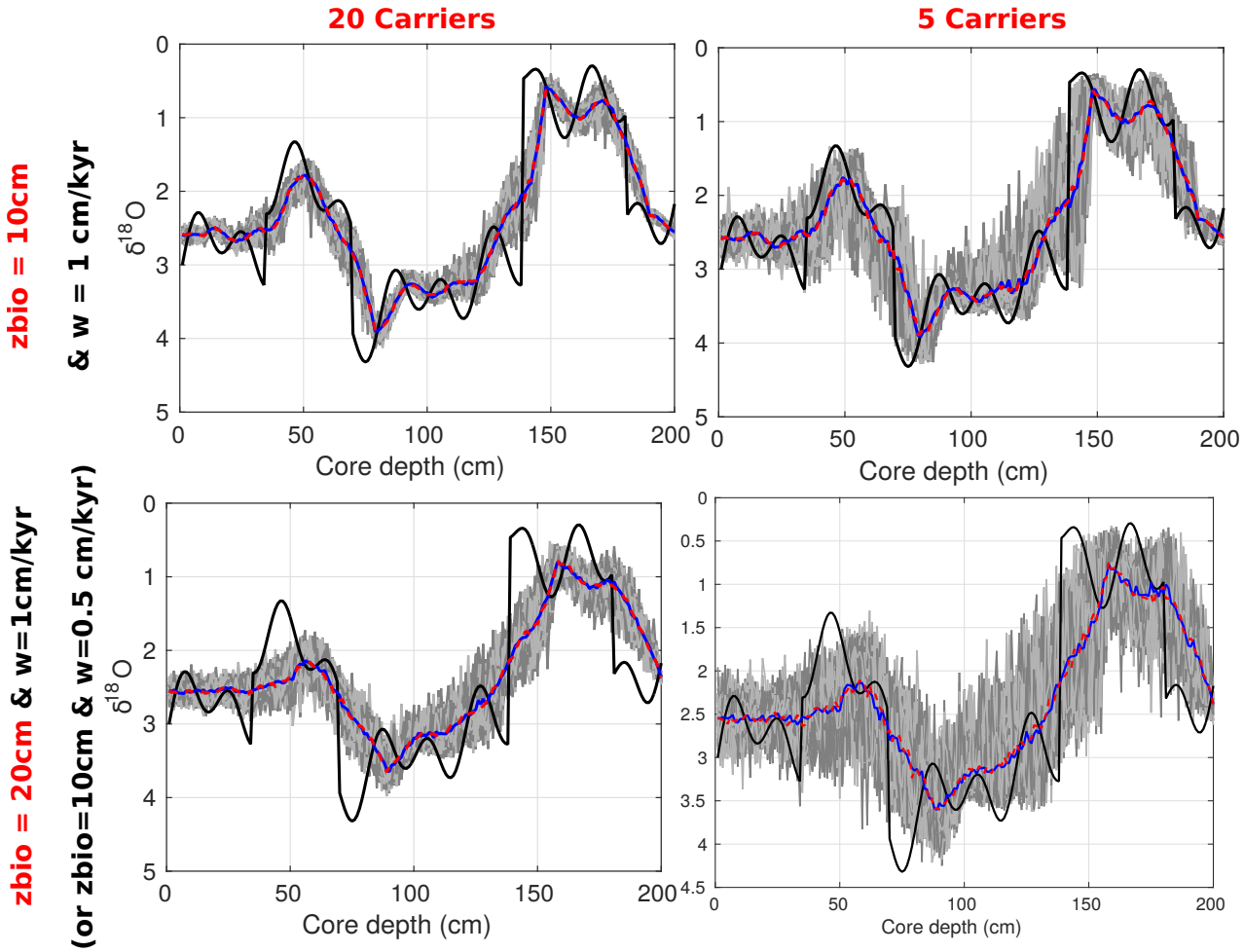

Figure 13: Example: Step changes - all cycles combined with $z_{bio} \in \{10, 20\}$cm and sample size of 20 and 5.