



## **Modelling the effects of temporally-variable production and bioturbation on age offsets between molluscan species in open-shelf sediment cores**

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Oceanographic and evolutionary inferences based on fossil assemblages in cores can be obscured by age offsets due to slow sedimentation or mixing. However, estimates of sedimentation can be biased by mixing and by variable production, thus obscuring estimates of temporal resolution of fossil assemblages. To identify the effects of sedimentation, mixing, preservation, and production on age offsets within and between two bivalve species, we simulate the effects of variable production and variable mixing on downcore age distributions, and compare them with downcore changes in postmortem age-frequency distributions (AFDs) observed on the southern California Shelf. We find that (1) within-species age offsets (inter-quartile age range) attain ~50-500 years in *Parvilucina* and ~2,000-4,000 years in *Nuculana* and between-species offsets (difference in median age) attain 1,000-2,000 years in the upper 25 cm, and (2) with increasing sediment depth, offsets within both species attain 2,000-5,000 years but between-species offsets become minor. Within-species offsets exceeding 2,000 years are in accord with the offsets expected under low sedimentation rate (~0.01 cm/y) and ~20 cm-thick fully-mixed layer. However, (1) sediment depths over which 1,000-yr cohorts are distributed exceed 20 cm and (2) thousand-year old shells in the top-core 25 cm demonstrate that they were exhumed from subsurface layers, indicating that mixing effects extend beyond the fully-mixed layer. Unmixed production trajectories show that abundance of *Nuculana* declined over the past centuries whereas abundance of *Parvilucina* increased in the 20th century. Out-of-phase production of these two species, coupled with upshifting of older *Nuculana* shells to surface, thus generates millennial-scale offsets between ages of these two species. Estimates of sedimentation rates and the mixed layer thickness can predict within-species temporal resolution to some degree but they do not fully account for incomplete mixing.