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Divergent trends in belowground microbial and animal biodiversity revealed across heterogeneous landscapes in a national-level metabarcoding survey

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Soil biota accounts for $\sim$25% of global biodiversity and is vital to nutrient cycling, soil fertility and primary production. There is a growing push to study the entirety of belowground biodiversity across large ecological scales to understand how habitat and soil properties interact to shape these communities. There is growing evidence that microbial and animal components of soil communities respond differently to shifts in soil properties and land uses. However, such evidence comes from largely homogeneous landscapes and often involves mixing modern molecular and traditional taxonomic methodologies to assess complete soil communities. Here, using a metabarcoding analysis of 436 locations across diverse temperate ecosystems in Wales, UK, we show that belowground richness of animal and microbial (bacteria, archaea, fungi, and protists) cohorts follow divergent trends across an intensity gradient of heterogeneous land uses, whereas β-diversity does not. Richness of soil animals was governed by intense land use and unaffected by soil properties, whereas microbial richness was largely driven by abiotic environmental properties across land uses. Our findings demonstrate the effectiveness of a standardized metabarcoding technique in capturing meaningful shifts soil biodiversity. Furthermore, we have extended our understanding of how soil communities are shaped by and respond to environmental factors and land use at the regional-scale, thereby providing a clearer understanding of macroecological processes governing the belowground biosphere.