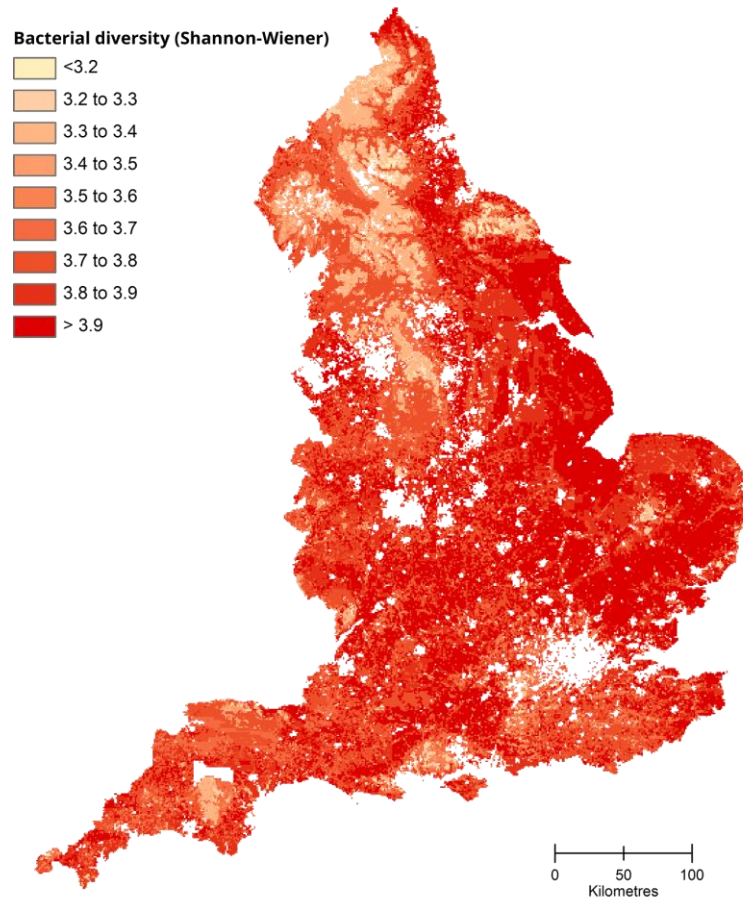
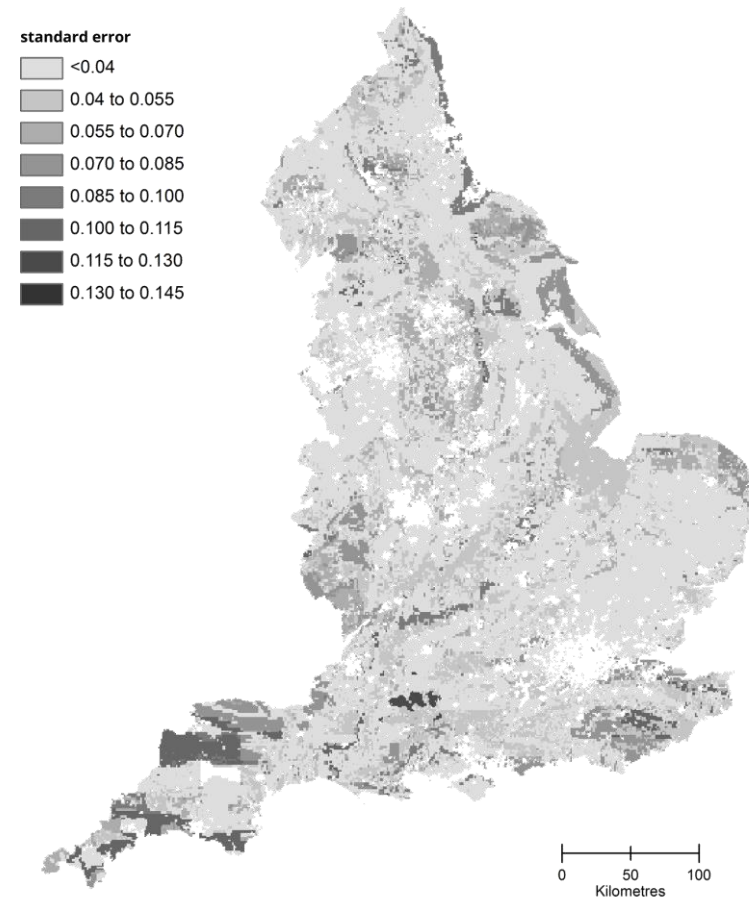


Soil bacteria

Mean estimates of soil bacterial diversity in topsoil (0-15cm depth)



Uncertainty: Standard error from the mean estimates



Soil bacteria

Mean estimates of soil bacterial diversity in topsoil.

What does this map show?

Mean estimates of bacterial diversity in topsoil (0-15cm depth) measured using the Shannon diversity index [\[1\]](#), a mathematical measure of species diversity in a given community. Soil bacteria represent a major portion of the biodiversity in soils. As they are at the bottom of the soil food web, the bacterial communities play an important role in soil processes such as nutrient cycling, carbon sequestration and the cycling of greenhouse gases as well as in biodegrading pollutants.

The UK National Ecosystem Assessment (UKNEA 2011) recognises the importance of soil bacterial diversity as a component of natural capital for supporting ecosystem services, in particular nutrient cycling, soil formation and primary production. The supporting services underpin the delivery of provisioning and regulating ecosystem services; soil bacterial diversity particularly influences food, fibre and energy from agriculture and forestry, soil quality and climate regulation.

A number of factors can have a strong influence on soil bacterial diversity [\[2,3\]](#), for example, environmental variables such as soil chemistry (e.g. pH), climate and plant community structure. The map reflects these factors with differences in bacterial diversity shown between upland habitats subject to harsh climatic conditions with distinct plant communities and acidic soils, and lowland habitats, which tend to have less acidic soils, agriculturally associated flora and a milder climate.

Soil bacterial diversity has high spatial variability. The standard error map gives an indication of the uncertainty in the estimated values shown on the mean bacterial diversity; the greater the standard error the greater the uncertainty.

How was this map produced?

This map was produced by using measurements of bacterial diversity from soil in the Centre for Ecology & Hydrology Countryside Survey (2007), at 1280 sample locations across GB within 256 1km squares. Measurements were extrapolated up to a national level using statistical analysis. This extrapolation was based on soil bacterial diversity values associated with a combination of habitat type and soil parent material: the geological material, bedrock, superficial and drift, from which soil develops.

What are the limitations of this map?

1. Areas such as urban and littoral rock are not sampled by Countryside Survey and therefore have no associated data. These areas are shown in white on the map.
2. In some circumstances sample sizes for particular habitat/parent material combinations were insufficient to estimate mean values. These areas are also shown in white on the map.
3. The map shows mean values at a 1 km square resolution. The standard error attributed to the mean estimates is only valid at 1km square resolution. The standard error at different resolutions is unknown.

4. The values for each 1 km square are generated from a statistical model of samples from approximately 256 1 km squares. Hence the map does not show direct measurements at all locations.

Further detail on the steps for creating this map

1. Top soil (0-15cm depth) cores were taken from 1280 Countryside Survey sample locations within 256 1km squares [\[4,5\]](#).
2. Bacterial communities were assessed using molecular DNA analysis [\[2\]](#). The Shannon diversity index was calculated for each sample [\[4,5\]](#). The Shannon diversity index is a mathematical measure of species diversity in a community which takes into account both species diversity and the relative abundance of different species.
3. Areas of each unique combination of broad habitat (as documented by JNCC [\[6\]](#)) and parent material were identified using data derived from the Land Cover Map 2007 [\[7\]](#) and Parent Material Model 2009 [\[8\]](#), respectively for each 1km square.
4. Values for the Shannon diversity index from Countryside Survey sampled locations were then combined with habitat/parent material data.
5. Using a statistical model (a generalized additive model [\[9\]](#)), a mean estimate of Shannon diversity for each unique combination of habitat and parent material, was extrapolated across the whole of England.
6. The statistical model was also used to produce an associated standard error map. High values reflect high variability and hence greater uncertainty in the mean estimates.

How to obtain the data

Data can be downloaded from <https://eip.ceh.ac.uk/naturalengland-ncmaps>.

Reuse of the data is subject to the terms of the [Open Government Licence](#) and you must cite:

Henrys, P.A.; Keith, A.M.; Robinson, D.A.; Emmett, B.A. (2014). Model estimates of topsoil microbes [Countryside Survey]. NERC Environmental Information Data Centre.
<http://doi.org/10.5285/53210c27-87fc-46e4-a3d6-e731003dc541>

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