

## Quantification of microbial life in the extreme subsurface

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Microbial life in the extreme subsurface is limited by various conditions such as the availability of nutrients, pH, temperature or toxic compounds. Examples for extreme subsurface environments are deeply-buried marine sediments, coal deposits, gas reservoirs or mine waste dumps. Over the last decade the microbiology in such environments has been studied in the BGR geomicrobiology lab using cultivation as well as molecular microbiological techniques. In deeply-buried marine sediments the abundance of cells strongly depends on the temperature and the availability of organic carbon down to a maximum sediment depth of almost 2 km below seafloor. The proportions of Bacteria and Archaea in marine sediments have shown to be highly variable in different sediments and sediment layers [1, 2]. In abandoned underground coal mines exists a complex microbial community responsible for the conversion of coal to methane [3, 4]. Gas reservoirs with very high salinity and temperature are hostile for life while a microbial community was found under less extreme conditions in this environment. In sulfidic mine waste tailings dumps microbial pyrite oxidation and metal mobilization preferentially occur in distinct tailings depth layers [5, 6]. No life was detected inside highly alkaline slag dumps while at less extreme conditions on the dump surface special new organisms were found [7].

- [1] Ciobanu *et al* (2014) *ISME J.*, published online.
- [2] Breuker (2013) *FEMS Microbiol. Ecol.* **85**, 578–592.
- [3] Krüger *et al* (2008) *Geomicrobiol. J.* **25**, 315–321.
- [4] Beckmann *et al* (2011) *Geomicrobiol. J.* **28**, 347–358.
- [5] Schippers *et al* (2010) *Hydrometallurgy* **104**, 342–350.
- [6] Korehi *et al* (2013) *Environ. Sci. Technol.* **47**, 2189–2196.
- [7] Schippers *et al* (2002) *Int. J. Syst. Evol. Microbiol.* **52**, 2291–2295.