The data contains 1 file:

1) The metadata: containing a) description of the samples, b) Soil potential substrate induced respiration, mineralisation, nitrification and denitrification, c) physicochemical properties of the soil and d) microbial gene abundances. The methods to obtain the values of this dataset are in the associated paper.

The datasets are associated with this paper (OA):
https://doi.org/10.1016/j.soilbio.2022.108709

The team that worked on this project gives you access to this data. As such, remember to cite the paper and this dataset whenever this data is reused.

Raw DNA sequencing data are available on the NCBI database under the accession number PRJNA790732.

DATASET info:

1) metadata

A .csv table containing a) description of the samples, b) Soil potential substrate induced respiration, mineralisation, nitrification and denitrification, c) physicochemical properties of the soil and d) microbial gene abundances. The methods to obtain the values of this dataset are in the associated paper.

Description of each column:

SampleID: sample identification number, which is the sample number used in all the datasets.

Treatment: Fertiliser application treatment applied to the plots

Date: date of sampling

SIR: Substrate induced respiration assay results (µg CO_2–C g^{-1} min^{-1})

Pot_N2O_produ: potential N2O production (µg N_2O–N g^{-1} dry soil min^{-1})

Pot_N2_produ: estimated potential N2 production (µg N_2–N g^{-1} dry soil min^{-1})

PN: soil potential nitrification (µg g fresh soil day^{-1})

N_mineralisation (µg NH_4^+-N g^{-1} dry soil)

NH4_mgL: ammonium (mg/L)

NO3_mgL: nitrate (mg/L)

P_morgans: phosphorus (mg/L soil)

K_Morgans: potassium (mg/L soil)

pH: soil pH

OM: organic matter or loss on ignition (%)

TOC: total organic carbon (%)

TN: total nitrogen (%)

TC: total carbon (%)

WHC: Water holding capacity of the soil (%)

GWC: Gravimetric water content of the soil (%)

X16s.Bact: Abundance of bacteria based on qPCR (gene copy number / ng DNA)

ITS: abundance of fungi (ITS) based on qPCR (gene copy number / ng DNA)

X16S.Archae: abundance of archaea (16S) based on qPCR (gene copy number / ng DNA)

AOA: abundance of ammonia-oxidizing archaea abundance based on qPCR (gene copy number / ng DNA)

AOB: abundance of ammonia-oxidizing bacteria based on qPCR (gene copy number / ng DNA)

COMAMMOX: complete ammonia-oxidizing bacterial abundance based on qPCR (gene copy number / ng DNA)

nirK: nirK genes' abundance based on qPCR (gene copy number / ng DNA)

nosZI: nosZI genes' abundance based on qPCR (gene copy number / ng DNA)

nosZII: nosZII genes' abundance based on qPCR (gene copy number / ng DNA)

nirS: nirS genes' abundance based on qPCR (gene copy number / ng DNA)