

Global Human Cryptosporidium Model Update

Data used:

Population: Worldpop 2018

Demographics: United Nations Waste Water Treatment: HydroWaste v1.0

Sanitation: Joint Monitoring Program (JMP) updated until 2024

Model updates:

- 1) Using point based WWTP data.
- 2) Waste water is distributed at country level based on WWTP capacity
- 3) WWTP emitted fraction calculated from treatment type.

Summary

	Current	Updated
gridded_population	Landscan 2010	Worldpop 2018
country_population	WUP 2018	WUP 2018
demographics	UN	UN
sanitation	JMP K2P	JMP WaterPath
wwtp	Every Grid Cell	HydroWaste WWTP locations
wwtp_distribution	Cell level	Country level by WWTP capacity
wwtp_femitted	vanPuijenbroek_2019	HydroWaste v1.0

Run Current Crypto Human Model

Run Updated Crypto Human Model

Compare Maps

```
par(mfrow = c(2, 1))

source("tests/testthat/helper-maps.R")
fpath <- file.path("output/global_human", "surface_water_emissions_crypto_global.tif")
rast_water <- terra::rast(fpath)
vect_borders <- terra::vect("inst/extdata/global_new_jmp/gadm/gadm.shp")
# helper_plot_map(rast_water, "Human Cryptosporidium Emissions", vect_borders)
terra::plot(log10(rast_water), main = "Current", col = rev(hcl.colors(50, palette = "RdYlBu")), breaks
terra::plot(vect_borders, add = TRUE)

fpath <- file.path("output/global_new_jmp", "surface_water_emissions_crypto_global.tif")
rast_water <- terra::rast(fpath)
# vect_borders <- terra::vect("inst/extdata/global_new_jmp/gadm/gadm.shp")
# helper_plot_map(rast_water, "Human Cryptosporidium Emissions", vect_borders)
terra::plot(log10(rast_water), main = "Updated", col = rev(hcl.colors(50, palette = "RdYlBu")), breaks
terra::plot(vect_borders, add = TRUE)
```

