Mehrabi et al. 2020. The global divide in data driven farming. Supplementary Information C: Geospatial overlays

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Contents

1 Reproducibility

We use the **R** packages `knitr` (Xie 2019) and `checkpoint` (Ooi 2019). The package `knitr` facilitates producing a dynamic document that contains all the steps required to analyze the data. `checkpoint()` will install all packages versions that we used in our analysis to avoid result discrepancies that may arise from software differences. Thus the reader is provided with all the code to fully reproduce the analysis, and adapt it for other analyses.

```r
require("checkpoint")
checkpoint(snapshotDate = "2020-07-20")
```

For the analysis in this document we will be using the **raster** (Hijmans 2020), `rgdal` (Bivand, Keitt, and Rowlingson 2019), `sp` (Pebesma and Bivand 2020), `sf` (Pebesma 2020), and `fasterize` (Ross 2020) packages.

```r
packages <- c("raster", "rgdal",
    "sp", "sf", "fasterize")
invisible(lapply(packages, require,
    character.only = TRUE))
```

2 Aims

This purpose of this document is to describe how we created a set of geospatial layers to assess the gaps in coverage of mobile network coverage for agricultural areas and vulnerable human populations targeted for data driven farming or health interventions. Specifically we will create seven key geospatial layers of global extent representing:

1. Hotspots of rainfall-dependent croplands (defined as the 90th percentile of the ratio of green water to total water used for crop production).
2. Arid cropland areas (defined as regions with annual precipitation <250mm).
3. The number of persons infected by Plasmodium falciparum.
4. Hotspots of yield gaps for four major crops (defined as the 90th percentile of the ratio of yield gaps to yield potentials).
5. Cropland areas with nutrient deficits for 17 major crops.
6. The number of food insecure persons (we used the prevalence of childhood stunting to proxy food insecurity).
7. The number of people with low well-being levels (defined as the 10th percentile of the subnational human development index).

The creation of these layers is a simple three step process. First we define a set of reference layers for cropland areas and human populations. Second we create a set of indicator layers representing the outcomes of interest in binary or prevalence units. Finally, we multiply the indicator layer by the reference layers to create the final output layers which represent absolute values of areas or people affected by each indicator. }

3 Load and preprocess data

3.1 Reference data

3.1.1 Population count

To represent population counts, we used LandScan 2017 (https://landscan.ornl.gov/documentation) ambient population distribution (Rose et al. 2018), which we aggregated to the target resolution for population based indicators (Malaria risk, Malnutrition, Subnational human development index) and areas based indicators

(Rainfall dependency, Arid Environments, Yield gaps, and Nitrogen deficiency) by calculating sums per grid cell.

```
PopCount_LandScan_25km2 <- raster::raster("./_00_ReferenceLayers/Population/ls_pop_25km2.tif")
PopCount_LandScan_100km2 <- raster::raster("./_00_ReferenceLayers/Population/ls_pop_100km2.tif")
PopCount_LandScan_100km2
```

```
## class      : RasterLayer
## dimensions : 2160, 4320, 9331200  (nrow, ncol, ncell)
## resolution : 0.08333333, 0.08333333  (x, y)
## extent     : -180, 180, -90, 90  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## source     : /Users/pumpkinjr/Sync/academic/projects/UBCload/projects/DDAbaselines/Data_scripts/Anal
## names      : ls_pop_100km2
## values     : 0, 4923381  (min, max)
```

```
# Target resolution
target_reso_pop25 <- raster::res(PopCount_LandScan_25km2)
target_reso_pop100 <- raster::res(PopCount_LandScan_100km2)
```

3.1.2 Cropland area

To represent cropland area, we used two different data sets that matched the respective indicator data. For Rainfall dependency, we used crop area and harvested crop area [ha] for the year 2000 (Siebert and Döll 2010). For Yield gaps, we used harvested crop area [ha] for the four main crops maize, rice, soy, and wheat for the year 2000 (Monfreda, Ramankutty, and Foley 2008). For all other indicators, we used crop area [ha] calculated from cropland cover [%] for the year 2000 (Ramankutty et al. 2008). All three data sources share the same spatial resolution, which we set as the target resolution for area-based indicators (Rainfall dependency, Arid Environments, Yield gaps, and Nitrogen deficiency).

```
# Siebert and Döll 2010
CropArea_MIRCA <- raster::raster("./_00_ReferenceLayers/Cropland/cropland_mirca.asc")
HarvArea_rf_MIRCA <- raster::raster("./_00_ReferenceLayers/IrrigatedArea/area_harv_rf_allcrops_ha.asc")

# Monfreda, Ramankutty, and
# Foley 2008
CropArea_maize <- raster::raster("./_00_ReferenceLayers/Cropland/maize_HarvestedAreaHectares.tif")
CropArea_rice <- raster::raster("./_00_ReferenceLayers/Cropland/rice_HarvestedAreaHectares.tif")
CropArea_soy <- raster::raster("./_00_ReferenceLayers/Cropland/soybean_HarvestedAreaHectares.tif")
CropArea_wheat <- raster::raster("./_00_ReferenceLayers/Cropland/wheat_HarvestedAreaHectares.tif")
CropArea_Top4Crops <- list(CropArea_maize,
    CropArea_rice, CropArea_soy,
    CropArea_wheat)

# Ramankutty et al. 2008
CropCover_EarthStat <- raster::raster("./_00_ReferenceLayers/Cropland/Cropland2000_5m.tif")
CellSize_EarthStat_km <- raster::area(CropCover_EarthStat)
CellSize_EarthStat_ha <- CellSize_EarthStat_km *
    100
CropArea_EarthStat <- CropCover_EarthStat *
    CellSize_EarthStat_ha

# Target resolution
target_reso_area <- raster::res(CropArea_EarthStat)
target_reso_area
```

```
## [1] 0.08333333 0.08333333
```

3.1.3   Define target extent

```
target_ext <- raster::extent(CropArea_EarthStat)
target_ext
```

```
## class      : Extent
## xmin       : -180
## xmax       : 180
## ymin       : -90
## ymax       : 90
```

3.2   Indicators

3.2.1   Rainfall dependency

To represent rainfall dependency, we used the consumptive crop water use of green water [mm/a] for the year 2000 (Siebert and Döll 2010). Data represented the average between 1998-2002.

```
green_water <- raster::raster("./_01_Rainfall_dependence/cwu_green_rainfed.asc")
```

3.2.2   Arid Environments

To represent arid environments, we used annual precipitation sums [mm/a] from the CHELSA data base (Karger et al. 2017), which we harmonized to the target extent and aggregated to the target resolution (area-based) by calculating the mean per grid cell.

```
precip <- raster::raster("./_02_HeatDrought/precip_FINAL_100km2.tif")
```

3.2.3   Malaria risk

To represent malaria risk, we used the nnual mean of Plasmodium falciparum incidence [%] in 2017 (Weiss et al. 2019).

```
pf_inci <- raster::raster("./_03_MalariaRisk/2019_Global_Pf_Incidence_2017_FINAL.tif")
```

3.2.4   Yield gaps

To represent yield gaps, we used yield gap data for 16 major crops [t/ha] for the year 2000 (Mueller et al. 2012). Data represented averages of census data between 1997-2003. We extracted data for the four major crops maize, rice, soy, and wheat and calculated yield gap fractions by calculating the quotient between actual yield gap and potential yields for each crop type individually.

```
folder_list <- as.list(list.dirs("./_04_YieldGap",
    full.names = TRUE, recursive = FALSE))

yield_gap_All16Crops <- list()
yield_pot_All16Crops <- list()

# load yield gap raster data
```

```r
# and store in list
for (i in 1:length(folder_list)) {
    # get all files for crop i
    temp_ras_list <- list.files(folder_list[[i]],
        pattern = "\\.tif$", full.names = TRUE)

    # select yield gap (2) and
    # yield potential (3)
    temp_ras_gap <- temp_ras_list[[2]]
    temp_ras_pot <- temp_ras_list[[3]]

    # read raster
    yield_gap_All16Crops[[i]] <- raster::raster(temp_ras_gap)
    yield_pot_All16Crops[[i]] <- raster::raster(temp_ras_pot)
}

# select only main crop types
# (production): maize (4), rice
# (9), soybean (12), wheat (16)
yield_gap_Top4Crops <- list(yield_gap_All16Crops[[4]],
    yield_gap_All16Crops[[9]],
    yield_gap_All16Crops[[12]],
    yield_gap_All16Crops[[16]])
yield_pot_Top4Crops <- list(yield_pot_All16Crops[[4]],
    yield_pot_All16Crops[[9]],
    yield_pot_All16Crops[[12]],
    yield_pot_All16Crops[[16]])

# calculate yield gap fractions
yield_gap_fraction_Top4Crops <- list()

for (i in 1:length(yield_gap_Top4Crops)) {
    temp_gap <- yield_gap_Top4Crops[[i]]
    temp_pot <- yield_pot_Top4Crops[[i]]
    temp_frac <- temp_gap/temp_pot
    yield_gap_fraction_Top4Crops[[i]] <- temp_frac
}
```

3.2.5 Nitrogen deficiency

To represent nitrogen deficiency, we used the nitrogen balance [kg] for 140 crops for the year 2000 (West et al. 2014). To only account for deficiencies, we set all positive values to *NA*.

```r
nitro_bal <- raster::raster("./_05_FertilizerBalance//NitrogenBalanceOnLandscape_140Crops.tif")
nitro_def <- nitro_bal
nitro_def[] <- ifelse(nitro_def[] <
    0, nitro_def[], NA)
```

3.2.6 Malnutrition

To represent malnutrition, we used the distribution of poor population [persons/km2] in developing countries, based on stunting among children (FAO 2011). We further used the prevalence of malnutrition [%] across the

African continent for the year 2015 (Osgood-Zimmerman et al. 2018) to increase thematic coverage. We used three indicators of malnutrition for our analysis: stunting, wasting, and underweight.

```r
stunt_glob <- raster::raster("./_06_Malnutrition/FAO_stunting_popdens.tif")
stunt <- raster::raster("./_06_Malnutrition/stunt_africa_FINAL.tif")
underweight <- raster::raster("./_06_Malnutrition/underweight_africa_FINAL.tif")
wasting <- raster::raster("./_06_Malnutrition/wasting_africa_FINAL.tif")
```

3.2.7 Subnational human development index

To represent human development, we used the sub-national human development index (SHDI, Smits and Permanyer 2019). The SHDI is a dimensionless, statistic composite index of life expectancy, education, and per-capita income. We converted SHDI data from its original polygon format to a spatial raster by assuming spatial homogeneity of the indicator within administrative units.

```r
shdi_data <- utils::read.csv("./_07_SHDI/SHDI_Complete_3.0.csv",
    stringsAsFactors = FALSE)

# remove national totals
shdi_data_clean <- shdi_data[-which(shdi_data$level ==
    "National"), ]

# select entries target year
# 2010 (most complete cases)
shdi_data_clean_2010 <- shdi_data_clean[which(shdi_data_clean$year ==
    2010), ]

# load shapefile with GDL
# (Global Data Lab) codes for
# joining
gdl_shp <- sf::st_read("./_07_SHDI/GDL-SHDI-SHP-2/GDL-SHDI-SHP-2.shp",
    quiet = TRUE)

# join data to shapefile (and
# export)
gdl_shdi_2010 <- merge(gdl_shp,
    shdi_data_clean_2010, by.x = "GDLCode",
    by.y = "GDLCODE")

# rasterize SHDI column
shdi_ras_2010 <- fasterize::fasterize(gdl_shdi_2010,
    CropCover_EarthStat, field = "shdi",
    fun = "first")
```

4 Spatial Overlay

We performed two separate analyses: 1) for area-based indicators, and 2) for population-based indicators.

1. Area-based indicators

- Step 1: Create hotspot maps for rainfall dependency and yield gaps using the highest decile of the indicator's distribution. For aridity, we used a fixed threshold value of 250mm precipitation per year. For nitrogen deficiency, we used the full data distribution. The resulting maps are binary layers.

- Step 2: Mask binary indicator hotspot maps to cropland extent (threshold: minimum 1ha cropland area).
- Step 3: Multiply masked binary indicator hotspot maps with harvested crop area to obtain area estimates of cropland affected by each indicator.

2. Population-based indicators

- Step 1: Create hotspot map for SHDI using the lowest decile of the indicator's distribution. The resulting map is a binary layer.
- Step 2: Multiply indicator maps (incidence of child stunting and prevalence of malaria infecions, and the presence of low human development) with population count data to obtain estimates of the number persons affected.

4.1   Area-based indicators

4.1.1   Map indicator hotspots using global thresholds (deciles or fixed)

```r
### Rainfall dependency
green_water_hotspot <- green_water

# convert 0 to NA to not bias
# quantile calculation
green_water_hotspot[] <- ifelse(green_water_hotspot[] ==
    0, NA, green_water_hotspot[])

# create binary mask using the
# top decile (i.e., highest
# crop water use)
green_water_hotspot[] <- ifelse(green_water_hotspot[] >=
    raster::quantile(green_water_hotspot,
        probs = 0.9)[[1]], 1, 0)


### Arid environments
precip_hotspot <- precip

# define arid environments with
# precipitation below 250mm/a
precip_hotspot[] <- ifelse(precip_hotspot[] <=
    250, 1, 0)


### Yield gaps
yield_gap_hotspot_list <- list()

# loop through list of four
# major crops and create binary
# masks using the top decile
# (i.e., largest yield gap
# fraction)
for (i in 1:length(yield_gap_fraction_Top4Crops)) {
    # create temporary raster
    temp_ras <- yield_gap_fraction_Top4Crops[[i]]
```

```r
    # create binary mask of top
    # decile (i.e., highest yield
    # gap fraction)
    temp_ras[] <- ifelse(temp_ras[] >=
        raster::quantile(temp_ras,
            probs = 0.9)[[1]],
        1, 0)

    # convert NAs to 0 for
    # summarizing
    temp_ras[is.na(temp_ras[])] <- 0

    # store in list
    yield_gap_hotspot_list[[i]] <- temp_ras
}


### Nitrogen deficiency
nitro_def_hotspot <- nitro_def

# create binary mask using all
# grid cells which are nitrogen
# deficient.
nitro_def_hotspot[] <- ifelse(nitro_def_hotspot[] <
    0, 1, 0)
```

4.1.2 Mask with cropland layer

```r
# create cropland masks using
# cut-off value of minimum 1ha
# per 10x10km grid cell
CropArea_MIRCA_mask1ha <- CropArea_MIRCA
CropArea_MIRCA_mask1ha[] <- ifelse(CropArea_MIRCA_mask1ha[] >
    1, 1, NA)

CropArea_EarthStat_mask1ha <- CropArea_EarthStat
CropArea_EarthStat_mask1ha[] <- ifelse(CropArea_EarthStat_mask1ha[] >
    1, 1, NA)

# mask indicator hotspots to
# cropland extent
green_water_hotspot_CLmask <- green_water_hotspot *
    CropArea_MIRCA_mask1ha
precip_hotspot_CLmask <- precip_hotspot *
    CropArea_EarthStat_mask1ha
nitro_def_hotspot_CLmask <- nitro_def_hotspot *
    CropArea_EarthStat_mask1ha
yield_gap_hotspot_CLmask <- list()
for (i in 1:length(yield_gap_hotspot_list)) {
    yield_gap_hotspot_CLmask[[i]] <- yield_gap_hotspot_list[[i]] *
        CropArea_EarthStat_mask1ha
}
```

4.1.3 Multiply cropland area layers with masked hotspot layers

```r
greenH2O_FINAL <- green_water_hotspot_CLmask *
    HarvArea_rf_MIRCA
aridity_FINAL <- precip_hotspot_CLmask *
    CropArea_EarthStat
Ndeficit_FINAL <- nitro_def_hotspot_CLmask *
    CropArea_EarthStat
yield_gap_hotspot_area <- list()
for (i in 1:length(yield_gap_hotspot_CLmask)) {
    # multiply yield gap hotspots
    # with respective harvested
    # crop area
    yield_gap_hotspot_area[[i]] <- yield_gap_hotspot_CLmask[[i]] *
        CropArea_Top4Crops[[i]]
}
# calculate area sums for the
# four major crops
yieldgap_FINAL <- yield_gap_hotspot_area[[1]] +
    yield_gap_hotspot_area[[2]] +
    yield_gap_hotspot_area[[3]] +
    yield_gap_hotspot_area[[4]]
```

4.2 Population-based indicators

4.2.1 Map SHDI hotspots

```r
shdi_hotspot <- shdi_ras_2010
shdi_hotspot[] <- ifelse(shdi_hotspot[] <=
    raster::quantile(shdi_hotspot,
        probs = 0.1)[[1]], 1, 0)
shdi_hotspot
```

```
## class      : RasterLayer
## dimensions : 2160, 4320, 9331200  (nrow, ncol, ncell)
## resolution : 0.08333333, 0.08333333  (x, y)
## extent     : -180, 180, -90, 90  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## source     : memory
## names      : layer
## values     : 0, 1  (min, max)
```

4.2.2 Multiply population counts with hotspot/prevalence layers

```r
pf_ppl_glob <- pf_inci * PopCount_LandScan_25km2
stunt_ppl_AFR <- stunt * PopCount_LandScan_25km2
underweight_ppl_AFR <- underweight *
    PopCount_LandScan_25km2
wasting_ppl_AFR <- wasting * PopCount_LandScan_25km2
shdi_ppl_glob <- shdi_hotspot *
    PopCount_LandScan_100km2
```

4.2.3 Multiply global stunting [pers/km2] with grid cell area [km] to obtain absolute numbers

```
stunt_ppl_glob <- stunt_glob *
    CellSize_EarthStat_km
```

4.3 Export final maps

```
raster::writeRaster(greenH2O_FINAL,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/AREA_BASED/greenH2O.tif")
raster::writeRaster(aridity_FINAL,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/AREA_BASED/aridity.tif")
raster::writeRaster(Ndeficit_FINAL,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/AREA_BASED/Ndeficit.tif")
raster::writeRaster(yieldgap_FINAL,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/AREA_BASED/yieldgap.tif")

raster::writeRaster(pf_ppl_glob,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/malaria_ppl_glob.tif")
raster::writeRaster(stunt_ppl_glob,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/stunt_ppl_glob.tif")
raster::writeRaster(stunt_ppl_AFR,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/stunt_ppl_AFR.tif")
raster::writeRaster(underweight_ppl_AFR,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/underweight_ppl_AFR.tif")
raster::writeRaster(wasting_ppl_AFR,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/wasting_ppl_AFR.tif")
raster::writeRaster(shdi_ppl_glob,
    format = "GTiff", overwrite = TRUE,
    "./RESULTS/POP_BASED/shdi_ppl_glob.tif")
```

5 Session info

```
sessionInfo()
```

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
```

```
##
## locale:
## [1] en_CA.UTF-8/en_CA.UTF-8/en_CA.UTF-8/C/en_CA.UTF-8/en_CA.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] fasterize_1.0.2 sf_0.9-5        rgdal_1.4-8     raster_3.1-5
## [5] sp_1.4-1        knitr_1.26
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.4        compiler_3.6.1   pillar_1.4.6     formatR_1.7
##  [5] class_7.3-15      tools_3.6.1      digest_0.6.23    evaluate_0.14
##  [9] lifecycle_0.2.0   tibble_3.0.3     lattice_0.20-41  pkgconfig_2.0.3
## [13] rlang_0.4.7       DBI_1.0.0        yaml_2.2.0       xfun_0.11
## [17] e1071_1.7-3       dplyr_1.0.2      stringr_1.4.0    generics_0.0.2
## [21] vctrs_0.3.4       classInt_0.4-3   grid_3.6.1       tidyselect_1.1.0
## [25] glue_1.4.2        R6_2.4.1         rmarkdown_1.18   purrr_0.3.3
## [29] magrittr_1.5      codetools_0.2-16 htmltools_0.4.0  ellipsis_0.3.0
## [33] units_0.6-5       KernSmooth_2.23-15 stringi_1.4.3  crayon_1.3.4
```

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