Ecosystem Service Change & Hotspot Extraction

vv0.5.0

Jerónimo Rodríguez Escobar

2025-12-16 14:58 Pacific Standard Time

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1 Overview

Prepares the processed 10 km grid, derives hotspot flags, and produces the bar/violin plots that summarize signed and absolute change by group (region, income, biome). Key steps: load helpers and paths, attach grouping attributes, pivot change fields to long form, define hotspots using the configured thresholds, export hotspot layers, and write the latest plots to `outputs/plots/latest/`.

2 Setup and Libraries

Load all core packages (tidyverse, spatial, plotting helpers) and initialize reproducibility settings. This chunk also sources `R/paths.R` and runs `devtools::load_all()` so downstream chunks can reuse helper functions.

3 Metadata Banner

Published: 2025-12-17 13:10 PST

> **Note**
>
> **Run metadata**
>
> - Analysis version: v0.5.0
> - Rendered: 2025-12-17 13:10 PST
> - Git: feat/ks-analysis @ 10146f9
> - Data root: /home/jeronimo/data/global_ncp

4 Add regional attributes to Grid (countries & biomes)

Attach country and biome IDs to the 10 km grid (`sf_f`) so downstream aggregation/hotspot steps can group by region. This chunk only runs if the processed GPKG is missing.

The input 10 km grid (`sf_f`) is enriched with country and WWF biome IDs to allow aggregation and comparisons of change by subregions (World Bank region, income group, continent, UN region, and biome). We use a point-on-surface join to avoid sliver/overlap issues, keep only the needed fields, and write a single enriched GPKG for downstream grouping, hotspot extraction, and plotting.

> **Tip**
>
> **What this step does**
>
> - Reads country and biome layers from `vectors/`.
> - Joins them to the 10 km grid via point-on-surface.
> - Writes `processed/10k_change_calc.gpkg` for downstream analysis (pivoting, hotspots, plots). **Inputs:** `sf_f` grid; `vectors/cartographic_ee_ee_r264_correspondence.gpkg`; `vectors/Biome.gpkg` **Output:** `processed/10k_change_calc.gpkg` (grid + regional attributes)
>
> **Why point-on-surface?** It's robust for odd cell shapes and avoids polygon–polygon sliver issues.

```
Skipping join: /home/jeronimo/data/global_ncp/processed/10k_change_calc.gpkg already exists.
```

5 Produce signed change bars

Bars are computed directly from `processed/10k_change_calc.gpkg`. We output two variants—zeros kept vs zeros dropped—both with trimmed tails and a dashed global mean. Pivoted `plt_long` is only necessary for hotspots/KS.

What this chunk does: - Read the processed GPKG and normalize IDs (`fid`, `c_fid`), dropping any `c_fid.x/y` artifacts. - Build a service mapping (`svc_map`) so raw column bases (with/without `_mean`) map to the canonical services; construct `col_pct/col_abs` names. - `agg_by_group()`: intersect requested `groupings` with available columns; for each grouping × service, pick the pct/abs change column, handle `Inf` pct values (`handle_inf`), optionally drop zeros (`drop_zero`), trim extremes at `cut_q`, then compute mean change by group. Returns tidy rows with `grouping, group, service, metric, mean_chg`. - Run `agg_by_group()` four ways: trimmed keep0/drop0 and no-trim keep0/drop0 → `signed_keep0`, `signed_drop0`, `signed_keep0_no_trim`, `signed_drop0_no_trim`. - A later chunk computes global reference means; plotting is in its own chunk so you can skip it when debugging.

```
services <- svc_order
groupings <- c("income_grp","region_wb","continent","region_un","WWF_biome")
cut_q <- 0.999
handle_inf <- "na"  # options: "na", "cap"
verbose <- TRUE
# helper for lightweight progress messages

vmsg <- function(...) if (isTRUE(verbose)) message(...)

gpkg <- file.path(Sys.getenv("GLOBAL_NCP_DATA"), "processed", "10k_change_calc.gpkg")
stopifnot(file.exists(gpkg))

vmsg("Reading: ", gpkg, " [layer: 10k_change_calc]")
sf_f <- sf::st_read(gpkg, layer = "10k_change_calc", quiet = TRUE)
sf_f <- sf::st_drop_geometry(sf_f)
if (!"fid" %in% names(sf_f)) sf_f$fid <- seq_len(nrow(sf_f))
if (!"c_fid" %in% names(sf_f)) {
  if ("c_fid.x" %in% names(sf_f)) sf_f <- dplyr::rename(sf_f, c_fid = c_fid.x)
  else if ("c_fid.y" %in% names(sf_f)) sf_f <- dplyr::rename(sf_f, c_fid = c_fid.y)
  else if ("id" %in% names(sf_f))      sf_f <- dplyr::rename(sf_f, c_fid = id)
}
sf_f <- dplyr::select(sf_f, -dplyr::any_of(c("c_fid.x","c_fid.y")))

# build mapping; include both raw base and no-_mean base, with ready-to-use columns
chg_cols <- grep("_(abs|pct)_chg$", names(sf_f), value = TRUE)
vmsg("Found ", length(chg_cols), " change columns; mapping services...")
services_raw   <- unique(sub("_(abs|pct)_chg$", "", chg_cols))     # as in file (may include _
services_clean <- stringr::str_remove(services_raw, "_mean$")
services_lower <- tolower(services_clean)
svc_map <- tibble::tibble(
  col_base  = c(services_raw, services_clean),
```

```
  canonical = dplyr::recode(c(services_lower, services_lower),
                            !!!canonical_lookup, .default = c(services_clean, services_clean))
) |>
  dplyr::distinct() |>
  dplyr::mutate(col_pct = paste0(col_base, "_pct_chg"),
                col_abs = paste0(col_base, "_abs_chg"))

agg_by_group <- function(df, services, groupings, cut_q = 0.999,
                         handle_inf = c("na","cap"), drop_zero = FALSE) {
  handle_inf <- match.arg(handle_inf)
  groupings <- intersect(groupings, names(df))
  vmsg("Groupings available: ", paste(groupings, collapse = ", "))
  out <- list()
  for (g in groupings) {
    vmsg("  Grouping: ", g)
    for (svc in services) {
      map_rows <- dplyr::filter(svc_map, canonical == svc)
      if (!nrow(map_rows)) next
      cols_pct <- map_rows$col_pct[map_rows$col_pct %in% names(df)]
      cols_abs <- map_rows$col_abs[map_rows$col_abs %in% names(df)]
      if (!length(cols_pct) && !length(cols_abs)) next

      add_one <- function(col, metric) {
        v <- df[[col]]
        if (metric == "pct" && any(is.infinite(v))) {
          if (handle_inf == "na") v[is.infinite(v)] <- NA_real_
        }
        if (isTRUE(drop_zero)) v[v == 0] <- NA_real_
        cap <- stats::quantile(abs(v), cut_q, na.rm = TRUE)
        v_trim <- pmax(pmin(v, cap), -cap)
        tibble::tibble(
          service = svc,
          group   = df[[g]],
          metric  = metric,
          val     = v_trim
        )
      }

      rows <- list()
      if (length(cols_pct)) rows[[length(rows)+1]] <- add_one(cols_pct[1], "pct")
      if (length(cols_abs)) rows[[length(rows)+1]] <- add_one(cols_abs[1], "abs")
      rows <- dplyr::bind_rows(rows)
      if (!nrow(rows)) next
      rows <- rows |>
        dplyr::filter(!is.na(group)) |>
        dplyr::group_by(service, metric, group) |>
        dplyr::summarise(mean_chg = mean(val, na.rm = TRUE), .groups = "drop") |>
```

```
        dplyr::mutate(grouping = g)
      out[[length(out)+1]] <- rows
    }
  }
  dplyr::bind_rows(out)
}

# trimmed means, zeros kept/dropped
signed_keep0 <- agg_by_group(sf_f, services, groupings, cut_q = cut_q,
                             handle_inf = handle_inf, drop_zero = FALSE)
signed_drop0 <- agg_by_group(sf_f, services, groupings, cut_q = cut_q,
                             handle_inf = handle_inf, drop_zero = TRUE)
# untrimmed (cut_q = 1) means, zeros kept/dropped
signed_keep0_no_trim <- agg_by_group(sf_f, services, groupings, cut_q = 1,
                                     handle_inf = handle_inf, drop_zero = FALSE)
signed_drop0_no_trim <- agg_by_group(sf_f, services, groupings, cut_q = 1,
                                     handle_inf = handle_inf, drop_zero = TRUE)
print(dplyr::count(signed_keep0, grouping, metric, service))
```

```
# A tibble: 80 x 4
   grouping  metric service              n
   <chr>     <chr>  <chr>            <int>
 1 WWF_biome abs    C_Risk              16
 2 WWF_biome abs    C_Risk_Red_Ratio    16
 3 WWF_biome abs    N_Ret_Ratio         16
 4 WWF_biome abs    N_export            16
 5 WWF_biome abs    Nature_Access       16
 6 WWF_biome abs    Pollination         16
 7 WWF_biome abs    Sed_Ret_Ratio       16
 8 WWF_biome abs    Sed_export          16
 9 WWF_biome pct    C_Risk              16
10 WWF_biome pct    C_Risk_Red_Ratio    16
# i 70 more rows
```

```
print(dplyr::count(signed_drop0, grouping, metric, service))
```

```
# A tibble: 80 x 4
   grouping  metric service              n
   <chr>     <chr>  <chr>            <int>
 1 WWF_biome abs    C_Risk              16
 2 WWF_biome abs    C_Risk_Red_Ratio    16
 3 WWF_biome abs    N_Ret_Ratio         16
 4 WWF_biome abs    N_export            16
 5 WWF_biome abs    Nature_Access       16
 6 WWF_biome abs    Pollination         16
 7 WWF_biome abs    Sed_Ret_Ratio       16
```

```
 8 WWF_biome abs    Sed_export          16
 9 WWF_biome pct    C_Risk              16
10 WWF_biome pct    C_Risk_Red_Ratio    16
# i 70 more rows
```

5.1 Diagnose sign flips (keep0 vs drop0)

Use this helper to see where dropping zeros changes the sign of the mean. Run interactively (set `eval: true`) after the direct bars chunk so `signed_keep0`/`signed_drop0` exist.

```
# Join trimmed keep/drop and untrimmed keep/drop, with clear column names
cmp <- signed_keep0 |>
  dplyr::rename(mean_keep_trim = mean_chg) |>
  dplyr::full_join(
    signed_drop0 |> dplyr::rename(mean_drop_trim = mean_chg),
    by = c("grouping","metric","service","group")
  ) |>
  dplyr::full_join(
    signed_keep0_no_trim |> dplyr::rename(mean_keep_notrim = mean_chg),
    by = c("grouping","metric","service","group")
  ) |>
  dplyr::full_join(
    signed_drop0_no_trim |> dplyr::rename(mean_drop_notrim = mean_chg),
    by = c("grouping","metric","service","group")
  ) |>
  dplyr::mutate(
    sign_keep_trim   = sign(mean_keep_trim),
    sign_drop_trim   = sign(mean_drop_trim),
    sign_keep_notrim = sign(mean_keep_notrim),
    sign_drop_notrim = sign(mean_drop_notrim),
    flipped_trim     = sign_keep_trim != sign_drop_trim &
                       !is.na(sign_keep_trim) & !is.na(sign_drop_trim),
    flipped_notrim   = sign_keep_notrim != sign_drop_notrim &
                       !is.na(sign_keep_notrim) & !is.na(sign_drop_notrim)
  )

flips_trim_only <- cmp |> dplyr::filter(flipped_trim == TRUE)
flips_no_trim_only <- cmp |> dplyr::filter(flipped_notrim==TRUE)
```

```
# Trimmed, zeros kept: compare pct vs abs signs
flips_pct_abs_keep_trim <- signed_keep0 |>
  tidyr::pivot_wider(names_from = metric, values_from = mean_chg) |>
  dplyr::mutate(
    sign_pct = sign(pct),
    sign_abs = sign(abs),
    flipped_pct_abs = sign_pct != sign_abs &
                      !is.na(sign_pct) & !is.na(sign_abs)
```

```
  ) |>
  dplyr::filter(flipped_pct_abs)

# Same for zeros dropped
flips_pct_abs_drop_trim <- signed_drop0 |>
  tidyr::pivot_wider(names_from = metric, values_from = mean_chg) |>
  dplyr::mutate(
    sign_pct = sign(pct),
    sign_abs = sign(abs),
    flipped_pct_abs = sign_pct != sign_abs &
                      !is.na(sign_pct) & !is.na(sign_abs)
  ) |>
  dplyr::filter(flipped_pct_abs)
```

```
# Trimmed, zeros kept: compare pct vs abs signs
flips_pct_abs_keep_no_trim <- signed_keep0_no_trim |>
  tidyr::pivot_wider(names_from = metric, values_from = mean_chg) |>
  dplyr::mutate(
    sign_pct = sign(pct),
    sign_abs = sign(abs),
    flipped_pct_abs = sign_pct != sign_abs &
                      !is.na(sign_pct) & !is.na(sign_abs)
  ) |>
  dplyr::filter(flipped_pct_abs)

# Same for zeros dropped
flips_pct_abs_drop_no_trim <- signed_drop0_no_trim |>
  tidyr::pivot_wider(names_from = metric, values_from = mean_chg) |>
  dplyr::mutate(
    sign_pct = sign(pct),
    sign_abs = sign(abs),
    flipped_pct_abs = sign_pct != sign_abs &
                      !is.na(sign_pct) & !is.na(sign_abs)
  ) |>
  dplyr::filter(flipped_pct_abs)
```

```
# after make-signed-bars-data, set eval: true on this once
#| label: export-flip-tables
#| eval: false
out_tbl <- file.path("outputs","tables"); dir.create(out_tbl, recursive = TRUE, showWarnings =

mk_pct_abs <- function(df, suffix) {
  df |> tidyr::pivot_wider(names_from = metric, values_from = mean_chg) |>
    dplyr::mutate(flipped_pct_abs = sign(pct) != sign(abs) & !is.na(pct) & !is.na(abs)) |>
    dplyr::filter(flipped_pct_abs) |>
    dplyr::rename(mean_abs = abs, mean_pct = pct) |>
    dplyr::mutate(source = suffix)
```

```
}

flips_keep_trim    <- mk_pct_abs(signed_keep0,           "keep_trim")
flips_drop_trim    <- mk_pct_abs(signed_drop0,           "drop_trim")
flips_keep_notrim  <- mk_pct_abs(signed_keep0_no_trim,   "keep_notrim")
flips_drop_notrim  <- mk_pct_abs(signed_drop0_no_trim,   "drop_notrim")

# save
saveRDS(list(flips_keep_trim, flips_drop_trim, flips_keep_notrim, flips_drop_notrim),
        file.path(out_tbl, "flips_pct_abs_all.rds"))
readr::write_csv(dplyr::bind_rows(flips_keep_trim, flips_drop_trim,
                                  flips_keep_notrim, flips_drop_notrim),
                 file.path(out_tbl, "flips_pct_abs_all.csv"))
```

6 Load cached long table (plt_long) for hotspots/KS

Hotspot export and KS still expect `plt_long`. To avoid the heavy pivot here, we load the cached table from `outputs/tables/plt_long.rds`. If it's missing, run `scratch/pivot_long.qmd` (or `scratch/pivot_long.R`) to regenerate it.

7 Hotspot extraction workflow (global + subregional)

We identify per-service hotspots using a 5% percentile rule and **direction vectors**: - `loss_services` (e.g., Nature_Access, Pollination, N/Sed_Ret_Ratio, C_Risk_Red_Ratio) → we flag the **lowest** values; - `gain_services` (Sed_export, N_export, C_Risk) → we flag the **highest** values.

We run this **once globally** and then **once per subregion** (World Bank region, income group, continent, UN region, WWF biome). For each run and for each metric (absolute and percent change) we write a compact **GPKG** containing only the hotspot cells, plus a CSV index:

- Output root: `processed/hotspots/`
  - `abs/global/hotspots_global_abs.gpkg`
  - `pct/global/hotspots_global_pct.gpkg`
  - `abs/<group_col>/hotspots_<group_col>_<group_val>_abs.gpkg`
  - `pct/<group_col>/hotspots_<group_col>_<group_val>_pct.gpkg`
- Index: `processed/hotspots/_hotspots_index.csv` (columns: scope, group_col, group_val, metric, n_hot, gpkg).

These files are meant for QGIS/QA and downstream stats (e.g., KS) without recomputing hotspots.

7.1 Hotspot rules & export configuration

The analysis uses a single, central configuration so the hotspot rules are consistent everywhere:

Thresholding: we flag hotspots using the top/bottom tails of the distribution per service. Here we use a percentile cutoff (e.g., 5%) rather than a fixed count.

Direction of concern: services in loss are "worse when they go down" (we keep the lowest tail); services in gain are "worse when they go up" (we keep the highest tail).

Combos (optional): grouped service sets that we count per cell for quick composite summaries.

Export switches: choose whether to write GPKGs and/or the CSV index.

```
HOTS_CFG <- list(
  analysis_name   = "global_NCP_hotspots",
  pct_cutoff      = 0.05,
  threshold_mode  = "percent",
  rule_mode       = "vectors",
  loss = c("Nature_Access","Pollination","N_Ret_Ratio","Sed_Ret_Ratio","C_Risk_Red_Ratio"),
  gain = c("Sed_export","N_export","C_Risk"),
  combos = list(
    deg_combo = c("Nature_Access","Pollination","N_export","Sed_export","C_Risk"),
    rec_combo = c("Nature_Access","Pollination","N_Ret_Ratio","Sed_Ret_Ratio","C_Risk_Red_Ratio
  ),
# centralize the grouping columns here
  groupings = c("income_grp","region_wb","continent","region_un","WWF_biome"),
  # IO
  write_layers = TRUE,
  write_index  = TRUE,
  out_dir      = file.path(data_dir(), "processed", "hotspots")
)
```

```
::: callout-note
**Hotspot configuration**

- Cutoff: 5% (percent)
- Rule mode: vectors
- Loss services: Nature_Access, Pollination, N_Ret_Ratio, Sed_Ret_Ratio, C_Risk_Red_Ratio
- Gain services: Sed_export, N_export, C_Risk
- Combos: **deg_combo**: Nature_Access, Pollination, N_export, Sed_export, C_Risk<br>**rec_comb
…
- Groupings: income_grp, region_wb, continent, region_un, WWF_biome
…- Write layers: TRUE | Write index: TRUE
- Output dir: `/home/jeronimo/data/global_ncp/processed/hotspots`
:::
```

7.2 Validate hotspot configuration

```
# stopifnot(exists("plt_long"))
# svc_all <- unique(plt_long$service)
# if (length(intersect(HOTS_CFG$loss, HOTS_CFG$gain)) > 0) {
#   stop("A service appears in BOTH `loss` and `gain`. Fix HOTS_CFG.")
# }
# miss_loss <- setdiff(HOTS_CFG$loss, svc_all)
# miss_gain <- setdiff(HOTS_CFG$gain, svc_all)
# if (length(miss_loss) > 0 || length(miss_gain) > 0) {
#   warning("Services in HOTS_CFG not found in `plt_long$service`:\n",
#           if (length(miss_loss)) paste0("  - missing loss: ", paste(miss_loss, collapse=", ", "
#           if (length(miss_gain)) paste0("  - missing gain: ", paste(miss_gain, collapse=", ", "
# }
```

7.3 Export hotspot layers

> **Note**
>
> **Hotspot export module**
> - Computes hotspot cells once (global + by subregion) for ABS and PCT change.
> - Writes compact GPKGs for mapping/QA and maintains `_hotspots_index.csv`.
> - Prereqs: `plt_long` in memory, `HOTS_CFG` defined (loss/gain/combos/etc.).

8 Trimmed change bar plots

> **Note**
>
> **How to read these bars**
>
> - Each bar shows the **trimmed mean absolute change** ($|\Delta|$) per service within each group; facet axes are free.
> - Bars are **always positive** by design: height = **magnitude of change**, not direction.
> - Direction-of-concern used elsewhere in the analysis:
>   - Worse when **up** `Sed_export`, `N_export`, `C_Risk`.
>   - Worse when **down** `Nature_Access`, `Pollination`, `N_Ret_Ratio`, `Sed_Ret_Ratio`, `C_Risk_Red_Ratio`.
> - These bars answer **"where is change largest?"**. See hotspot maps/violins for **up vs. down** patterns.

Short answer: your current barplots use all grid cells (the full 10-km population), not just hotspots. They summarize trimmed means per subregion/global from plt_long via aggregate_change_simple(),

with cut_q=0.999 to cap outliers and (optionally) drop_zeros=TRUE. That's why every bar is positive—those bars are the magnitude of change, not the direction.

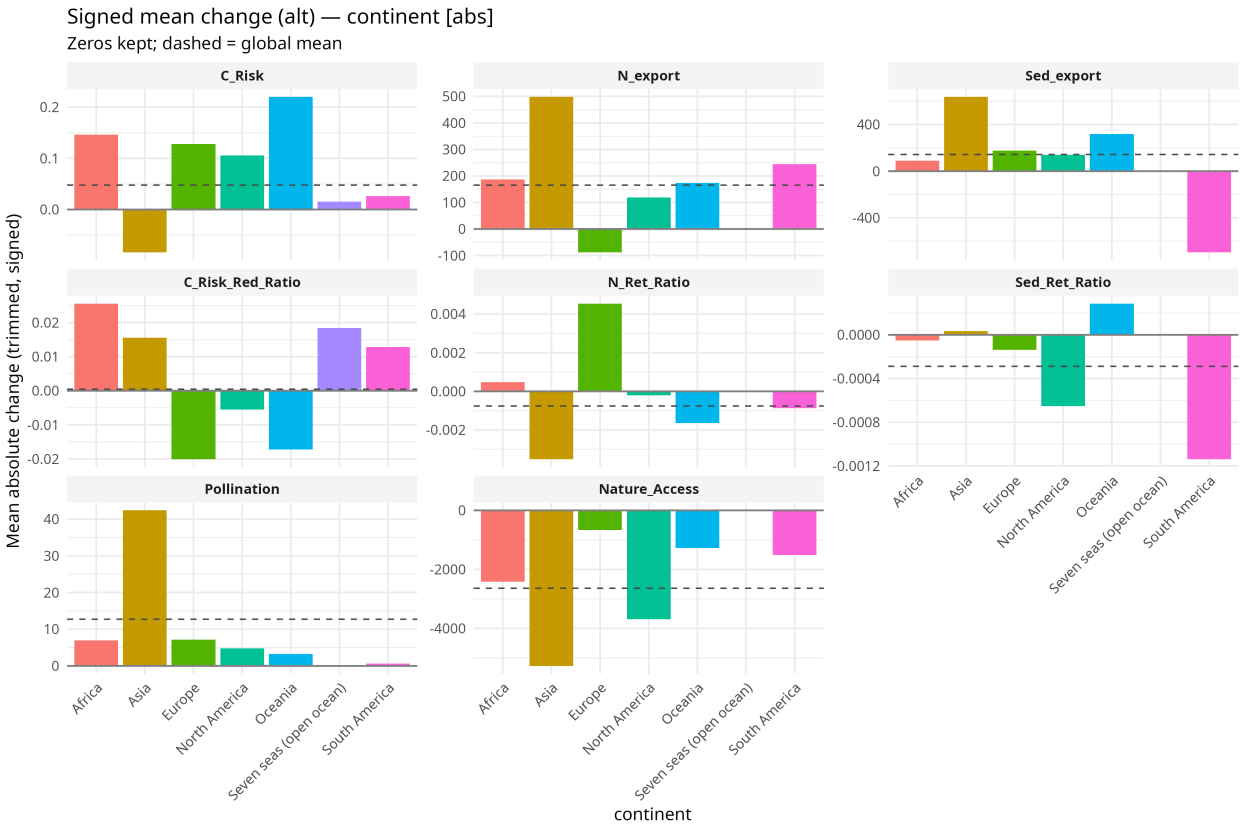
Outputs: PNGs land in `outputs/plots/{abs|pct}/<group_col>/bars_*.png` plus a flat copy in `outputs/plots/latest/bars/` for embedding here. The legacy global-only single-bar chart was removed to keep the gallery focused on grouped views.

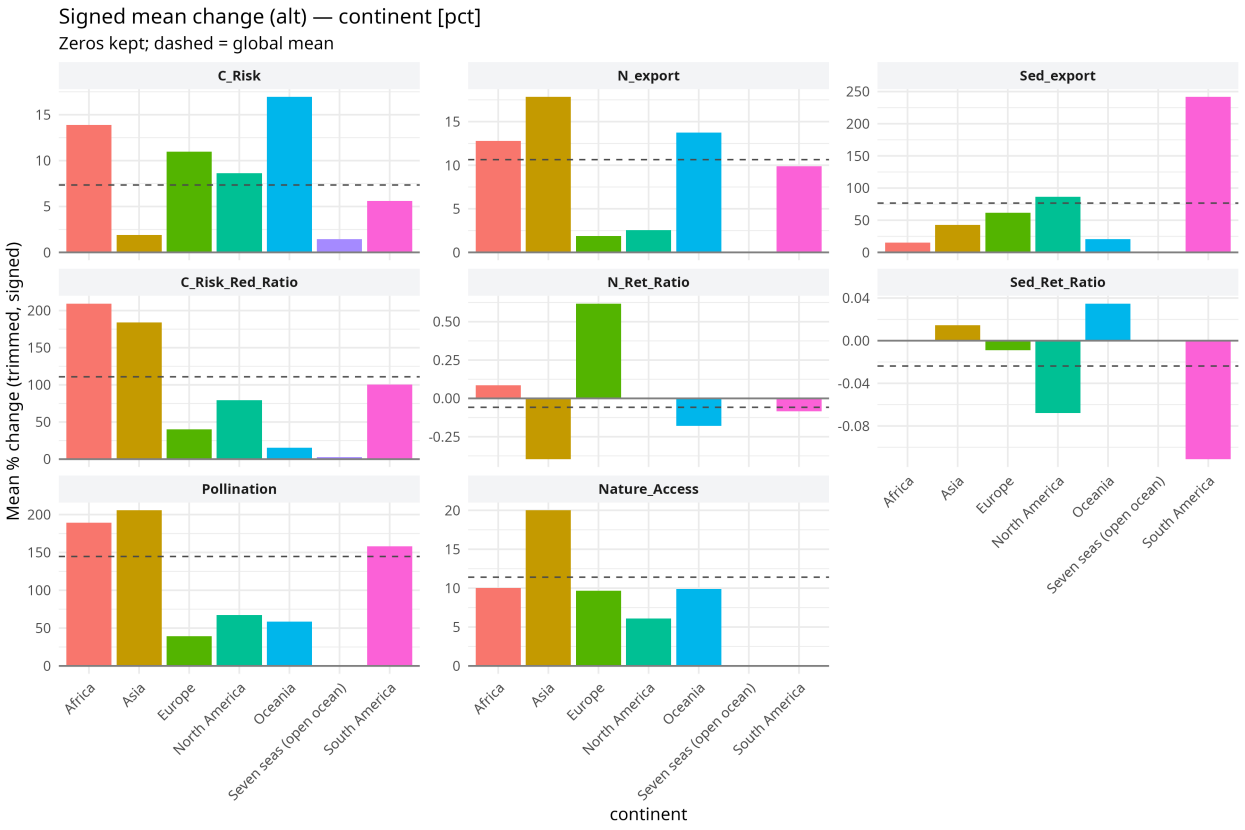
Generate trimmed-mean bar plots (abs & pct) for each grouping. Plots save to `outputs/plots/...` and are embedded below.

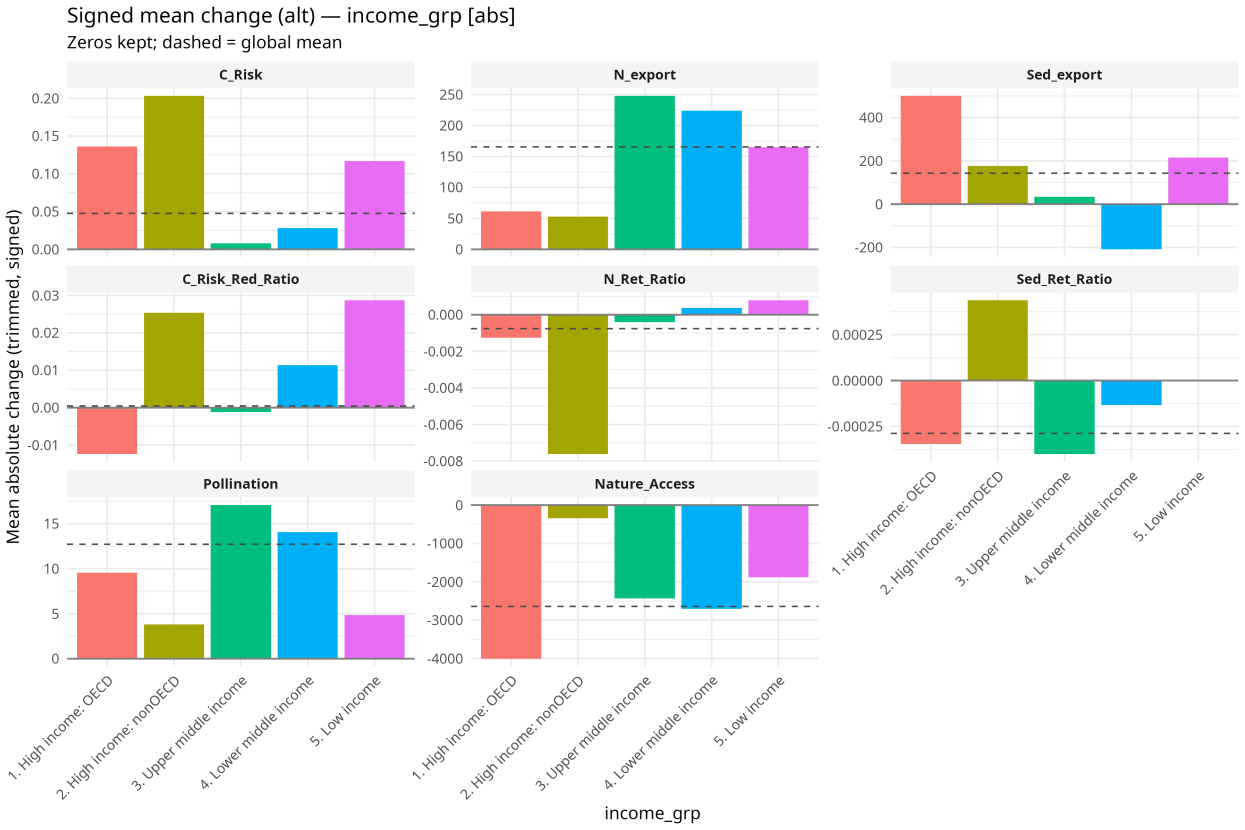
8.1 TODO: Hotspot vs non-hotspot contribution bars

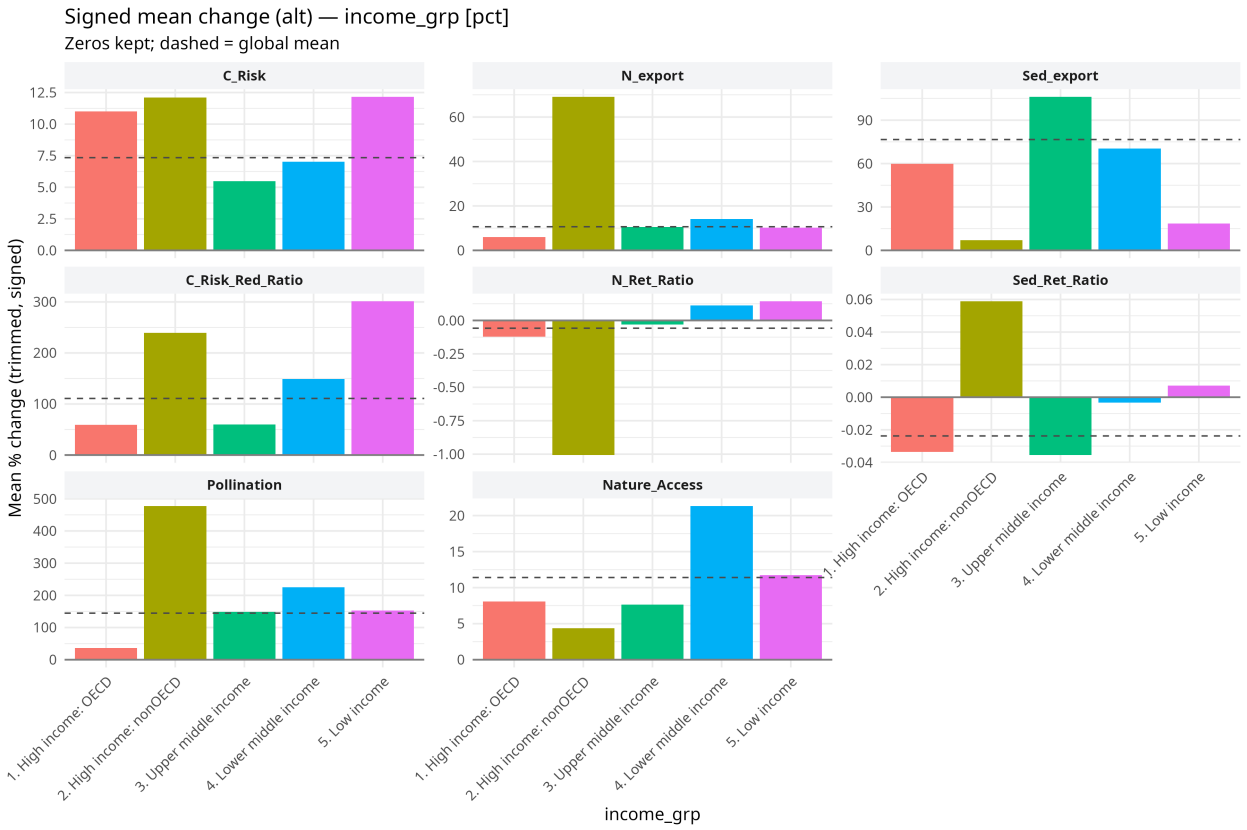
Future idea: stack bars to show how much of each group's total signed change comes from hotspot cells vs the complement. Steps: compute group means separately for hotspot and non-hotspot subsets (using the same 5% rules), then plot stacked bars (hotspot share + non-hotspot share) per service/group. Keep both absolute and percent-change variants; avoid overwriting existing plots (write to `outputs/plots/signed_hotshare/`).

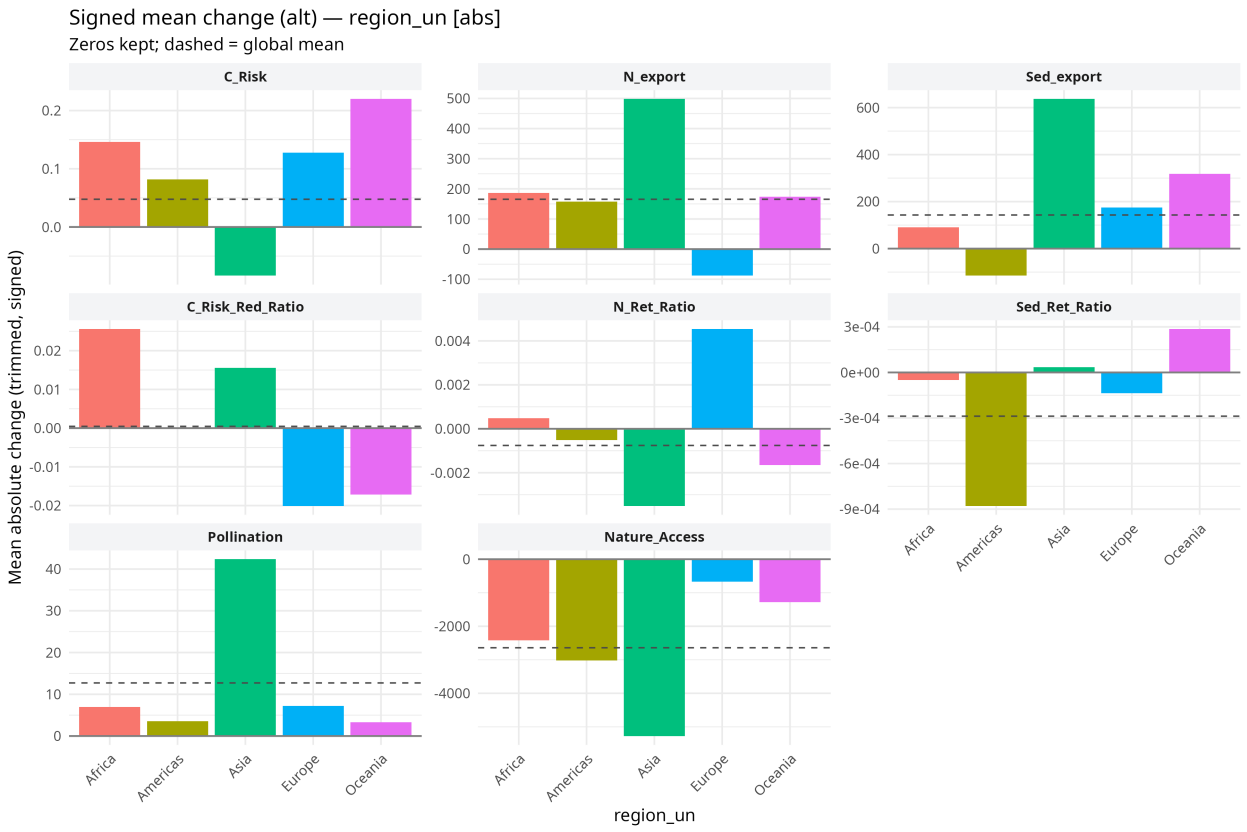
8.2 Signed means (alt variants: keep0 vs drop0; dashed = global mean)

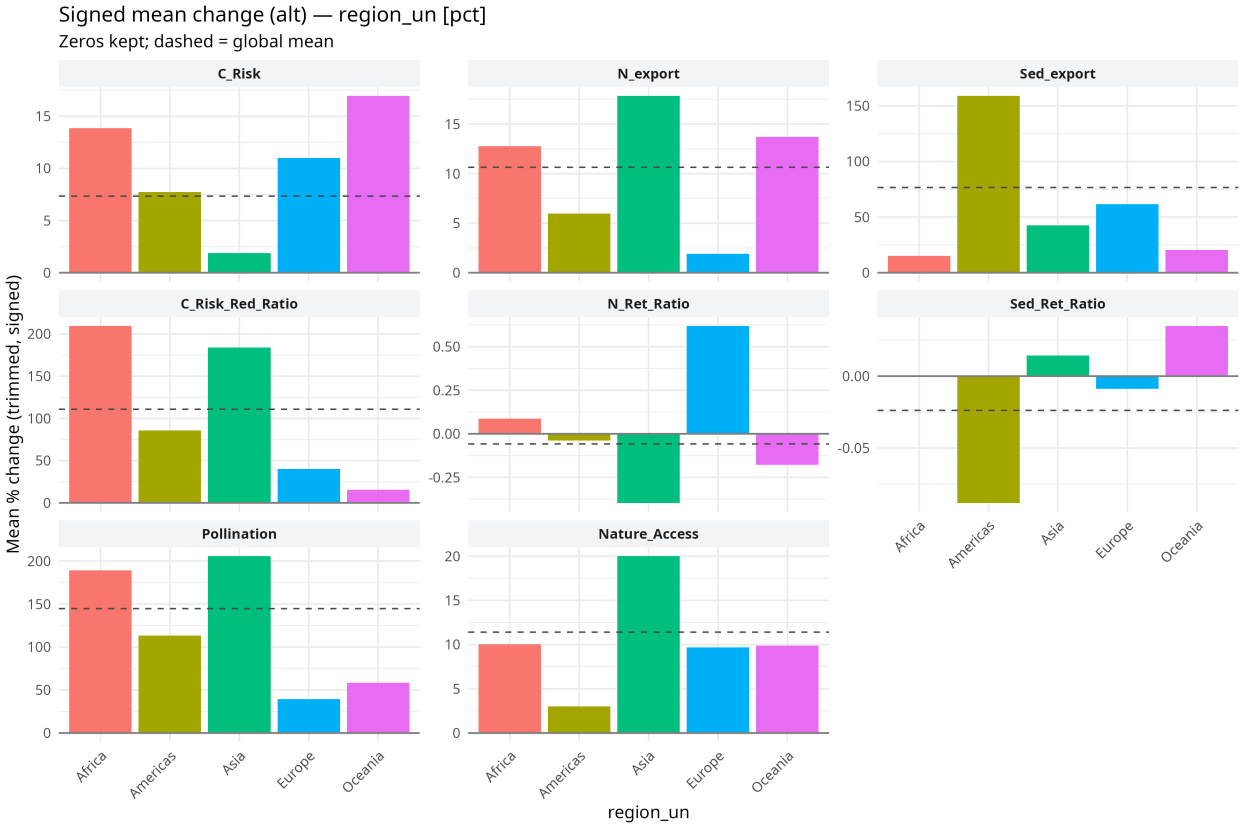



Signed mean change (alt) — continent [pct]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
Africa
Asia
Europe
North America
Oceania
Seven seas (open ocean)
South America
continent

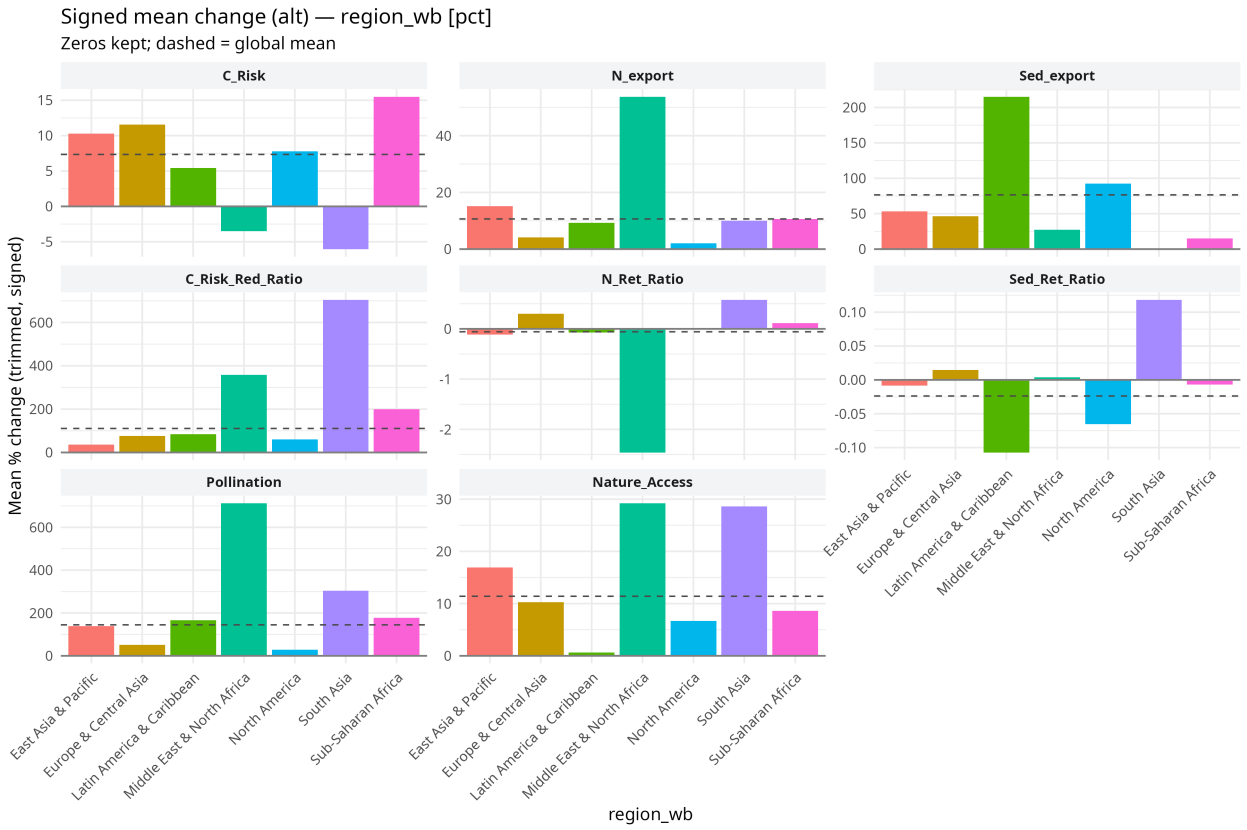

Signed mean change (alt) — income_grp [abs]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income
income_grp


Signed mean change (alt) — income_grp [pct]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income
income_grp

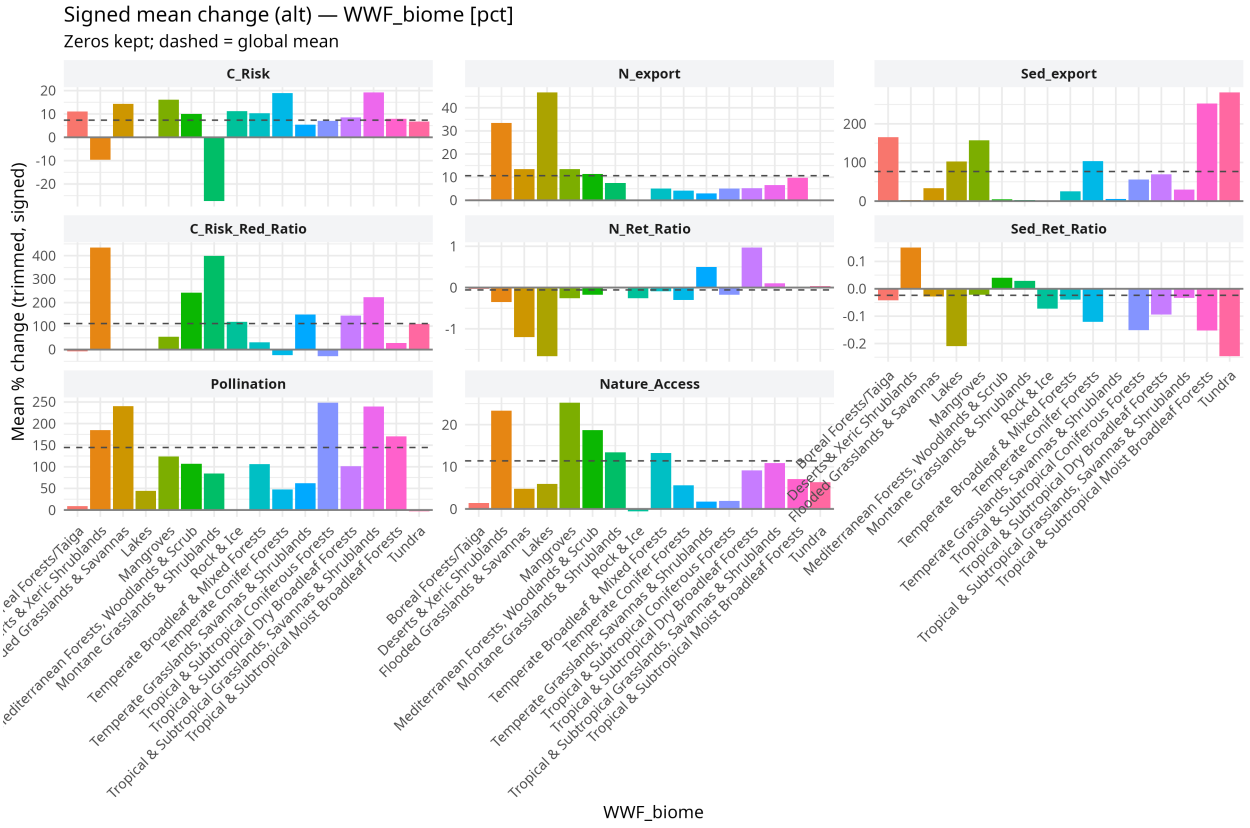

Signed mean change (alt) — region_un [abs]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
Africa
Americas
Asia
Europe
Oceania
region_un

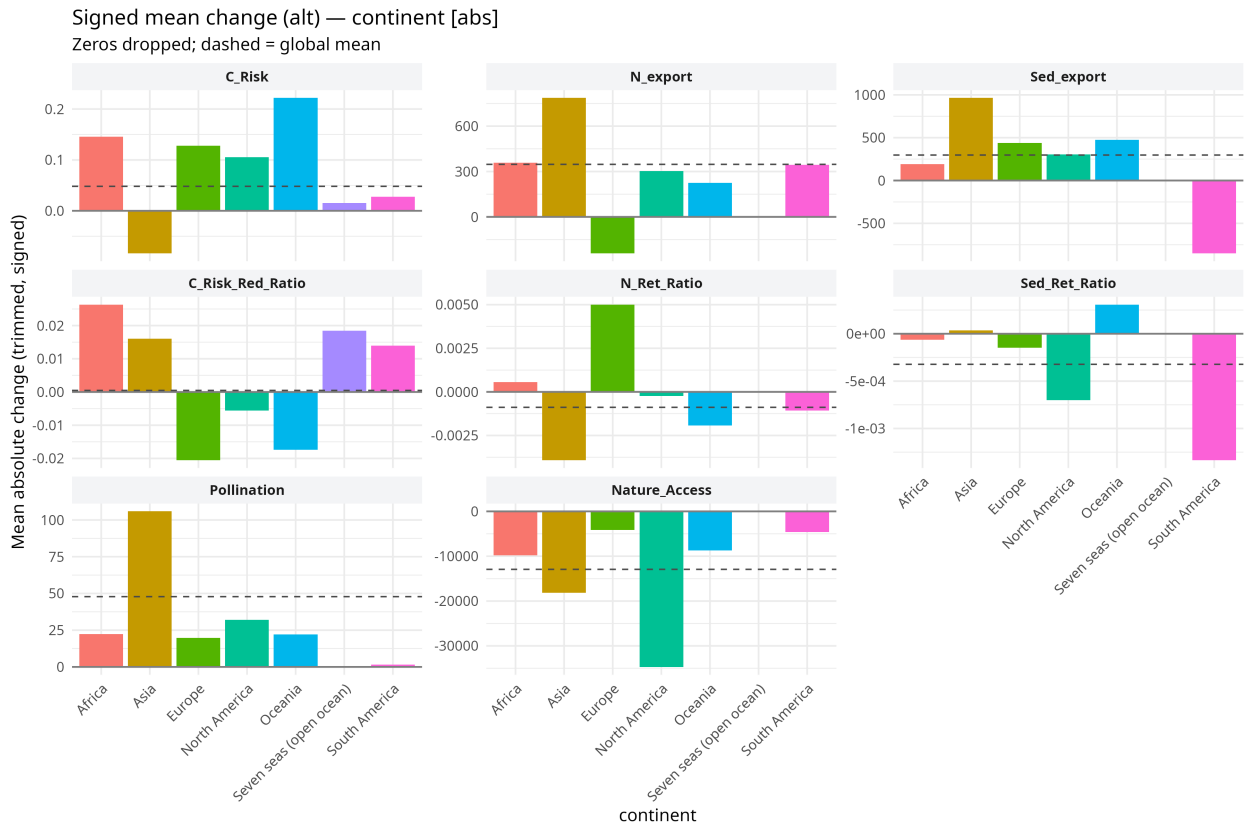

Signed mean change (alt) — region_un [pct]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
Africa
Americas
Asia
Europe
Oceania
region_un

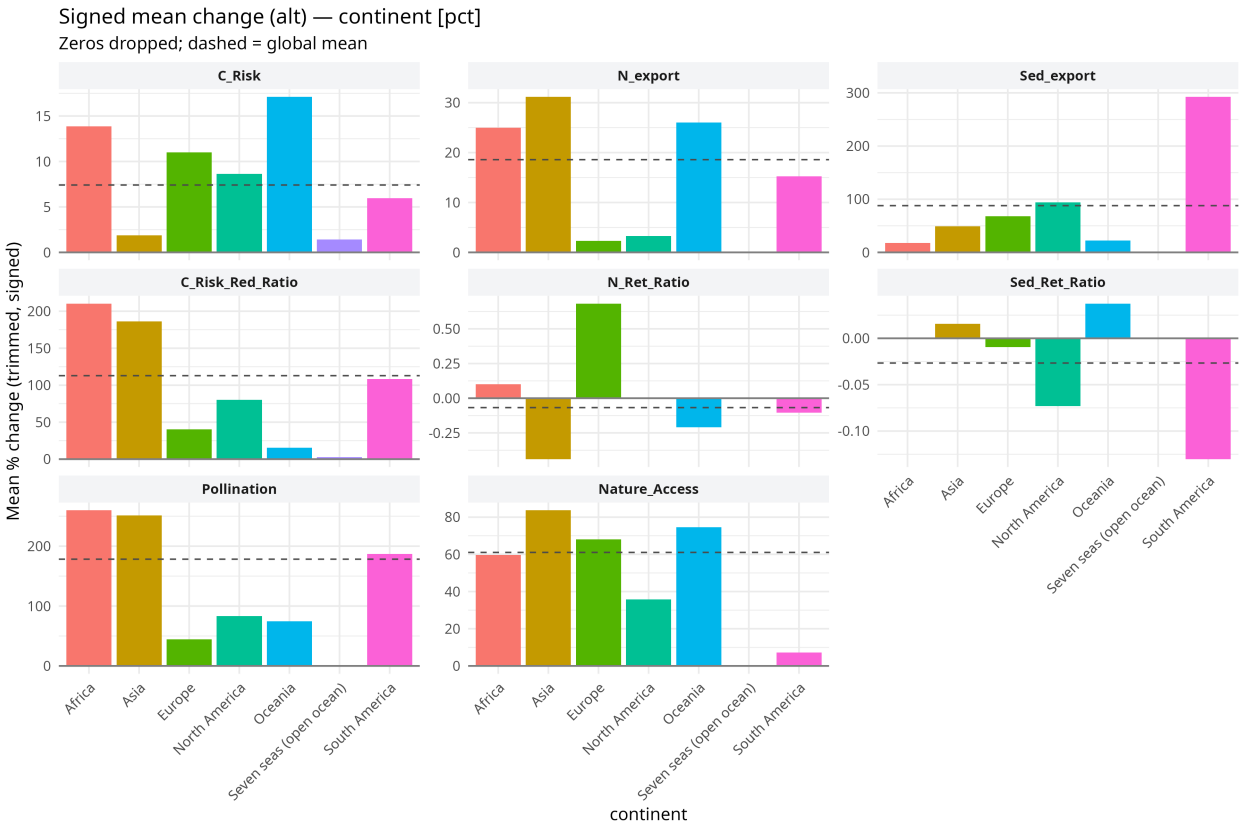

Signed mean change (alt) — region_wb [abs]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa
region_wb

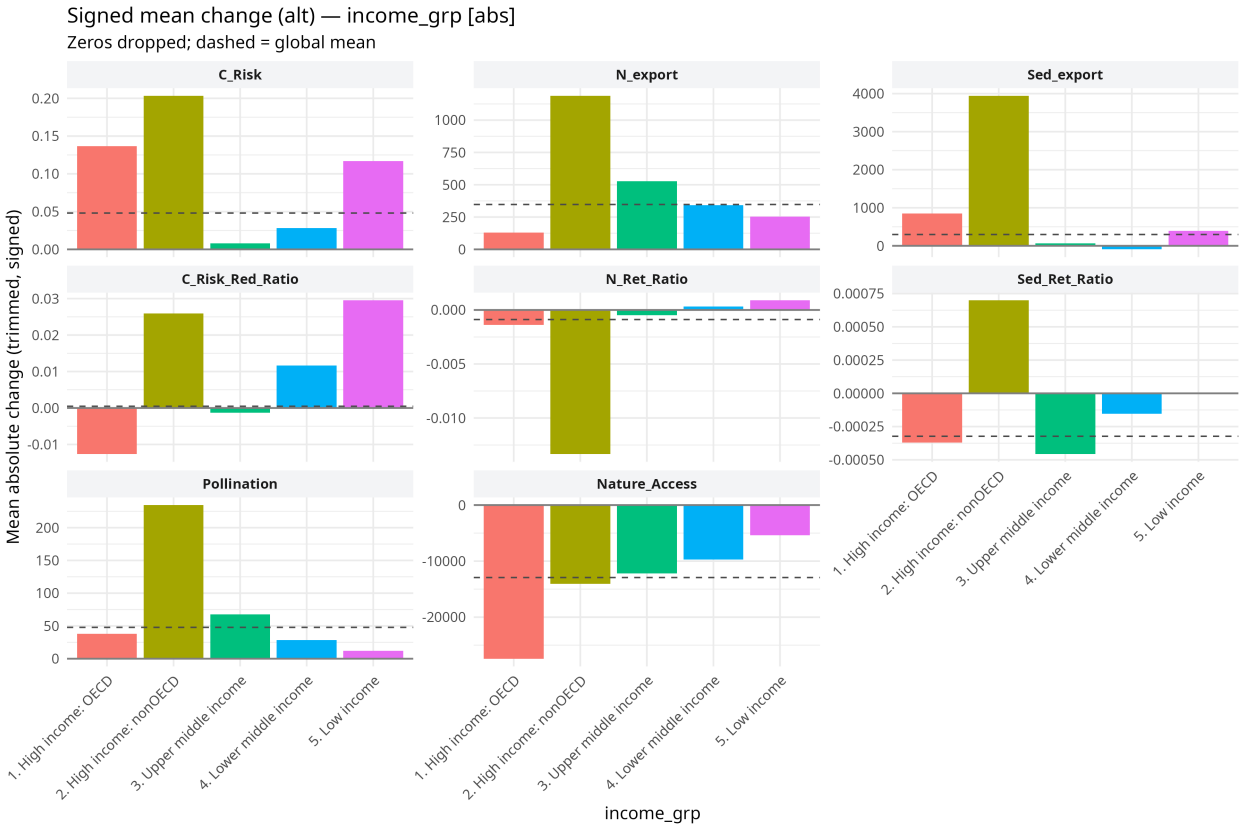

Signed mean change (alt) — region_wb [pct]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa
region_wb

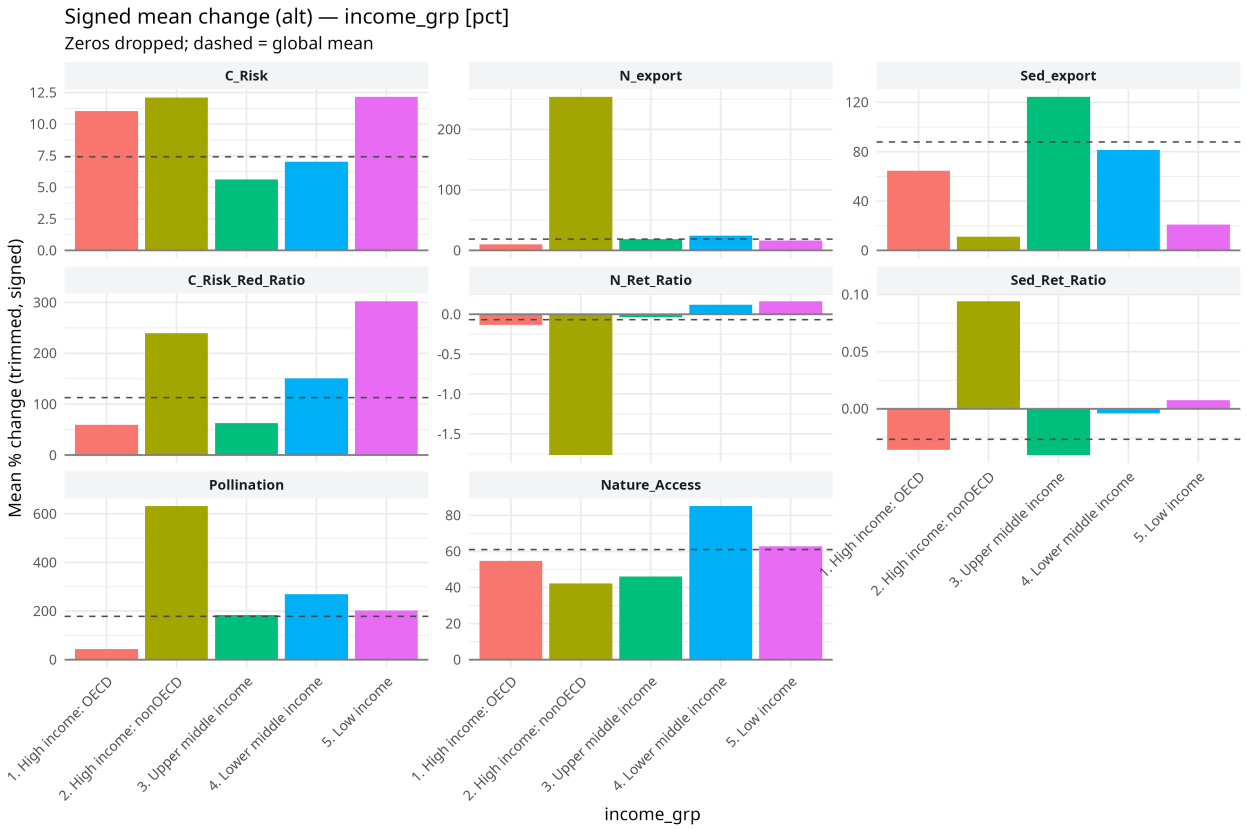

Signed mean change (alt) — WWF_biome [abs]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
Boreal Forests/Taiga
Deserts & Xeric Shrublands
Flooded Grasslands & Savannas
Lakes
Mangroves
Mediterranean Forests, Woodlands & Scrub
Montane Grasslands & Shrublands
Rock & Ice
Temperate Broadleaf & Mixed Forests
Temperate Conifer Forests
Temperate Grasslands, Savannas & Shrublands
Tropical & Subtropical Coniferous Forests
Tropical & Subtropical Dry Broadleaf Forests
Tropical & Subtropical Grasslands, Savannas & Shrublands
Tropical & Subtropical Moist Broadleaf Forests
Tundra
WWF_biome

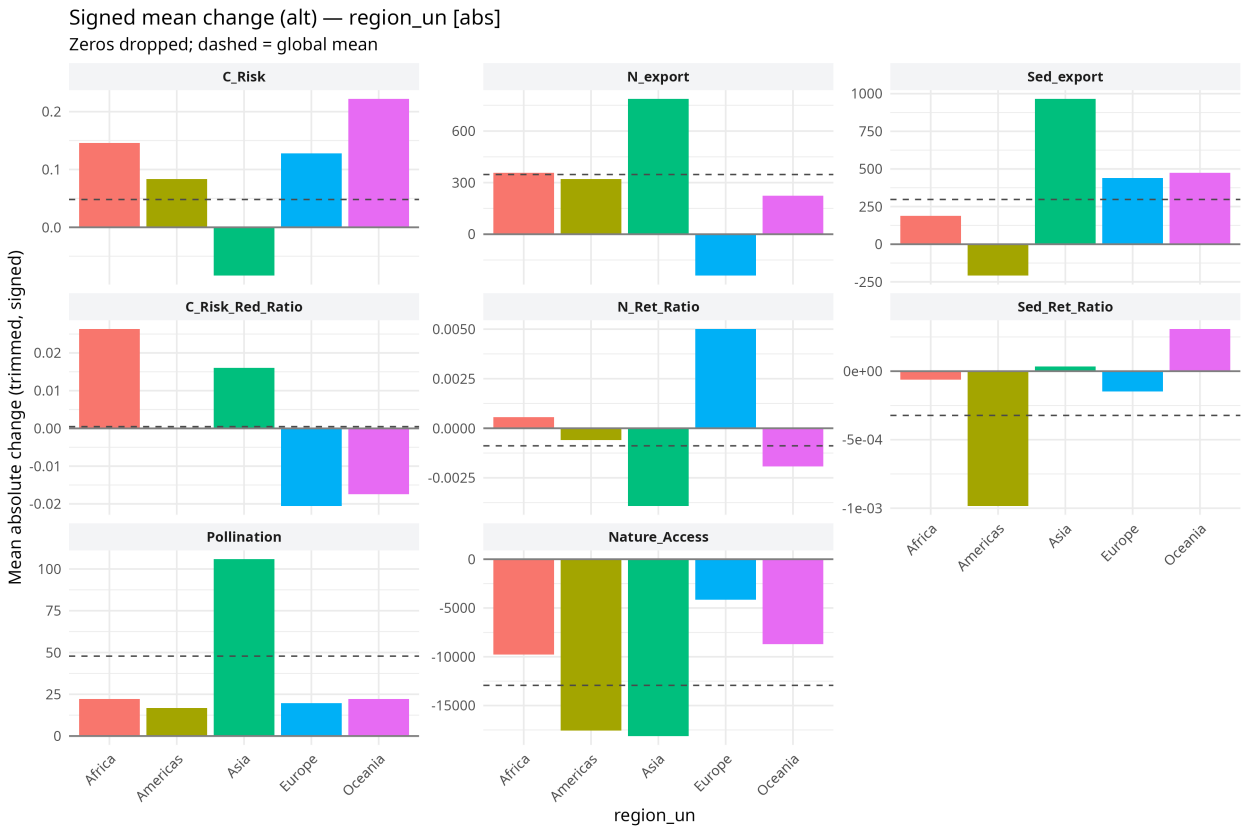

Signed mean change (alt) — WWF_biome [pct]
Zeros kept; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
Boreal Forests/Taiga
Deserts & Xeric Shrublands
Flooded Grasslands & Savannas
Lakes
Mangroves
Mediterranean Forests, Woodlands & Scrub
Montane Grasslands & Shrublands
Rock & Ice
Temperate Broadleaf & Mixed Forests
Temperate Conifer Forests
Temperate Grasslands, Savannas & Shrublands
Tropical & Subtropical Coniferous Forests
Tropical & Subtropical Dry Broadleaf Forests
Tropical & Subtropical Grasslands, Savannas & Shrublands
Tropical & Subtropical Moist Broadleaf Forests
Tundra
WWF_biome

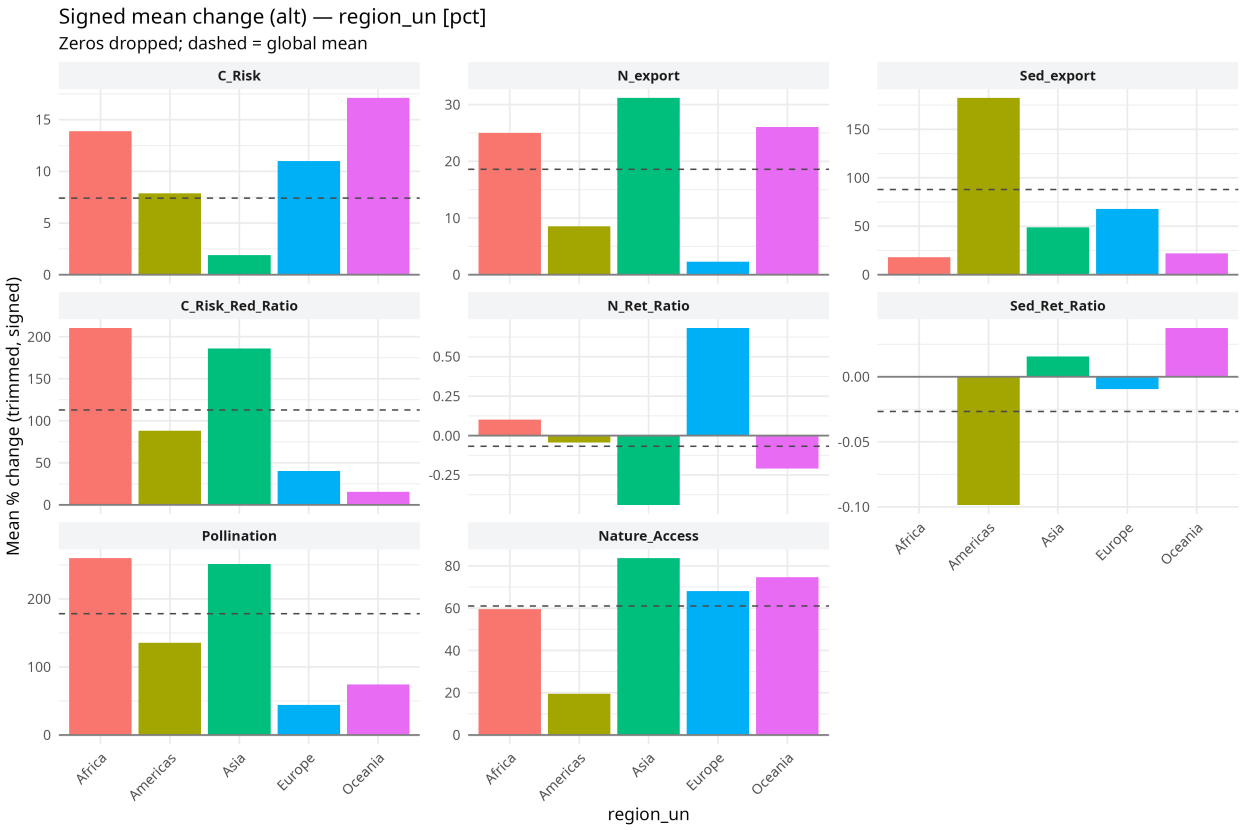

Signed mean change (alt) — continent [abs]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
Africa
Asia
Europe
North America
Oceania
Seven seas (open ocean)
South America
continent

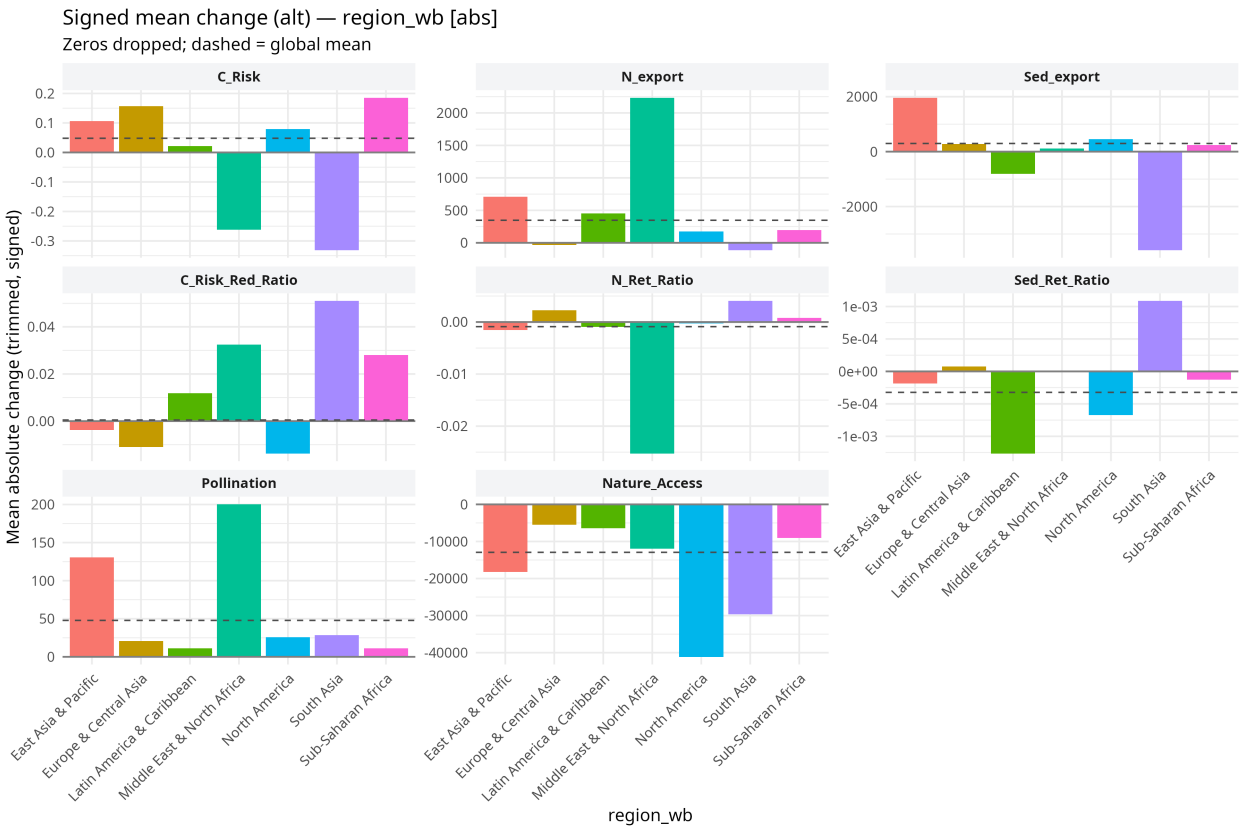

Signed mean change (alt) — continent [pct]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
Africa
Asia
Europe
North America
Oceania
Seven seas (open ocean)
South America
continent

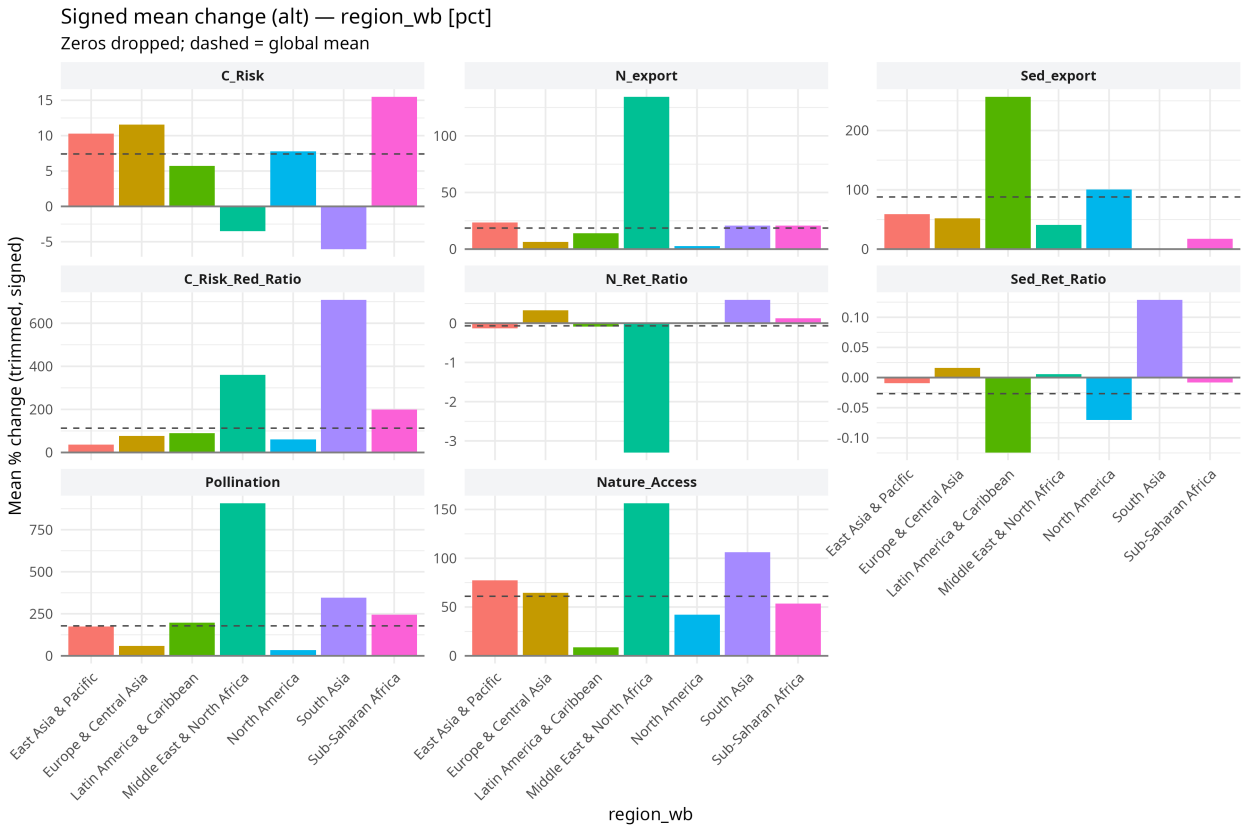

Signed mean change (alt) — income_grp [abs]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income
income_grp

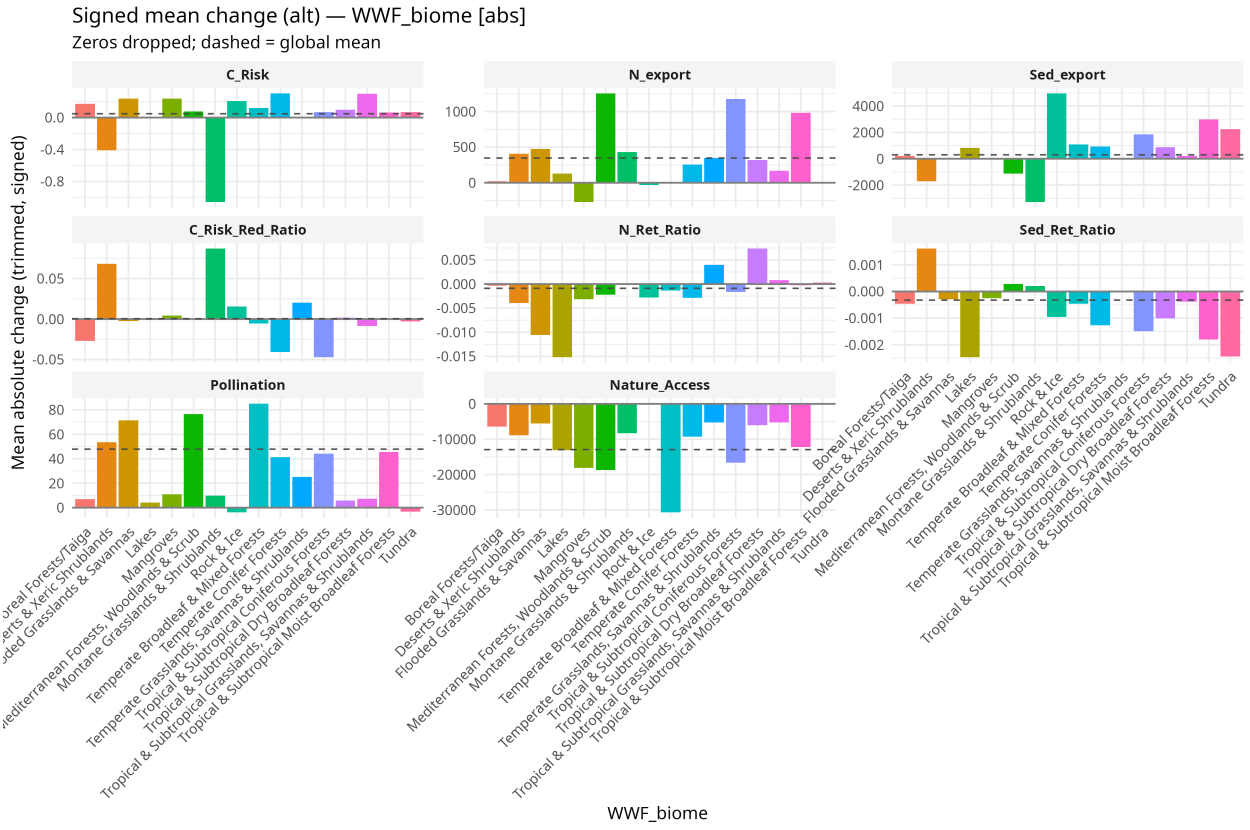

Signed mean change (alt) — income_grp [pct]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income
income_grp

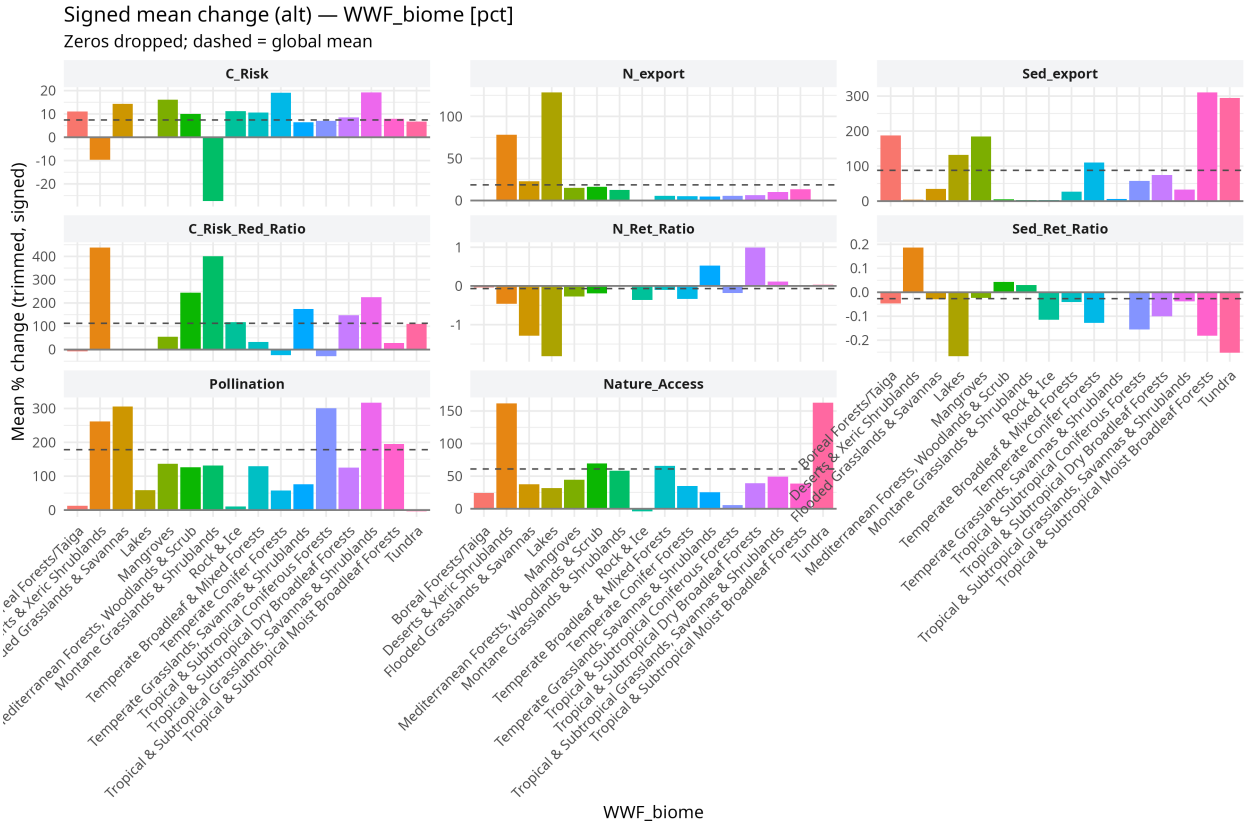

Signed mean change (alt) — region_un [abs]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
Africa
Americas
Asia
Europe
Oceania
region_un


Signed mean change (alt) — region_un [pct]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
Africa
Americas
Asia
Europe
Oceania
region_un


Signed mean change (alt) — region_wb [abs]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa
region_wb


Signed mean change (alt) — region_wb [pct]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean % change (trimmed, signed)
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa
region_wb

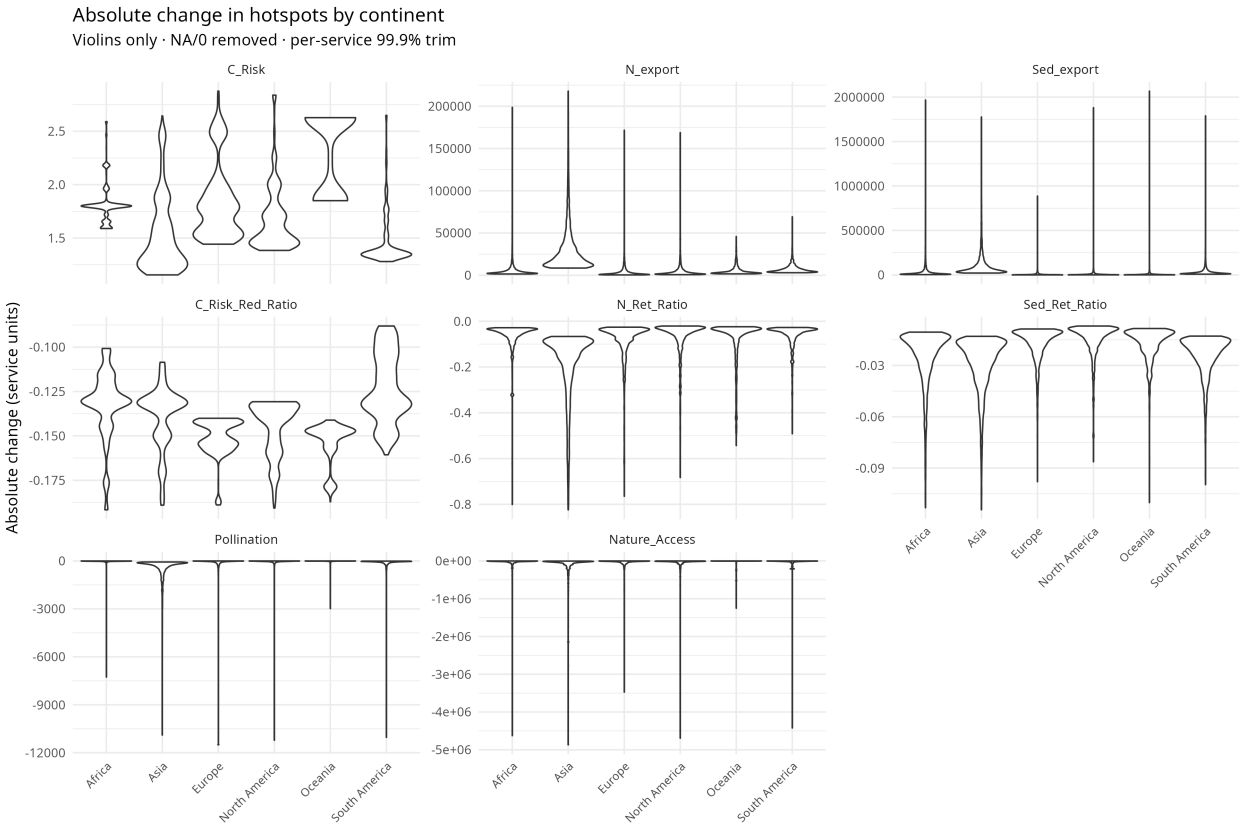

Signed mean change (alt) — WWF_biome [abs]
Zeros dropped; dashed = global mean
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Mean absolute change (trimmed, signed)
Boreal Forests/Taiga
Deserts & Xeric Shrublands
Flooded Grasslands & Savannas
Lakes
Mangroves
Mediterranean Forests, Woodlands & Scrub
Montane Grasslands & Shrublands
Rock & Ice
Temperate Broadleaf & Mixed Forests
Temperate Conifer Forests
Temperate Grasslands, Savannas & Shrublands
Tropical & Subtropical Coniferous Forests
Tropical & Subtropical Dry Broadleaf Forests
Tropical & Subtropical Grasslands, Savannas & Shrublands
Tropical & Subtropical Moist Broadleaf Forests
Tundra
WWF_biome

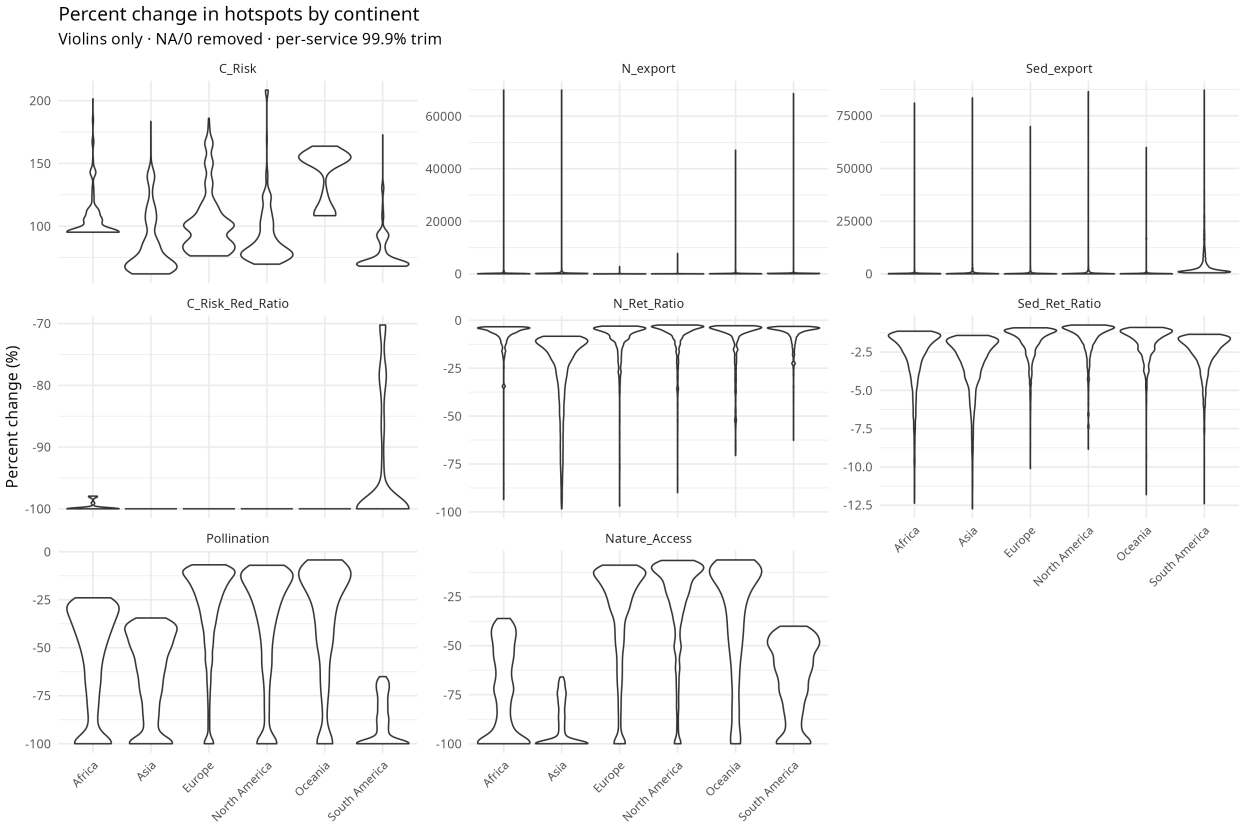


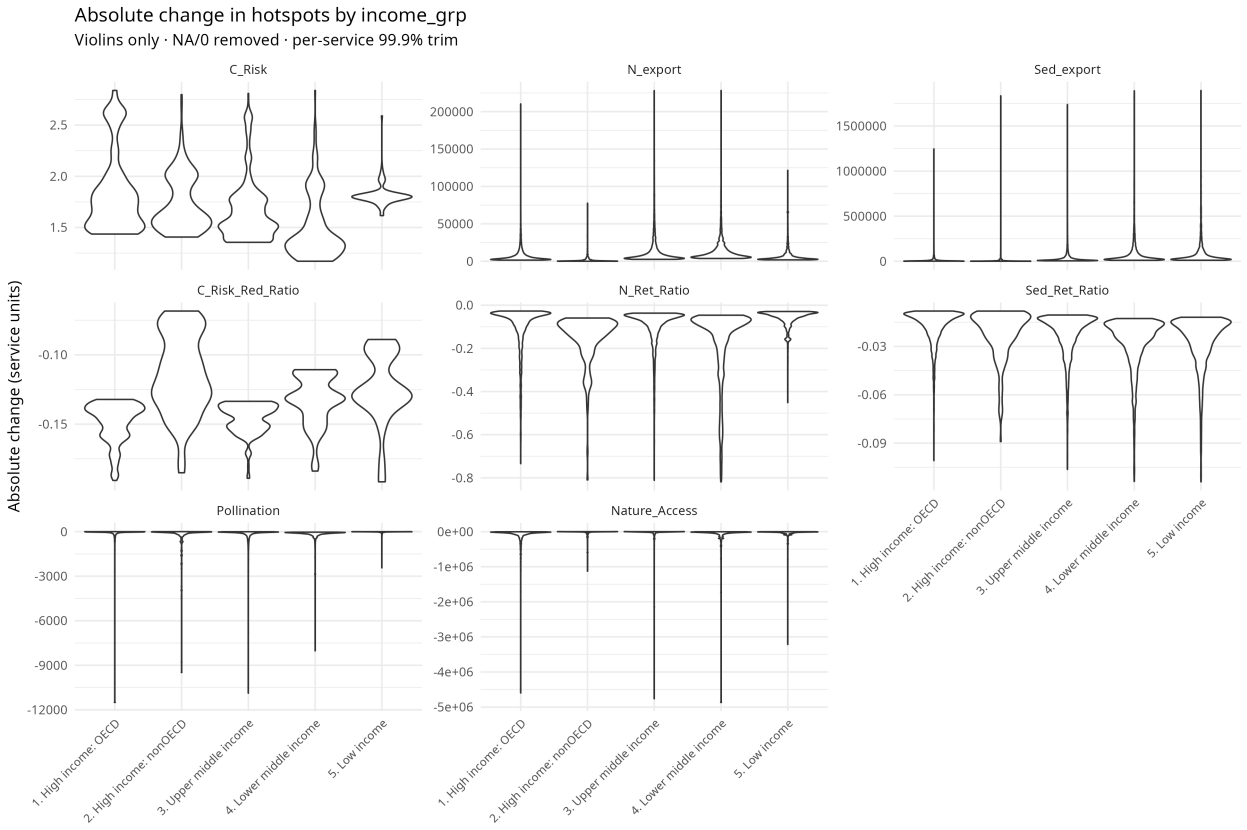
9 Hotspot violin plots

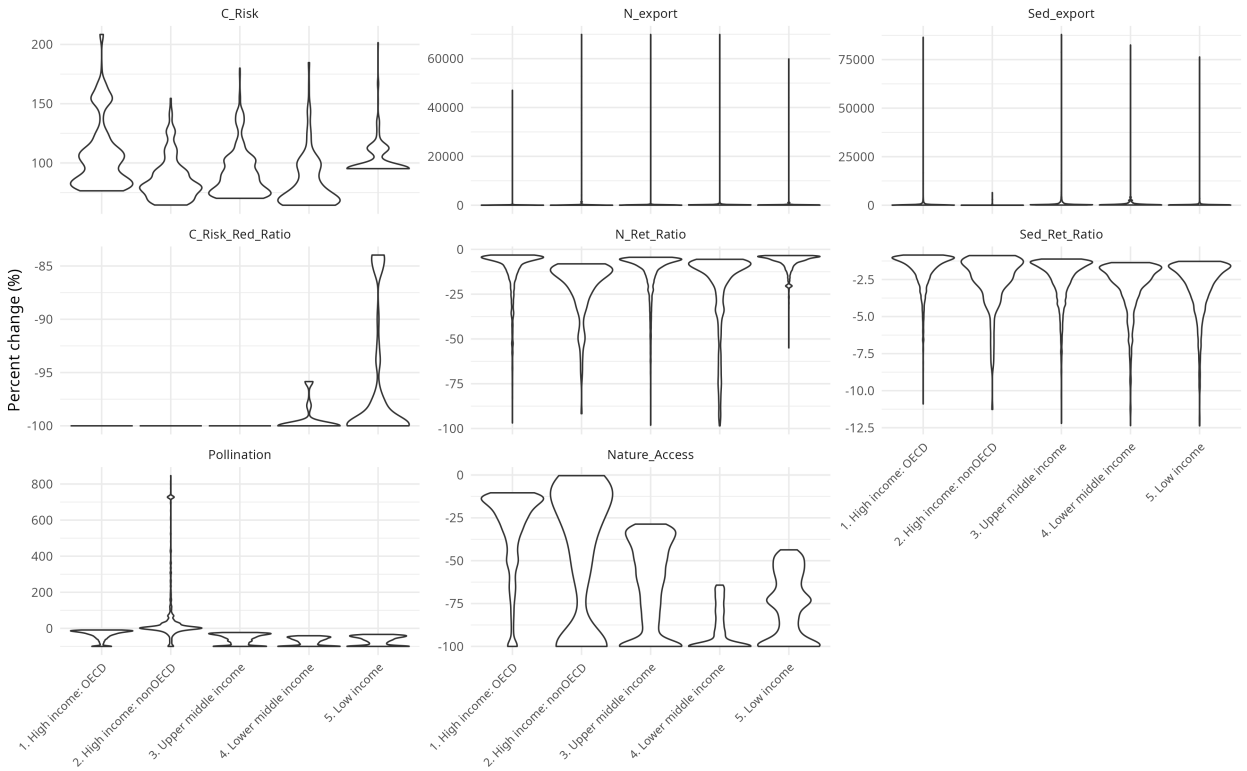
Summarize hotspot distributions by group using saved PNGs; skip computation if group columns are absent. Helper `run_hotspot_violins_by()` now lives in `R/hotspot_violins.R`, so we just call it from this report.

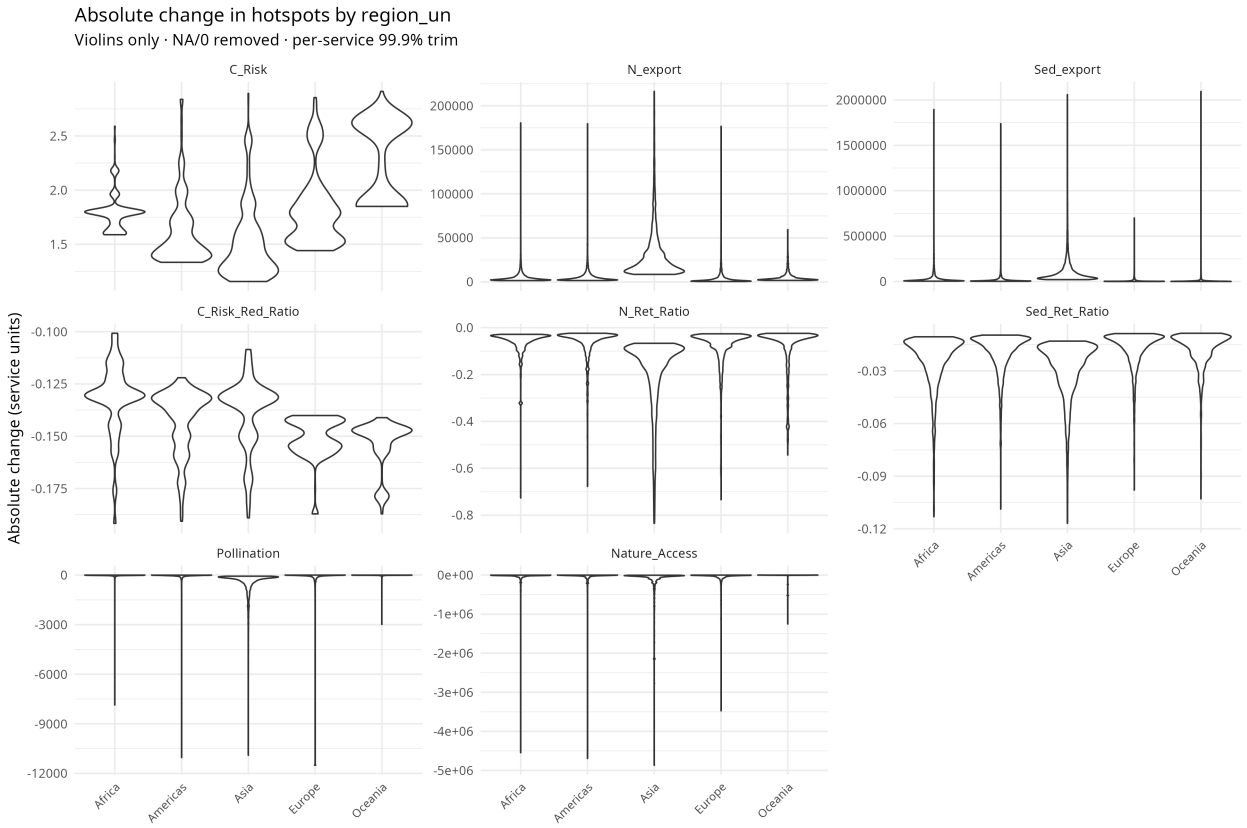
Outputs: PNGs are written to `outputs/plots/{abs|pct}/<group_col>/violins_*.png` and mirrored into `outputs/plots/latest/violins/` for embedding.

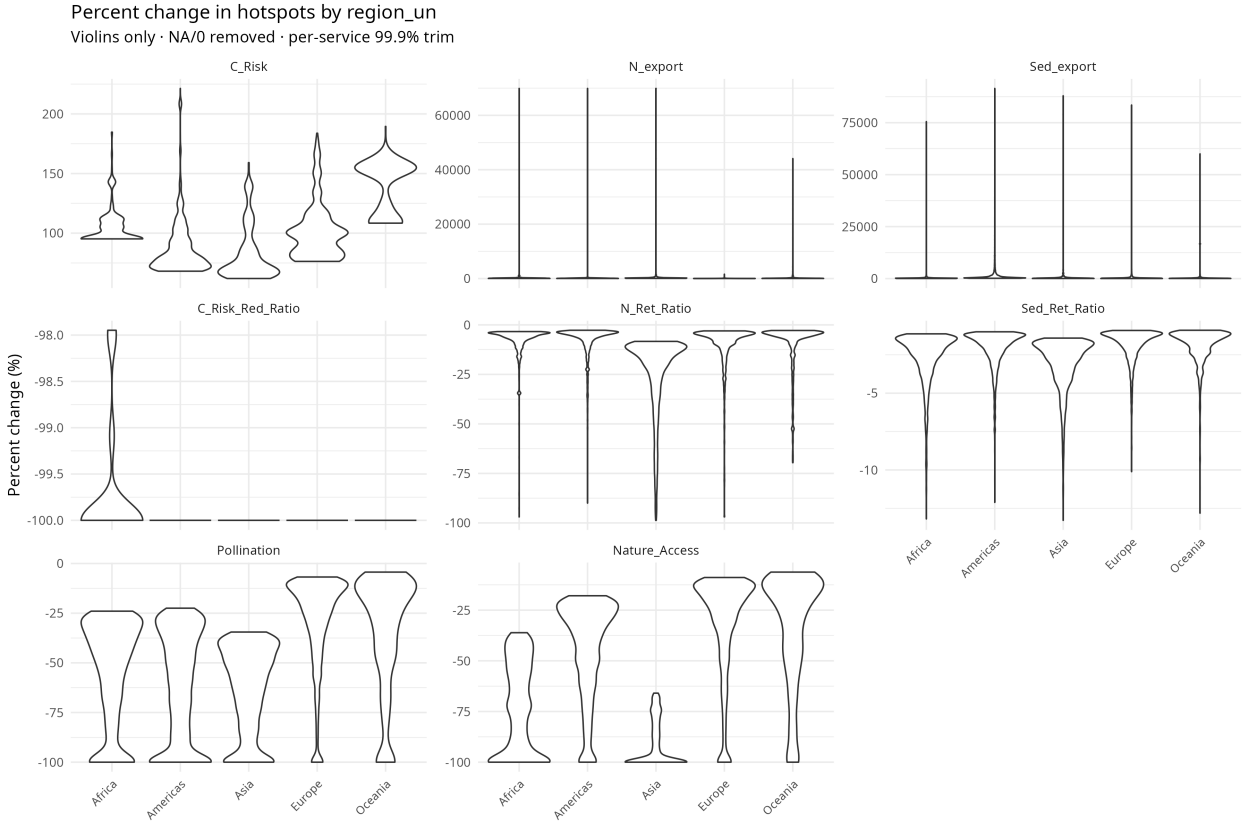

Absolute change in hotspots by continent
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Absolute change (service units)
Africa
Asia
Europe
North America
Oceania
South America

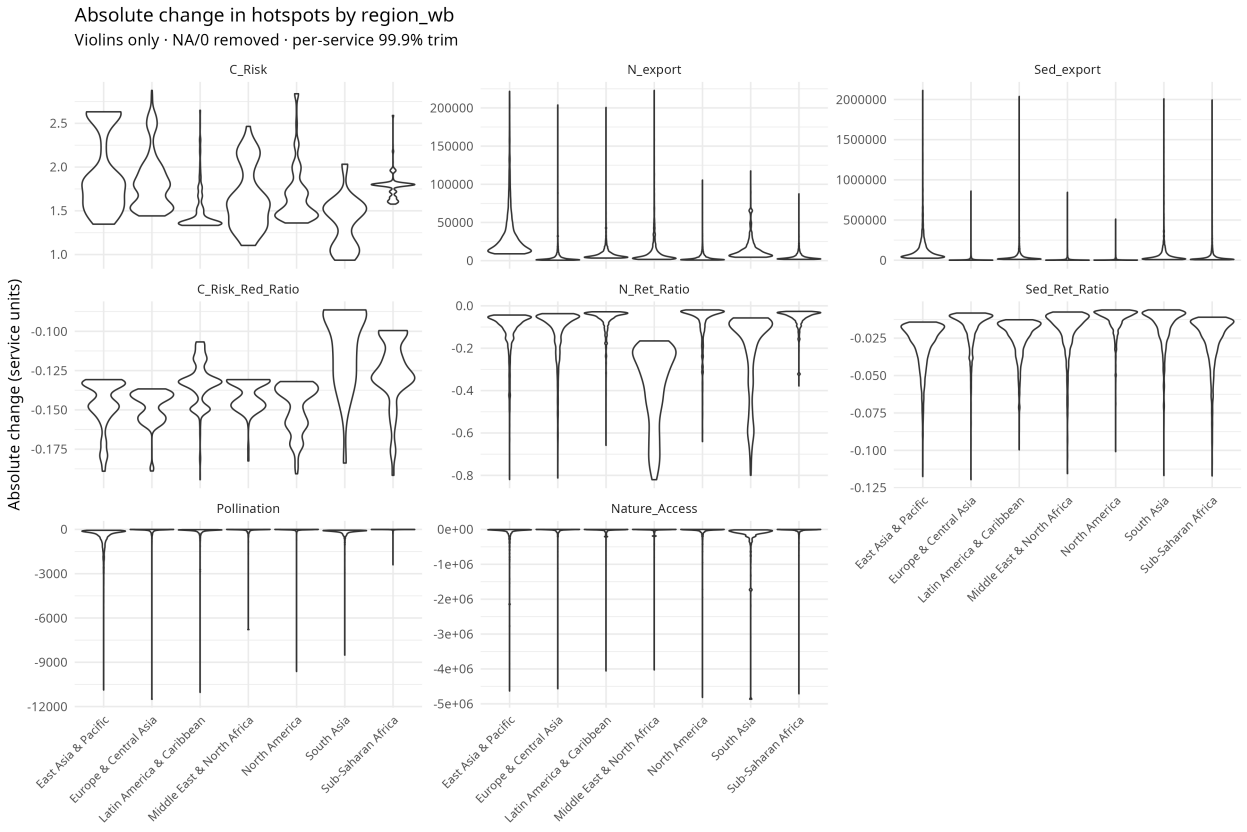

Percent change in hotspots by continent
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Percent change (%)
Africa
Asia
Europe
North America
Oceania
South America

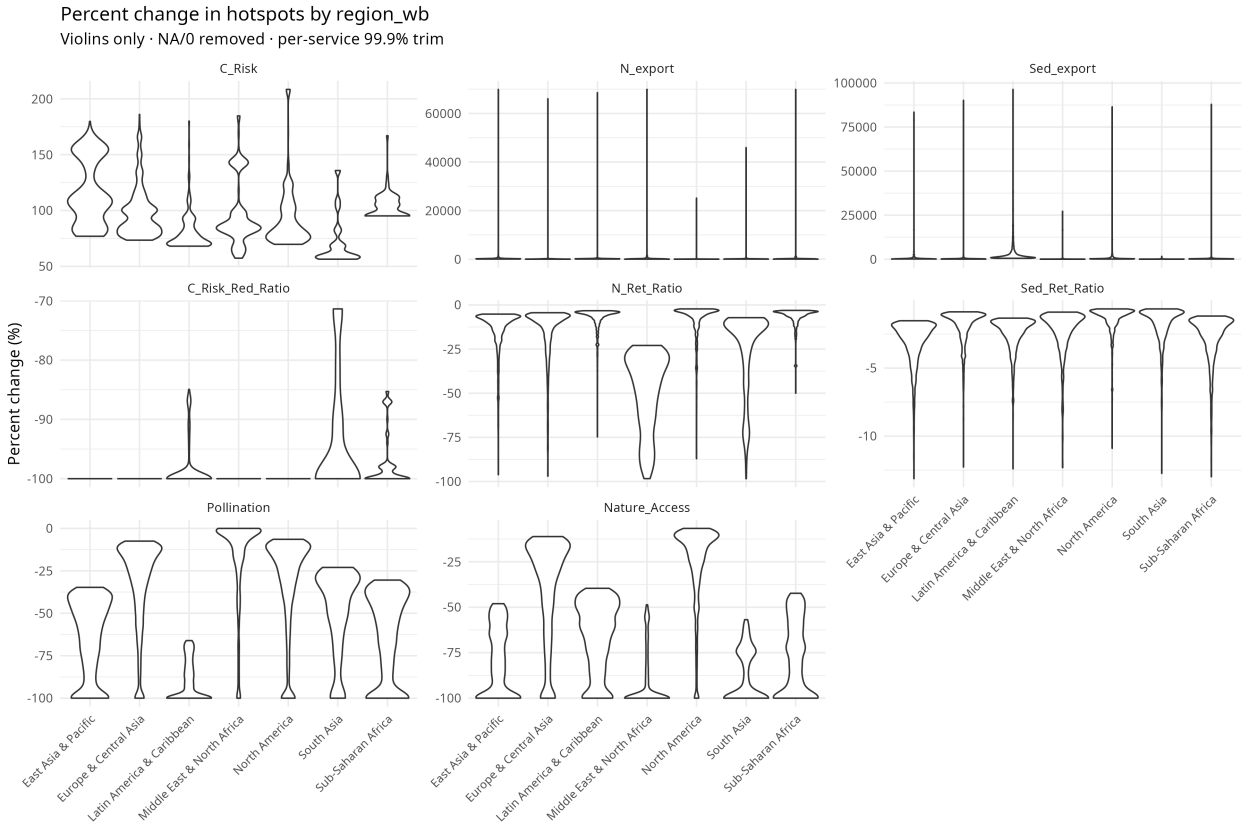

Absolute change in hotspots by income_grp
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Absolute change (service units)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income

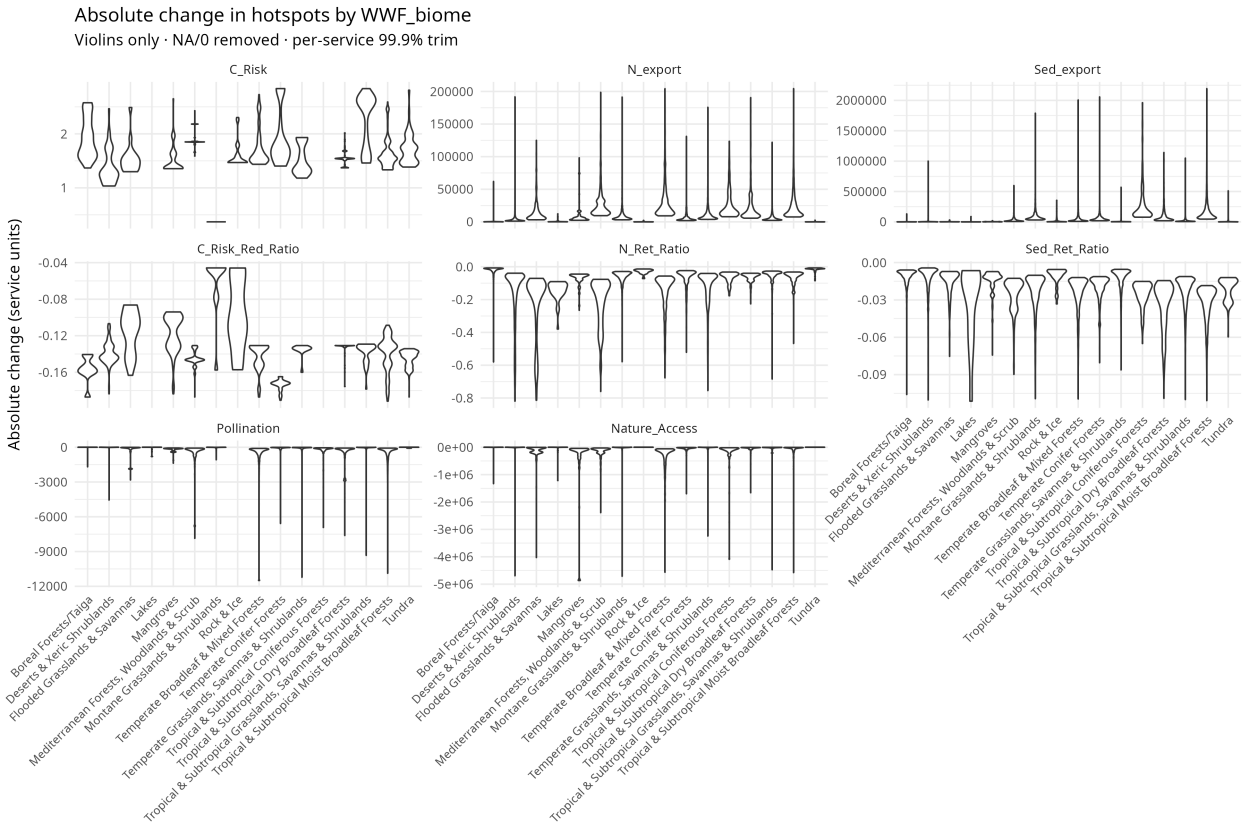

Percent change in hotspots by income_grp
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Percent change (%)
1. High income: OECD
2. High income: nonOECD
3. Upper middle income
4. Lower middle income
5. Low income

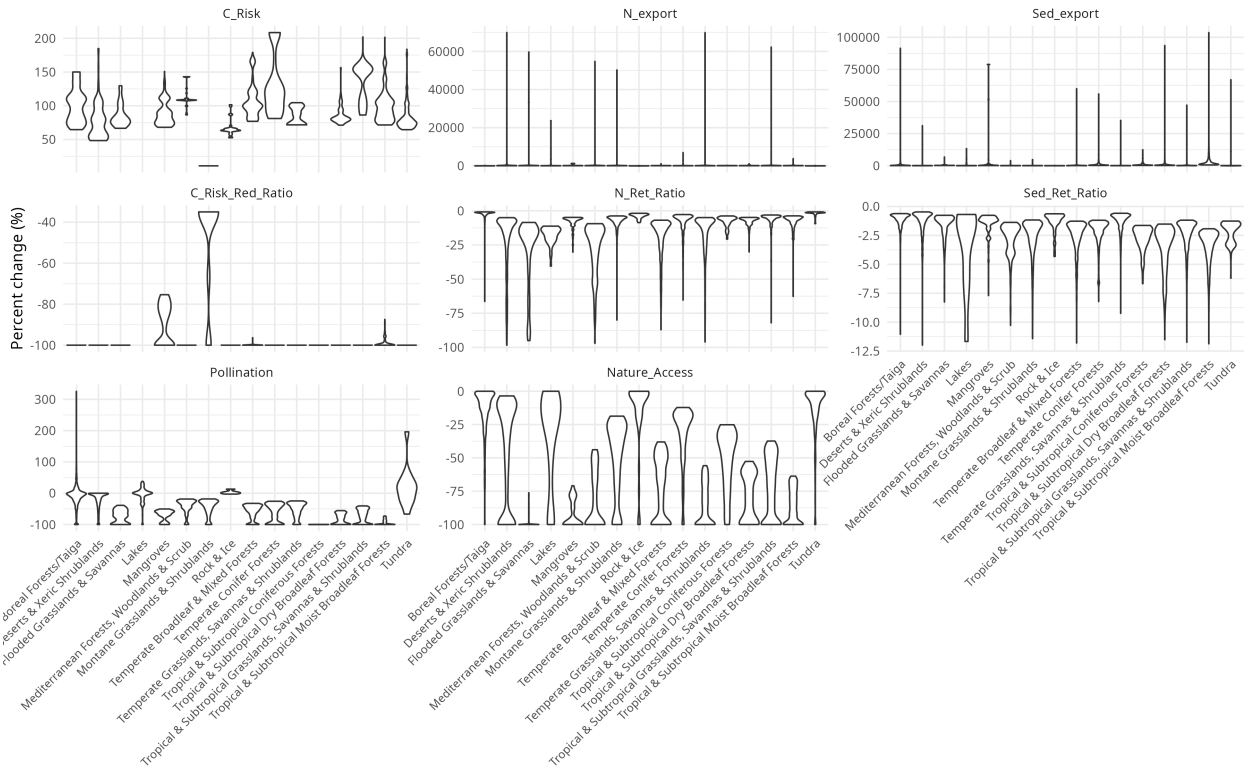

Absolute change in hotspots by region_un
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Absolute change (service units)
Africa
Americas
Asia
Europe
Oceania


Percent change in hotspots by region_un
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Percent change (%)
Africa
Americas
Asia
Europe
Oceania


Absolute change in hotspots by region_wb
Violins only · NA/0 removed · per-service 99.9% trim
Absolute change (service units)
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa


Percent change in hotspots by region_wb
Violins only · NA/0 removed · per-service 99.9% trim
Percent change (%)
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
East Asia & Pacific
Europe & Central Asia
Latin America & Caribbean
Middle East & North Africa
North America
South Asia
Sub-Saharan Africa


Absolute change in hotspots by WWF_biome
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Absolute change (service units)
Boreal Forests/Taiga
Deserts & Xeric Shrublands
Flooded Grasslands & Savannas
Lakes
Mangroves
Mediterranean Forests, Woodlands & Scrub
Montane Grasslands & Shrublands
Rock & Ice
Temperate Broadleaf & Mixed Forests
Temperate Conifer Forests
Temperate Grasslands, Savannas & Shrublands
Tropical & Subtropical Coniferous Forests
Tropical & Subtropical Dry Broadleaf Forests
Tropical & Subtropical Grasslands, Savannas & Shrublands
Tropical & Subtropical Moist Broadleaf Forests
Tundra


Percent change in hotspots by WWF_biome
Violins only · NA/0 removed · per-service 99.9% trim
C_Risk
N_export
Sed_export
C_Risk_Red_Ratio
N_Ret_Ratio
Sed_Ret_Ratio
Pollination
Nature_Access
Percent change (%)
Boreal Forests/Taiga
Deserts & Xeric Shrublands
Flooded Grasslands & Savannas
Lakes
Mangroves
Mediterranean Forests, Woodlands & Scrub
Montane Grasslands & Shrublands
Rock & Ice
Temperate Broadleaf & Mixed Forests
Temperate Conifer Forests
Temperate Grasslands, Savannas & Shrublands
Tropical & Subtropical Coniferous Forests
Tropical & Subtropical Dry Broadleaf Forests
Tropical & Subtropical Grasslands, Savannas & Shrublands
Tropical & Subtropical Moist Broadleaf Forests
Tundra