

Sa2RAGE B1 correct

Sriranga Kashyap

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Set working directory

```
working_dir <- "~/mp2rage_data"
```

Provide input NIfTI filenames

```
# MP2RAGE UNI
in_uni <- paste0(working_dir, "/MP2RAGE_UNI.nii.gz")

# Sa2RAGE B1 map
in_b1_map <- paste0(working_dir, "/sub01_sa2rage_2p0mm_iso_B1map_reg-to-mp2rage.nii")
```

Provide output NIfTI filenames

```
# MP2RAGE B1 Corrected UNI
out_uni <- paste0(working_dir, "/MP2RAGE_UNI_B1_corrected.nii.gz")

# MP2RAGE B1 Corrected T1
out_t1 <- paste0(working_dir, "/MP2RAGE_T1map_B1_corrected.nii.gz")
```

Provide MP2RAGE sequence parameters from protocol

```
# MP2RAGE parameters
slices_per_slab <- 240
slice_partial_fourier <- 8 / 8

mp2rage_params <-
  list(
    mprage_tr = 5.0,
    flash_tr = 6.9e-3,
    inv_times_a_b = c(900e-3, 2750e-3),
    flip_angle_a_b_deg = c(5, 3),
    num_z_slices = NULL
  )

mp2rage_params$num_z_slices <-
  slices_per_slab * c(slice_partial_fourier - 0.5, 0.5)
```

Provide Sa2RAGE sequence parameters from protocol

```
# Sa2RAGE parameters
base_resolution <- 128
phase_partial_fourier <- 6 / 8
phase_ipat <- 2
ref_lines <- 24

sa2rage_params <- list(
  mprage_tr = 2.4,
  flash_tr = 2.2e-3,
  inv_times_a_b = c(58e-3, 1800e-3),
  flip_angle_a_b_deg = c(4, 10),
  num_z_slices = NULL
)

sa2rage_params$num_z_slices <-
  base_resolution * c(phase_partial_fourier - 0.5, 0.5) /
  phase_ipat + c(ref_lines / 2, ref_lines / 2) * (1 - 1 / phase_ipat)
```

Register B1 map to MP2RAGE

```
## If b1 map is not registered, do this first:

mp2rage_register_sa2rage(
  in_sa2rage_inv2 = "Sa2RAGE_INV2.nii.gz",
  in_sa2rage_b1_map = "Sa2RAGE_B1map.nii.gz",
  in_mp2rage_inv2 = "MP2RAGE_INV2.nii.gz",
  out_reg_b1_map = "Sa2RAGE_B1map_reg-to-mp2rage.nii.gz")

# Skip if already in register
```

B1 correction

```
# Load data
nii_uni <- readnii(in_uni)
data_uni <- nii_uni@.Data

nii_b1_map <- readnii(in_b1_map)
data_b1_map <- nii_b1_map@.Data

# Start B1 correction
b1_corrected_list <- mp2rage_b1_correct(
  in_b1_map_data = data_b1_map,
  is_sa2rage = TRUE,
  in_uni_data = data_uni,
  param_list_sa2rage = sa2rage_params,
  param_list_mp2rage = mp2rage_params,
  inversion_efficiency = 0.96,
  b0 = 7
)

# b1_corr_data <- b1_corrected_list$b1_corr
```

```
t1_corr_data <- b1_corrected_list$t1_corr  
uni_corr_data <- b1_corrected_list$uni_corr
```

Write outputs

```
# Load NIfTI structure for output files  
nii_t1_corr <- nii_uni  
nii_t1_corr@.Data <- t1_corr_data  
writenii(nim = nii_t1_corr, filename = out_t1)  
  
nii_uni_corr <- nii_uni  
nii_uni_corr@.Data <- uni_corr_data  
writenii(nim = out_uni_corr, filename = out_uni)
```