Appendix 1 Radiomics feature extraction

Radiomics feature extraction was carried out using the widely used Pyradiomics package (version 3.0.1, available at https://pyradiomics.readthedocs.io/en/latest/). The extraction process consisted of preprocessing and feature computation stages. During preprocessing, the images were resampled to a consistent 1×1×1 mm^3 resolution to ensure rotational invariance. Gray values were discretized with a bin width of 10 to mitigate computational complexity. Additionally, the images were normalized via the μ±3σ method to exclude outlier gray values. The parameters for the feature extraction settings were as follows:

```
# This is an example of settings that can be used as a starting point for analyzing MR data with small (~3mm) slice
# thickness. This is only intended as a starting point and is not likely to be the optimal settings for your dataset.
# Some points in determining better values are added as comments where appropriate

# When adapting and using these settings for an analysis, be sure to add the PyRadiomics version used to allow you to
# easily recreate your extraction at a later timepoint:

############################## Extracted using PyRadiomics version: <version> ##############################
########

imageType:
  Original: {}

featureClass:
  # redundant Compactness 1, Compactness 2 an Spherical Disproportion features are disabled by default, they can be
  # enabled by specifying individual feature names (as is done for glcm) and including them in the list.
  firstorder:

setting:
  # Normalization:
  # MR signal is usually relative, with large differences between scanners and vendors. By normalizing the image before
  # feature calculation, this confounding effect may be reduced. However, if only one specific scanner is used, or the
  # images reflect some absolute world value (e.g. ADC maps, T2maps (NOT T2 weighted)), consider disabling the
  # normalization.
  normalize: true
  normalizeScale: 100  # This allows you to use more or less the same bin width.

  # Resampling:
  # If slices are very thin (~1mm), such as in 3D scanned (isotropic) volumes, resampledPixelSpacing may be reduced to
  # (1, 1, 1). Furthermore, in case of isotropic volumes, consider disabling resampling.
  # On a side note: increasing the resampled spacing forces PyRadiomics to look at more coarse textures, which may or
  # may not increase accuracy and stability of your extracted features.
  interpolator: 'sitkBSpline'
  resampledPixelSpacing: [1, 1, 1]

  # Mask validation:
  # correctMask and geometryTolerance are not needed, as both image and mask are resampled, if you expect very small
  # masks, consider to enable a size constraint by uncommenting settings below:
  #minimumROIDimensions: 2
  #minimumROISize: 50

  # Image discretization:
  # The ideal number of bins is somewhere in the order of 16-128 bins. A possible way to define a good binwidt is to
   # extract firstorder:Range from the dataset to analyze, and choose a binwidth so, that range/binwidth remains
approximately
  # in this range of bins.
  binWidth: 10

  # first order specific settings:
  # When normalizing, gray values below the mean will be negative. Shifting by 300 (3 StdDevs * 100) ensures that the
  # majority of voxels is positive (only outliers >3 SD lower than the mean will be negative).
  voxelArrayShift: 300

  # Misc:
  # default label value. Labels can also be defined in the call to featureextractor.execute, as a commandline argument,
  # or in a column "Label" in the input csv (batchprocessing)
  label: 1
```


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