Supplementary S1

Pyradiomics definitions file for ADC radiomic features calculations.

imageType:

  Original: {}

featureClass:

  firstorder:

  shape:

  glcm:

   - 'Autocorrelation'

   - 'JointAverage'

   - 'ClusterProminence'

   - 'ClusterShade'

   - 'ClusterTendency'

   - 'Contrast'

   - 'Correlation'

   - 'DifferenceAverage'

   - 'DifferenceEntropy'

   - 'DifferenceVariance'

   - 'JointEnergy'

   - 'JointEntropy'

   - 'Imc1'

   - 'Imc2'

   - 'Idm'

   - 'Idmn'

   - 'Id'

   - 'Idn'

   - 'InverseVariance'

   - 'MaximumProbability'

   - 'SumEntropy'

   - 'SumSquares'

  glrlm:

  glszm:

  gldm:

  ngtdm:

setting:

  normalize: false

  interpolator: 'sitkLinear'

1

resampledPixelSpacing: [1.6796875, 1.6796875, 6.0]

padDistance: 10

preCrop: true

minimumROISize: 10

force2D: true

force2Ddimension: 2

binWidth: 100

voxelArrayShift: 0

symmetricalGLCM: true

Supplementary S2

Pyradiomics definitions file for fat fraction radiomic features calculations.

imageType:

 Original: {}

featureClass:

 firstorder:

 shape:

 glcm:

  - 'Autocorrelation'

  - 'JointAverage'

  - 'ClusterProminence'

  - 'ClusterShade'

  - 'ClusterTendency'

  - 'Contrast'

  - 'Correlation'

  - 'DifferenceAverage'

  - 'DifferenceEntropy'

  - 'DifferenceVariance'

  - 'JointEnergy'

  - 'JointEntropy'

  - 'Imc1'

  - 'Imc2'

  - 'Idm'

  - 'Idmn'

  - 'Id'

  - 'Idn'

  - 'InverseVariance'

  - 'MaximumProbability'

  - 'SumEntropy'

  - 'SumSquares'

 glrlm:

 glszm:

 gldm:

 ngtdm:

setting:

 normalize: false

 interpolator: 'sitkLinear'

 resampledPixelSpacing: [1.6796875, 1.6796875, 5.0]

 padDistance: 10

preCrop: true

minimumROISize: 10

force2D: true

force2Ddimension: 2

binWidth: 3.333

voxelArrayShift: 0

symmetricalGLCM: true

Supplementary S3

Below is the Stan script for drawing parameter samples given input data.

```
data {
  int<lower=0> N_tot; // Total number of samples (lesions)
  int<lower=0> N;    // Number of patients
  int<lower=0> M[N]; // Number of samples per patient (Note sum(M) == N)
  vector[N_tot] x1;  // Baseline measurements 1
  vector[N_tot] x2;  // Baseline measurements 2
}
parameters {
  real mu_0;          // Population mean
  real<lower=0> sigma_0; // Inter-patient variation standard deviation
  vector[N] mu_i;       // Patient means
  real<lower=0> sigma_p; // Intra-patient variation standard deviation
  vector[N_tot] mu_ij;   // Lesion means
  real<lower=0> sigma_r; // Repeatability standard deviation
  real bias;          // Bias between double baseline measurements
}
model {
  // Priors
  mu_0 ~ normal(0, 10);
  bias ~ normal(0, 10);
  sigma_0 ~ cauchy(0, 5);
  sigma_p ~ cauchy(0, 5);
  sigma_r ~ cauchy(0, 5);

  // Likelihoods
  int pos = 1;
  for (n in 1:N) {
    mu_i[n] ~ normal(mu_0, sigma_0);
    for (m in pos:pos+M[n]-1) {
      mu_ij[m] ~ normal(mu_i[n], sigma_p);
      x1[m] ~ normal(mu_ij[m], sigma_r);
      x2[m] ~ normal(mu_ij[m] + bias, sigma_r);
    }
    pos = pos + M[n];
  }
}
```