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Description and usage

- src/scripts/compute_features.py Run this script to compute the features. At the end of the process the resulting features will be stored in the cache/feature.db file. The calculation may require from a few minutes to several hours depending on the number of features and the combinations of parameters requested. The main paramers are:
 - features_to_compute the radiomics features to compute (see feature_lut in src/functions for accepted values);
 - CT_window a tuple of two elements (CTmin, CTmax) used to window the input CT signal. Values less or equal than
 CTmin are set to CTmin; those greater or equal than CTmax to CTmax;
 - number_of_levelss a list of positive integers each representing the number of levels used to resample the CT signal between CTmin and CTmax;
 - noise_scales a list of non-negative floats each representing the amplitude of the Gaussian noise as a percentage of the spread (standard deviation) of the input signal.
- src/scripts/patient_population.py Use this script to retrieve data about the study population at the scan level (patient id, age, gender, in-plane pixel spacing, slice thickness and slice spacing) and at the nodule level (patient id, nodule id, number of annotations) and at the annotation level (annotation id, subtetly, internal structure, calcification, sphericity, margin, lobulation, spiculation, texture and malignancy see pylide documentation for details about the maing of each parameter). The results will be stored in the cache/scans_metadata.csv and cache/noduless_metadata.csv files, respectively.
- src/scripts/stability_analysis_delineation.py Use this script to assess the features' stability to lesion delineation. The results will be stored in the cache/stability_against_delineation.csv file. The main parameters are:
 - num_requested_annotations limit the analysis to those nodules that have exactly the requested number of annotations (default = 4);
 - noise_scale the noise scale at which the analysis is carried out (the value needs to have been included during feature calculation parameter noise_scales of src/scripts/compute_features.py , default = 0.0);
 - num_levels the number of discretization levels at which the analysis is carried out (the value needs to have been included during feature calculation parameter num_levelss of src/scripts/compute_features.py , default = 256).

NOTE: Any of the src/scripts/stability_analysis_delineation.py scripts can be launched only after the features have been computed via src/scripts/compute_features.py make sure the ... and can

Dependencies

- NumPy 1.18.5
- Pandas 1.1.3
- pinguoin 0.3.10
- pylidc 0.2.2
- pynrrd 0.4.2
- pyradiomics 3.0.1
- SQLite

How to cite this work

 Bianconi, F., Palumbo I., Fravolini M.L. et al. Radiomics analysis of lung lesions on CT: experimental evaluation of the stability of texture features against delineation, intensity discretisation and noise (to appear)

References

- 1. Armato III, S.G.; McLennan, G.; Bidaut, L. et al. Data From LIDC-IDRI. The Cancer Imaging Archive. (2015). http://doi.org/10.7937/K9/TCIA.2015.LO9QL9SX
- 2. Armato III, S.G., McLennan, G., Bidaut, L. *et al.*; **The Lung Image Database Consortium (LIDC) and Image Database Resource Initiative (IDRI): A completed reference database of lung nodules on CT scans** (2011) Medical Physics, 38 (2), pp. 915-931. DOI: https://doi.org/10.1118/1.3528204
- 3. Clark, K., Vendt, B., Smith, K., Freymann, J., Kirby, J., Koppel, P., Moore, S., Phillips, S., Maffitt, D., Pringle, M., Tarbox, L., Prior, F.; **The cancer imaging archive (TCIA): Maintaining and operating a public information repository** (2013) Journal of Digital Imaging, 26 (6), pp. 1045-1057. DOI: https://doi.org/10.1007/s10278-013-9622-7
- 4. Van Griethuysen, J.J.M., Fedorov, A., Parmar, C., et al.; Computational radiomics system to decode the radiographic phenotype (2017) Cancer Research, 77 (21), pp. e104-e107. DOI: https://doi.org/10.1158/0008-5472.CAN-17-0339