Data Science / Medical Imaging & Big Data

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Medical images are one of the largest and fastest growing resources of information and present some of the biggest challenges for data science due to their volume, multimodality and complexity. The explosion in data collection from different sources makes their unaided processing and interpretation by humans impossible, and requires the development of **automated** storage, management, **processing and analysis algorithms**.

Moreover, medical imaging devices (such as magnetic resonance tomography or positron emission tomography) do not immediately provide physicians with the kind of information relevant to their needs, e.g. **imaging biomarkers for diagnosis, prognosis and therapy**.
Image processing algorithms are needed to extract this information from the physical and statistical laws that relate the measurements with the image.

New image analyses, from theory and algorithm design to the development of advanced methods for feature extraction, selection and classification, are crucial to reduce image dimensionality problem to the most informative features that can be used to **support the clinical diagnostic process**.

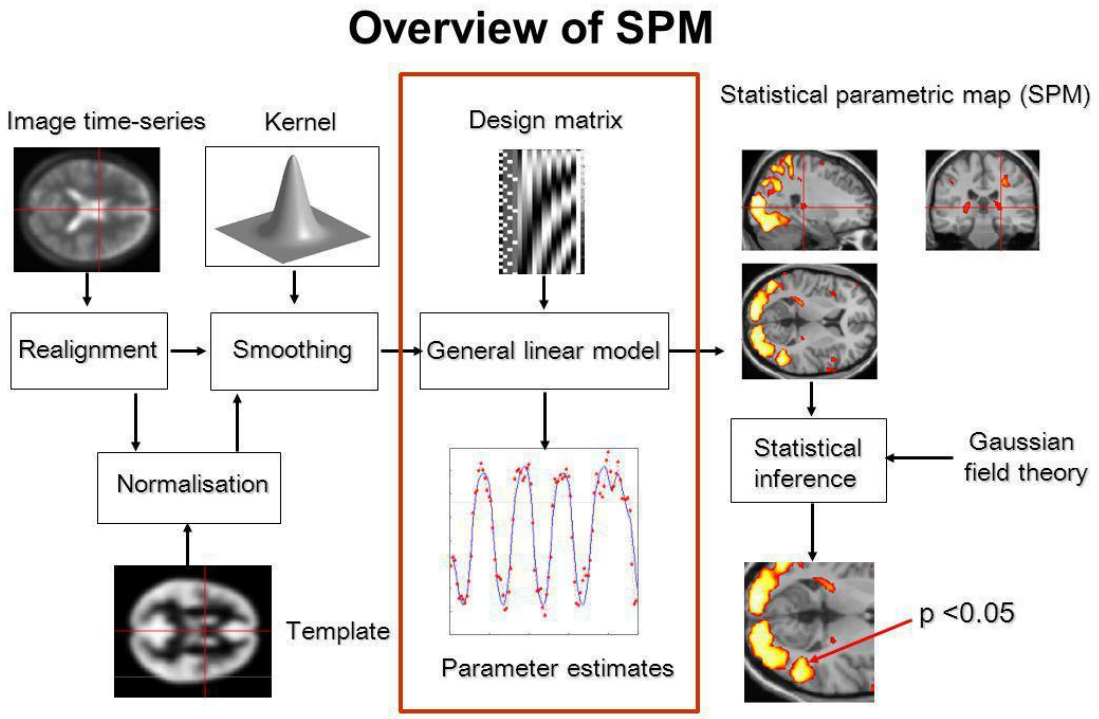
The course will present several image processing methods and their potential for managing big medical-imaging data, facing dimensionality problems by extracting image features relevant to clinical needs as candidate disease biomarkers.

Each topic will be addressed in two parallel sessions, i.e. academic lessons and laboratory activities.

Data Science / Medical Imaging & Big Data

Main topics

- **Statistical Parametric Mapping**
- Texture analysis
- Segmentation of medical images
- Feature reduction and selection techniques
- Radiomics / Radiogenomics
- From medical images to disease biomarkers
- Predictive models



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Main topics

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- **Texture analysis**
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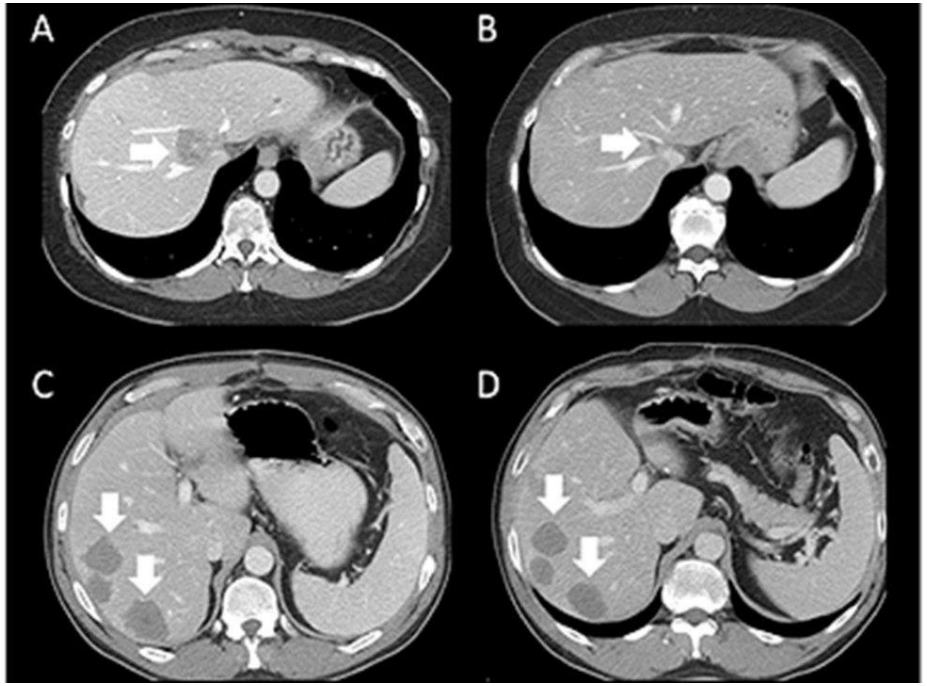

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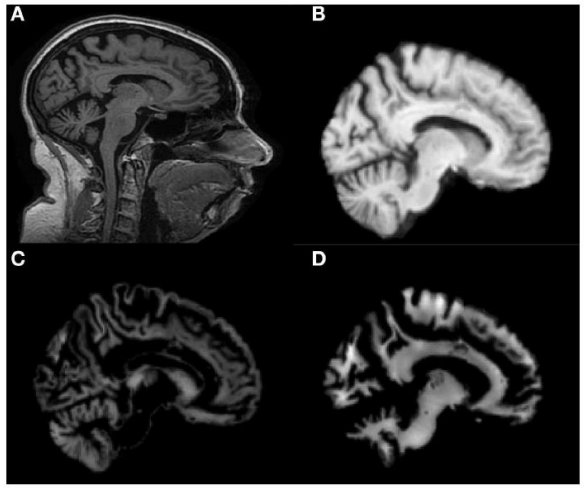

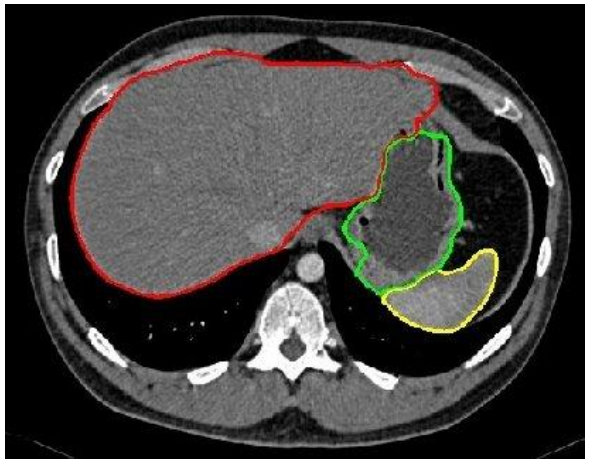

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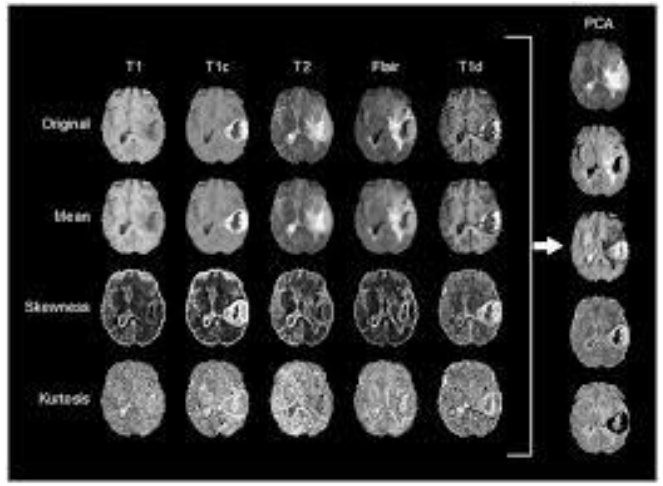

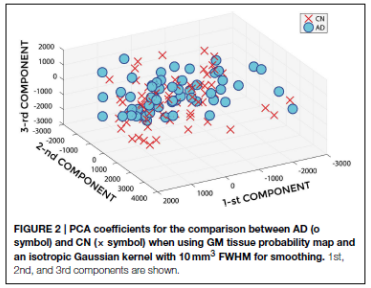

FIGURE 2 | PCA coefficients for the comparison between AD (o symbol) and CN (× symbol) when using GM tissue probability map and an isotropic Gaussian kernel with 10 mm^3 FWHM for smoothing. 1st, 2nd, and 3rd components are shown.

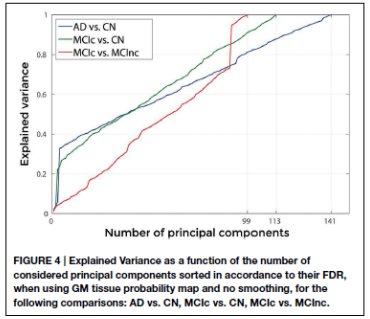

FIGURE 4 | Explained Variance as a function of the number of considered principal components sorted in accordance to their FDR, when using GM tissue probability map and no smoothing, for the following comparisons: AD vs. CN, MCIc vs. CN, MCIc vs. MCInc.

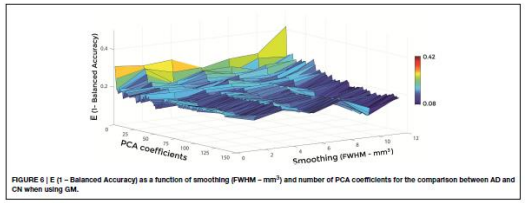

FIGURE 6 | E (1 – Balanced Accuracy) as a function of smoothing (FWHM – mm^3) and number of PCA coefficients for the comparison between AD and CN when using GM.

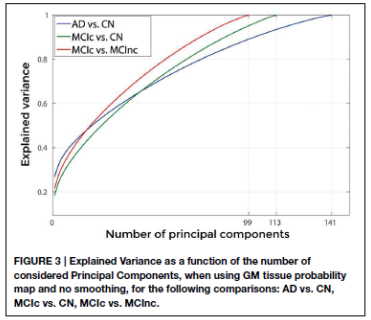

FIGURE 3 | Explained Variance as a function of the number of considered Principal Components, when using GM tissue probability map and no smoothing, for the following comparisons: AD vs. CN, MCIc vs. CN, MCIc vs. MCInc.

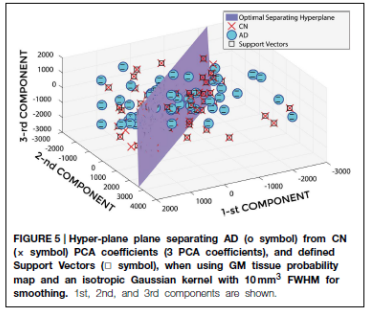

FIGURE 5 | Hyper-plane plane separating AD (o symbol) from CN (× symbol) PCA coefficients (3 PCA coefficients), and defined Support Vectors (□ symbol), when using GM tissue probability map and an isotropic Gaussian kernel with 10 mm^3 FWHM for smoothing. 1st, 2nd, and 3rd components are shown.

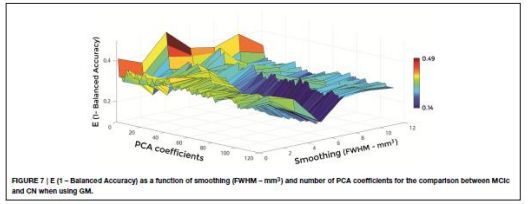

FIGURE 7 | E (1 – Balanced Accuracy) as a function of smoothing (FWHM – mm^3) and number of PCA coefficients for the comparison between MCIc and CN when using GM.

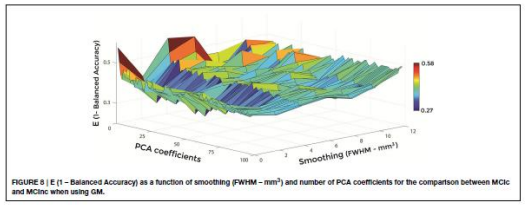

FIGURE 8 | E (1 – Balanced Accuracy) as a function of smoothing (FWHM – mm^3) and number of PCA coefficients for the comparison between MCIc and MCInc when using GM.

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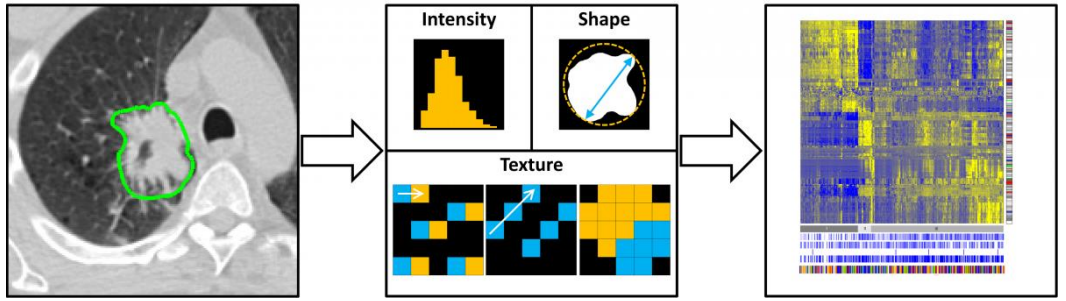

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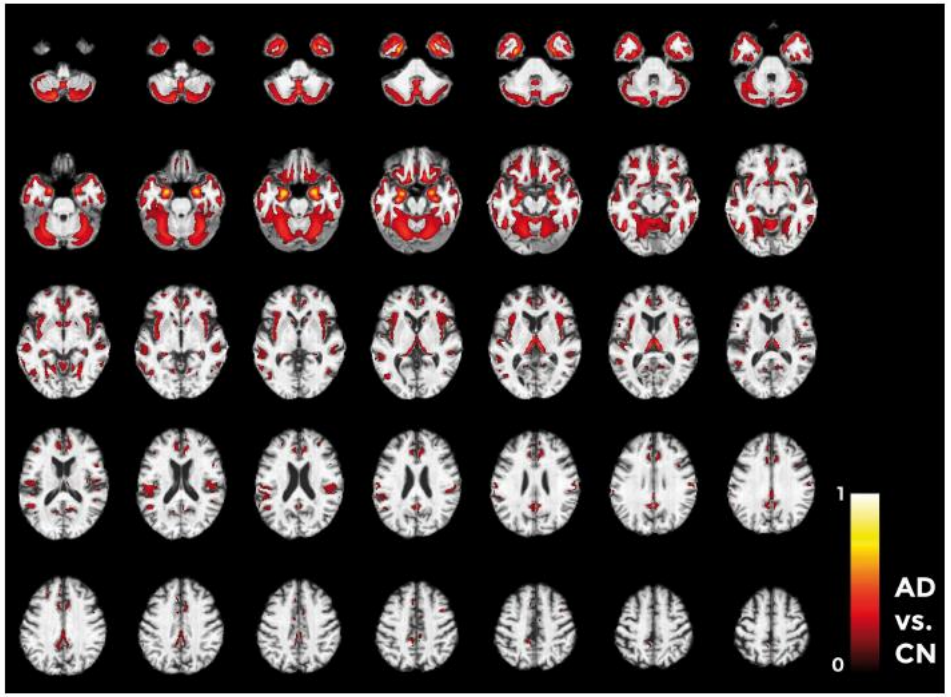

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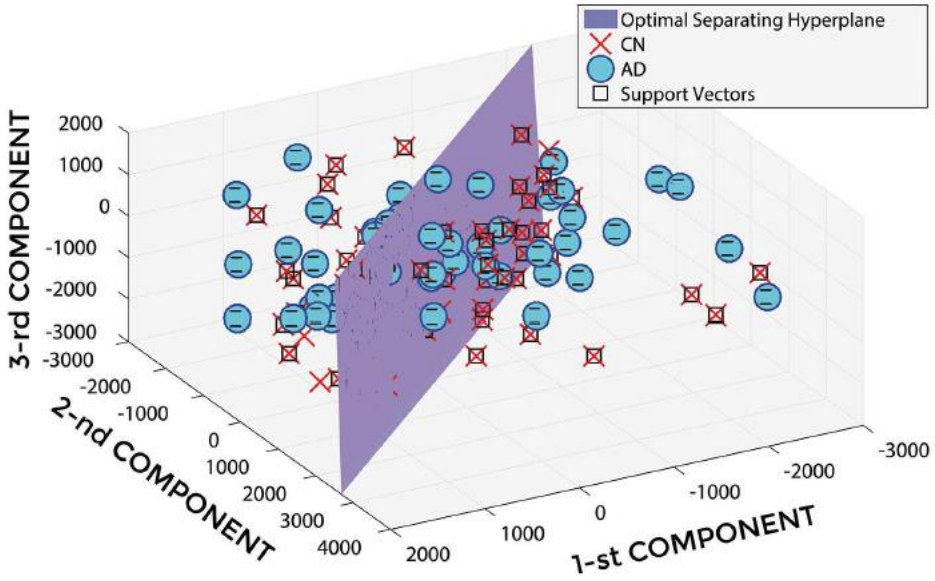

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Requirements

- Matlab
- Statistical Parametric Mapping
- Data available (for each practical session) at
  https://christiansalvatore.github.io/medicalimaging-bigdata/
  or
  https://github.com/christiansalvatore/medicalimaging-bigdata/