

Scientific programmer in neuroimage analysis and machine learning (University of Texas Southwestern, Dallas, USA)

Background:

The laboratory of Albert Montillo (<http://www.utsouthwestern.edu/labs/montillo>) in the Bioinformatics Department of UT Southwestern Medical Center is seeking a full time Scientific Programmer for studies of mental & neurodevelopmental disorders and neurodegenerative diseases. The Scientific Programmer will use multimodal MRI, and MEG/EEG data to study structural and functional circuit changes, and PET/SPECT, CT to study metabolic and pathophysiological changes associated with diagnosis and prognoses. The main responsibilities of the position include: implementing and optimizing image processing, computational and analyses pipelines for large-scale multimodal brain imaging data and corresponding clinical data. The lab is an interactive and collaborative team directed by Albert Montillo, Ph.D., conducting cutting-edge research to advance the theory and application of machine learning for the analysis of medical images. The lab addresses unmet clinical needs by forming predictive models that make diagnoses and prognoses more precise and advance neuroscience by furthering the understanding of mechanisms in disease and intervention. You will work directly with him and an array of principle investigators, collaborators and trainees.

Medical image analysis software the lab has developed include machine learning-based methods for labeling structures throughout the brain (parcellation), versions of which are used worldwide and FDA approved. The lab has built deep learning methods to label networks in resting state fMRI and detect artifacts in MEG. The lab has pioneered deep learning decision forests that increase prediction accuracy while reducing prediction time and outcome prediction methods using advanced brain connectomics.

Job responsibilities

- Design, implement and optimize image processing, computational and analyses pipelines for large-scale multimodal brain imaging, including resting and task-based fMRI, diffusion MRI, PET/SPECT, CT, and MEG/EEG data on our high performance compute cluster.
- Implement machine learning models to automate preprocessing, quality control, and computational data analysis of imaging, metabolic, genetic, behavioral, and clinical data.
- Integrate third party pipelines with tailored in-house pipelines.
- Build tools to organize and visualize the growing database of analysis results.
- Contribute to writing of journal and conference papers. Participate fully in collaborative research.
- Attend lab meetings, stay abreast of developments in image analysis and machine learning.
- Coordinate data integration from ongoing studies.
- Teach lab members about image processing steps, outputs and to quality control approaches.
- A minimum three-year commitment is strongly encouraged.
- Anticipated start date: immediate

Experience of ideal applicants:

- B.A. or B.S. Degree in Computer Science, Electrical Engineering, Biomedical Engineering or a related field with three (3) years scientific software development; Master's or Ph.D. preferred. Software development experience on high performance compute clusters or GPU-based machine learning is a strong plus. Will consider record of success in publishing computational results in lieu of experience.
- Familiarity with at least 1 image data type: MRI, PET/SPECT, CT, MEG/EEG & format: NIFTI, DICOM.
- Experience in at least 1 neuroimage analysis pipeline: NiPype, SPM, FSL, AFNI, FreeSurfer; for diffusion MRI: Camino, DTI-TK, DiPy, TrackVis, DTI/DSI studio, ExploreDTI; for MEG/EEG: Brainstorm, EEGLAB, FieldTrip, MNE, NUTMEG.
- Experience in brain connectivity, graph theory, and genomic data analyses are significant advantages.

- Experience developing image processing or image analysis software and algorithms using Linux. Solid understand of standard CS data structures.
- At least 2 years of experience in Python and 1 other language (Matlab, R, C/C++)
- Proficient at the Linux command line, bash scripting, and revision control e.g. Git or SVN.
- Practical ML experience applying at least 1 of the following: deep learning neural nets (RNN,CNN,DNN, UNet/VNet), DCGAN, deep reinforcement learning, transfer learning, autoencoders; classical learning: SVM, random forest, boosting, ensemble methods; Generative and probabilistic modeling: probabilistic graphical models, RBM, GMM; optimization; image/object recognition; time series analysis.
- Experience in at least one of these Python libraries: Keras, scikit-learn, TensorFlow, PyTorch, Nilearn, PyMMPA.
- Optional but helpful: Experience in C/C++ (ITK library), cMake, software development. Familiarity with XNAT.

Salary compensation is very competitive and enhanced by the low cost of living in Dallas. Benefits include health insurance. The candidate will also benefit from membership in vibrant national and international research communities through our on-going collaborations with UCLA, UCSF, UPenn, Stanford, Philips and Siemens Research, as well as a large local neuroscience communities through UTSW's O'Donnell Brain Institute, and UTD's Centers for Vital Longevity, Brain Health, and Brain Performance.

Please apply by email to Dr. Montillo [Albert.Montillo@UTSouthwestern.edu] and include your CV and names and addresses of three references. Use the subject line "ScientificProgrammer: <your name>".

The Montillo lab is co-located within the Bioinformatics Department on UT Southwestern's south campus and embedded in the Radiology Department on north campus. We are an integral part of the Advanced Imaging Research Center, and work closely with research groups within Neuroscience, Neurology, Psychiatry, Radiation Oncology, and Surgery. Montillo lab members have access to considerable computational resources, including the >6,800-core cluster with >8 Petabyte of storage available through UTSW's high-performance infrastructure (BioHPC – <https://portal.biohpc.swmed.edu>). Future lab members will have the opportunity to work on a broad range of image analysis, machine learning and modeling on interdisciplinary teams, and participate in all aspects of method development, software implementation, data analysis, and validation with lab collaborators.

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