A standardised representation for non-parametric fMRI results

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Introduction

Reuse of data collected and analysed at another site is becoming more prevalent in the neuroimaging community (cf. for example (Milham et al. 2017)) but this process usually relies on intensive data and metadata curation. Given the ever-increasing number of research datasets produced and shared, it is desirable to rely on standards that will enable automatic data and metadata retrieval for large-scale analyses (Wilkinson et al. 2016).

We recently introduced NIDM-Results (Maumet et al. 2016), a data model to represent and publish data and metadata created as part of a mass univariate neuroimaging study (typically functional magnetic resonance imaging). Here we extend this model to allow for the representation of non-parametric analyses and we introduce a JSON API that will facilitate export into NIDM-Results.

Methods

This work was developed within NIDASH, an international collaboration dedicated to projects advancing neuroimaging data sharing. The group works openly and meets weekly through videoconferences; minutes of online discussions are publicly available (cf. https://github.com/incf-nidash/nidm). We also received feedback from other members of the neuroimaging community.

NIDM-Results relies on semantic web technologies. Although those techniques are very powerful, they are not yet widespread in our scientific community and the learning curve with these tools can be steep. In order to facilitate the development of export tools into NIDM-Results, we created a simple JSON API that can be used by neuroimaging software developers as an intermediate step to generate a NIDM-Results document.

Results

Fig. 1. provides an overview of the extension for non-parametric tests. Briefly, a new object was created to store information about the non-parametric null distribution, including the number of permutations used and the size of the exchangeability blocks. In addition, a new statistic type was created to represent smoothed-T statistic, a variant of the T-Statistic in which the variance is smoothed also sometimes referred to as "pseudo-T Statistic". To test the usability of the specification, we added capabilities to the SnPM software package (Nichols and Holmes 2002) to export its results into NIDM-Results.

The JSON API is publicly available and open for comments at https://tinyurl.com/y84uxobq. The document is divided into two main subsections describing mandatory and optional fields respectively. Fig. 2 provides an example of a compliant JSON file including information about the neuroimaging

software, data scaling, design matrix, error model, contrasts and statistics as well as a list of the peaks and clusters found in the thresholded map. We have built libraries in Python (https://github.com/incf-nidash/nidmresults) and MATLAB (as part of SPM (Penny et al. 2011)) that can be used to create an NIDM-Results document from a document created in agreement with the JSON API. The MATLAB library is used by SnPM to generate its NIDM-Results export.

Conclusions

We have provided a data model to represent data and metadata created by mass-univariate nonparametric studies. We hope that this model will ease realization of large-scale image-based meta-analyses. We also welcome feedback and new contributions from the community on the specifications and the various implementations. In the future, we would like to extend the list of nonparametric neuroimaging tools (e.g. AFNI's (Cox 1996) 3dttest++ or FSL's (Jenkinson et al. 2012) randomise) that provide export to NIDM-Results. By providing an easy mechanism to export to NIDM-Results, our goal is to increase interoperability between existing neuroimaging software packages and to facilitate the development of generic tools. As an example of such tool, we have started developing viewers in MATLAB and Python that can be used to display a NIDM-Results pack, regardless of the neuroimaging software package that was used for the analysis.
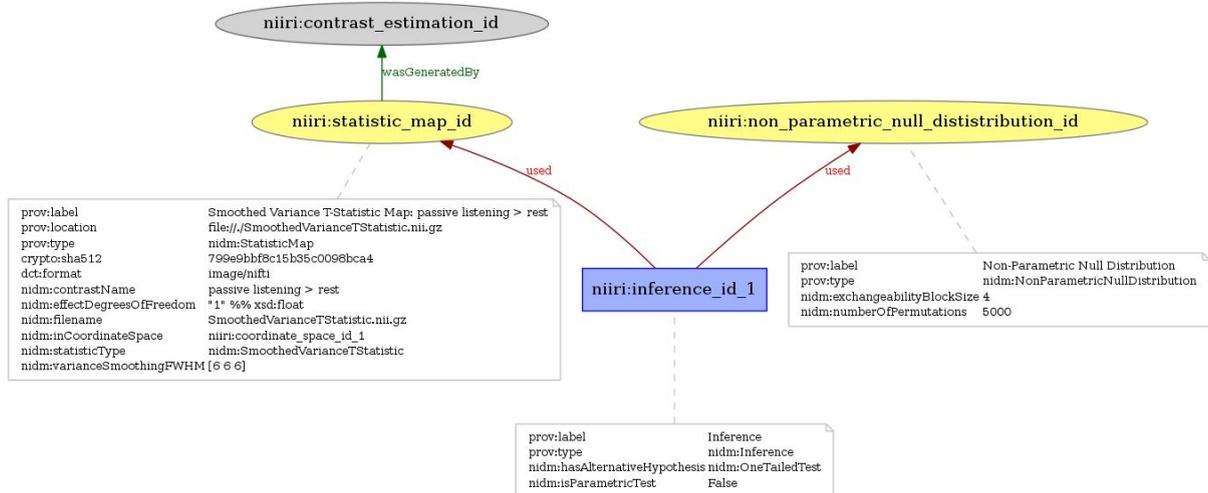
Figures

Fig. 1. Proposed extension of NIDM-Results for non-parametric tests.

```json
{
  "NeuroimagingAnalysisSoftware_type": "scr_SPM",
  "NeuroimagingAnalysisSoftware_softwareVersion": "12.6906",
  "Data_grandMeanScaling": false,
  "Data_hasMRIProtocol": "nlx_FunctionalMRIProtocol",
  "Groups": {
    "StudyGroupPopulation_groupName": "Control",
    "StudyGroupPopulation_numberOfSubjects": 14
  },
  "DesignMatrix_atLocation": "./design.csv",
  "DesignMatrix_regressorNames": ["mean"],
  "ParameterEstimateMaps": ["./beta_0001.nii"],
  "ErrorModel_hasErrorDistribution": "obo_NormalDistribution",
  "ErrorModel_errorVarianceHomogeneous": true,
  "ErrorModel_varianceMapWiseDependence": "nidm_IndependentParameter",
  "ErrorModel_hasErrorDependence": "nidm_IndependentError",
  "ModelParameterEstimation_withEstimationMethod": "obo_OrdinaryLeastSquaresEstimation",
  "ResidualMeanSquaresMap_atLocation": "./ResMS.nii",
  "GrandMeanMap_atLocation": "./GrandMean.nii.gz",
  "MaskMap_atLocation": "./mask.nii",
  "CoordinateSpace_inWorldCoordinateSystem": "nidm_Ixi549CoordinateSystem",
  "CoordinateSpace_voxelUnits": ["mm", "mm", "mm"],
  "Contrasts": {
    "StatisticMap_contrastName": "Group_mean",
    "ContrastWeightMatrix_value": 1,
    "StatisticMap_statisticType": "obo_TStatistic",
    "StatisticMap_errorDegreesOfFreedom": 13,
    "StatisticMap_atLocation": "./spmT_0001.nii",
    "ContrastMap_atLocation": "./con_0001.nii",
    "ContrastStandardErrorMap_atLocation": "./ContrastStandardError.nii.gz"
  },
  "ClusterDefinitionCriteria_hasConnectivityCriterion": "nidm_voxel18connected",
  "PeakDefinitionCriteria_minDistanceBetweenPeaks": 8,
  "PeakDefinitionCriteria_maxNumberOfPeaksPerCluster": 3,
  "Inferences": {
    "StatisticMap_contrastName": ["Group_mean"],
    "HeightThreshold_type": "nidm_PValueUncorrected",
    "HeightThreshold_value": 0.001,
    "ExtentThreshold_type": "obo_Statistic",
    "ExtentThreshold_clusterSizeInVoxels": 120,
    "Inference_hasAlternativeHypothesis": "nidm_OneTailedTest",
    "SearchSpaceMaskMap_atLocation": "./mask.nii",
    "SearchSpaceMaskMap_searchVolumeInVoxels": 160902,
    "SearchSpaceMaskMap_searchVolumeInUnits": 1287216,
    "ExcursionSetMap_atLocation": "./ExcursionSet.nii.gz",
    "Clusters": [
      {
        "SupraThresholdCluster_clusterSizeInVoxels": 565,
        "SupraThresholdCluster_pValueUncorrected": 4.22e-09,
        "Peaks": [
          {
            "Peak_value": 9.02,
            "Coordinate_coordinateVector": [-10,18,42],
          },
          ... More peaks ...
        ]
      },
      ... More clusters ...
    ]
  }
}
```

Fig. 2. Example of JSON file for a group fMRI inference with an uncorrected voxelwise threshold p<0.001.

Acknowledgments

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