

Online open neuroimaging mass meta-analysis

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Abstract. We describe a system for meta-analysis where a wiki stores numerical data in a simple format and a web service performs the numerical computation. We initially apply the system on multiple meta-analyses of structural neuroimaging data results. The described system allows for mass meta-analysis, e.g., meta-analysis across multiple brain regions and multiple mental disorders.

1 Introduction

The scientific process aggregates a large number of scientific results into a common scientific consensus. *Meta-analysis* performs the aggregation by statistical analysis of numerical values presented across scientific papers. Collaborative systems such as wikis may easily aggregate text and values from multiple sources. However, so far they have had limited ability to apply numerical analysis as required, e.g., by meta-analysis.

Researchers have discussed the advantages and disadvantage of the tools for conducting systematic reviews from “paper and pencil”, over spreadsheets to RevMan and web-based specialized applications [10]: Setup cost, versatility, ability to manage data, etc. In 2009 they concluded that “no single data-extraction method is best for all systematic reviews in all circumstances”. For example, RevMan and Archie of the Cochrane Library provide an elaborate system for keeping track and analyzing textual and numerical data in meta-analyses, but the system could not import information from electronic databases [10]. Our original meta-analyses [4, 5] relied on the Microsoft Excel spreadsheets later distributed on public web sites. Compared to an ordinary spreadsheet a wiki solution provides data entry provenance and collaborative data entry with immediately update. Shareable folders on cloud-based storage systems would help collaboration on spreadsheets, but yield no provenance. Online services, such as the spreadsheet of Google Docs, may lack meta-analytic plotting facility. Web-based specialized applications for systematic reviews may have a high setup cost [10].

We have previously explored a simple online meta-analysis system—a “fielded wiki”—in connection with personality genetics [8]. As implemented specifically

* Thanks to the Lundbeck Foundation for the funding of the *Center for Integrated Molecular Brain Imaging* (CIMBI).

system for recording structured bibliographic data about the publication and to annotate the CSV information, see Figure 2.

The bulk of the data currently presented in the wiki comes from the large mass meta-analysis of volumetric studies on major depressive disorder reporting over 50 separate meta-analyses for individual brain regions [4]. Further data comes from mass meta-analyses across multiple brain regions on

bipolar disorder [5] and first-episode schizophrenia [6], a meta-analysis on longitudinal development in schizophrenia [7] as well as data from individual original studies on obsessive-compulsive disorder.

Apart from neuroimaging studies the Brede Wiki also records data from meta-analyses from a few other studies outside neuroimaging [2], allowing us to test the generality of the framework. The data is distributed under ODbL.

3 Web script and meta-analysis

The web script for meta-analysis reads the CSV information, identifies the required columns for meta-analysis, performs the statistical computations and makes meta-analytic plots—the so-called forest and funnel plots—in the SVG format, see Figure 3. From either the title information or a PubMed identifier the script generates back-links from the generated page to pages on the wiki. The script may also export the computed results as JSON or CSV. Furthermore, it may generate a small *R* script that sets up the data in variables and use the *meta* library for meta-analysis.

The web script attempts to guess the separator used on the CSV page and also tries to match the elements of the column header, e.g., the strings “control n”, “controls number”, “number of controls”, etc. match for number of control subjects. With no matches the user needs to explicitly specify the relevant columns via URL parameters, which in turn a wiki template can setup.

Standard meta-analysis computes an *effect size* from each result in a paper and computes a combined meta-analytic effect size and its confidence interval. Although the methodological development continues, there exist established statistical analysis approaches for ordinary meta-analysis [2]. Our system implements computations on the standardized mean difference for continuous variables and on the natural logarithm of the odds ratio for categorical variables with fixed and random effects methods using an inverse-weighted variance model, — following the approach in the Stata program. As an extra option we provide meta-analysis on the natural logarithm of the variance ratio [3], for comparison of the standard deviations between two groups of subjects.

```

{{Metaanalysis csv begin}}
{{Metaanalysis csv
| title = Major Depressive Disorder Neuroimaging Database - Pituitary, total
| topic1 = Pituitary
| topic2 = Major depressive disorder
| topic3 = MaND
}}
{{Metaanalysis csv
| title = Obsessive-compulsive disorder Neuroimaging Database - Pituitary
| topic1 = Pituitary
| topic2 = Obsessive-compulsive disorder
| topic3 = ObND
}}
{{Metaanalysis csv end}}

```

Fig. 2. Template to annotate the CSV data and define the links to the meta-analysis.

4 Results

We have added 124 pages with CSV data, — most of which contain data suitable for meta-analysis. For individual analyses the reading, computation and download finish within seconds. With multiple calls to the web script and JSON output another script can plot multiple meta-analytic results together as in Figure 4. Generating such a plot takes several minutes. For generating the page show in Figure 3 we need only the CSV data and the web

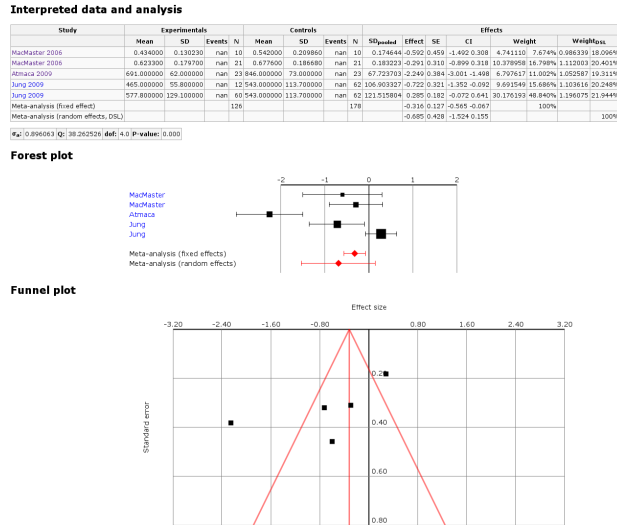


Fig. 3. Screenshot of web script showing the meta-analytic results with forest and funnel plots.

script, while the script that generated Figure 4 used information defined in templates, CSV data and the web script with no further adaption of MediaWiki.

5 Discussion

By using MediaWiki in our present system we exploit the template facility to capture structured information, and free-form wikitext for annotation and comment on the individual scientific papers, — as in semantic academic annotation wikis *AcaWiki* and *WikiPapers*. It is also possible to use the pages of the wiki as a simple means to keep track of the status of the papers considered for the meta-analysis: potentially eligible, eligible, partially entered and fully entered.

Why not Semantic MediaWiki? Semantic MediaWiki (SMW) may query text and numerical data, though has not had the ability to make complex computations. The *Semantic Result Formats* extension includes average, sum, product and count result formats enabling simple computations of a series of numerical values, but insufficient for the kind of computations we require. The data for meta-analysis form a n-ary data record (mean, standard deviation, number of subjects, labels) so either individual SMW pages should store each data record or we should invoke the n-ary functionality in *Semantic Internal Objects* SMW extension, SMW *record* or the recently-introduced *subobject* SMW functionality. We have not investigated whether these tools provide convenient means for representing our data. The Brede Wiki can export its ontologies defined in MediaWiki template to SKOS. Our future research can consider RDFication of the CSV information through the SCOVO format [9].

We wrote the web service in Python, where Numpy makes vector computation available and Scipy provides statistical methods, necessary for the computation. In a future PHP implementation the script could more closely integrate with the wiki as either a MediaWiki or a SMW extension.

A wiki built from standard components provides an inexpensive solution with means to manage meta-analytic data in a collaborative environment. The general framework allows not only the meta-analysis of neuroimaging-derived data but has the potential for managing and analyzing data from many other domains.

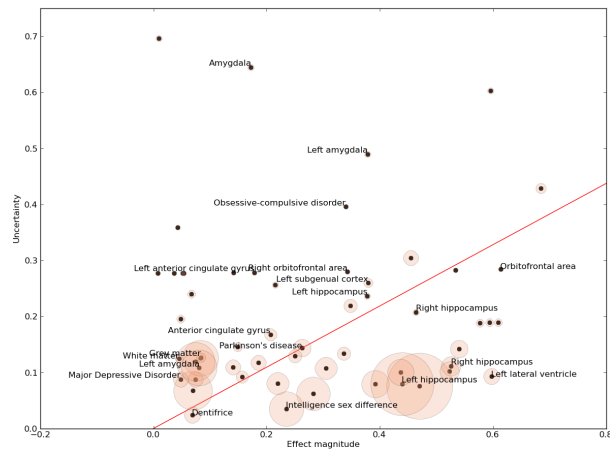


Fig. 4. Results from mass meta-analyses shown in a L'Abbé-like plot and constructed by calling the web script multiple times. Each dot corresponds to a meta-analysis. Uncertainty as a function of effect size with size of each dot determined by the number of subjects. The line indicates 0.05-significance.

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