**Minutes conference call ENIGMA-ADHD-MA, 3rd of Sept 2013**

**Participants (in random order):**

Barbara Franke, Martine Hoogman, Maarten Mennes, Marcel Zwiers, Janneke Dammers, Janita Bralten, Patrick de Zeeuw, Paul Thompson, Annette Conzelmann , Mitul Metha, Sarah Medland, Ben Neale, Eric Newman (for Terry Jernigan), Maria Hovic, Phil Asherson, Jan Buitelaar, Kerstin von Plessen, Theo van Erp, Andreas Reif, Steve Faraone, Thomas Frodl, Yannis Paloyelis, Katya Rubia, Kerstin Konrad, Neda Jahanshad.

Joanna Kuntsi and Phillip Shaw tried to join but had difficulties joining the TC.

*Note: there seemed to be some technical difficulties during the TC due to which not everyone could attend the meeting. We apologize for the inconvenience.*

**Agenda:**

1. Introduction of project aims
2. Do we miss researchers (at least 50 samples from patients with ADHD required)?
3. MoU: are there any essential changes necessary
4. Which questions do we want to address as a group:
    a. Current project/paper:
        i. Do differences exist between patients with ADHD and controls?
        ii. Do differences depend on age?
        iii. Do ADHD-subtype/gender/medication/comorbidity affect differences?
        iv. Can we add longitudinal aspects to the mainly cross-sectional design?
5. Procedure, distribution of tasks and timelines
6. Ideas for future projects/papers (e.g. cortical analyses/genetics/……)

**1. Introduction of the project aims**

The main aim of this project is to understand the structure of the ADHD brain. We will do this by joining forces and work along existing protocols for analyzing brain imaging data (from the ENIGMA Consortium) to maximize power and to minimize the effort. Secondary aims are to do deeper phenotyping by also looking at effects of factors like co-morbidity, age, medication, and possibly longitudinal effects etc.

The problem of quality assessment was mentioned; how do we deal with the different T1 protocols for obtaining structural scans. ENIGMA has dealt with the same issues and it was mentioned that we should be able to rely on the expertise of each separate site. Bad scans should be taken out by the site prior to analysis, which everyone would do for their own analysis anyway. We will put together a protocol on how to deal with outlier issues, together with experts from the ENIGMA team. Differences in scanner protocols can be dealt with by taking these as covariates. Main message from ENIGMA (Thompson), seconded by Faraone was: just do your own QC and decide within your group which data you would use for your own analysis. When this expertise is not available in your own group, you can rely on the experts in our working group.

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*Note; we will make sure we have clear protocols for the analysis and suggestions for your QC.*

2. **Do we miss researchers?**

Suggested were: Joel Nigg (USA), Marina Danckaerts (Belgium), David Coghill (UK), Daniel Brandeis (GER). Please email Martine Hoogman (m.hoogman@gen.umcn.nl) if you have any additional suggestions.

*Note: we have contacted these researchers in the meantime.*

3. **MoU: are there any essential changes necessary?**

No changes to the MoU were suggested. The procedure for ethical approval was discussed. The sites should have approval for sharing data. There will be no issues if only summary data is shared, if we decide to share the estimated volumes per person, ethical approval for data sharing is important. In some cases, even a receiving site is required to have approval for working with the data, everyone should check this with their ethics committee.

There will be a central support group consisting of the people who will run the actual analyses (up to now: Martine Hoogman, Maarten Mennes, Marcel Zwiers) and senior people looking into the design issues. This latter group should include clinicians to make sensible decisions on e.g., how to treat medication and comorbidity issues. We will gauge interest in active participation in this central support group via a poll.

4. **Which questions do we want to address as a group:**

The main question will be: Can we find differences in subcortical volumes comparing ADHD patients and controls?

Additional questions: Are there effects of age, gender, comorbidity, subtype, and medication on subcortical volumes? Are there effects of development (longitudinal analysis)? Are the effects obserced quantitative in nature and extend to ADHD symptoms in the general population?

The first paper for this initiative should address the main question and possibly one or two secondary questions (to be decided yet). All the other questions can be studied in subsequent papers. To address the main question well (and acknowledge the content of other meta-analyses already in the literature), effects of medication should already be included.

5. **Procedure, distribution of tasks and timelines**

The following procedure was presented:

I. To maximize homogeneity, the preferred method to segment the subcortical volumes is FreeSurfer, for people who still have to start segmentation (version 5.3); if segmentation has been performed already with another version of FreeSurfer or with FSL-First and people are not able to resegment, we will also be able to include those datasets. This is based on the possibility to extend to cortical volumes in the future. We will make use of the protocols of ENIGMA available on their website. The current ENIGMA protocols were written for version 5.1 but are easily transformed to version 5.3.

*Note: ENIGMA website is down for now given a move of the Loni group, new link will distributed asap.*

II. It was discussed whether to share summary data of each site for given volumes or to share volumes of individual samples with relevant covariates. Sharing individual volume results will increase the possibilities for analysis and better guard against outliers and low quality data. We decide to do a poll to probe the view of the working group members on this issue.

III. Data will be stored in a secure SQL database at the Donders Centre for Cognitive Neuroimaging in Nijmegen.

IV. QC will be performed by the central support group of the working group based on ENIGMA's protocols.

**6. Ideas for future projects/papers (e.g. cortical analyses/genetics/……)**

Ideas for cortical analysis, influence of environmental factors, endocrine effects, translation to general population symptom scores.

**Points of action:**

A Google form will be made to get a good overview of the cohorts and decide on the issues mentioned above. Included in the form:

- Which segmentation method have you used or are you intending to use, are you prepared to resegment to increase homogeneity of the sample? What is the estimated timeline if you have not segmented yet (possible before Christmas 2013)?
- Are you willing and able to share the subcortical volumes per subject, or just the summary data?
- Who is interests in which additional analyses (e.g., environmental data, endocrine data, genetics) and has data for such work?
- Who wants to be actively involved in the central support group and what is your specific expertise etc?

To be decided based on the info from the Google form:

- How to deal with summary versus individual data
- Segmentation procedure homogeneity
- Timeline