



Summary of the MAQC March-23-2006 Teleconference

The MAQC Project: Calibrated RNA Samples, Reference Datasets, and QC Metrics/Thresholds for Microarray Quality Control

Teleconference Date: March 23, 2006 (9 am PST/11 am CST/12 pm EST/17:00 GMT)
Summary Date: March 27, 2006
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MAQC Website: <http://edkb.fda.gov/MAQC/>

1. “12,091” mapping table based on Mar-8-06 RefSeq (Damir):
 - Truly one-to-one: one gene, one NM, and one probe(set) ID per row; No repeating gene ID, NM, or probe(set) ID; File name: `one_to_one_mapping.zip`.
 - Data files (full rows and 12,091 rows) are ready for download at the MAQC site; File name: `uniform_MAQC_data.zip`.
 - All manuscript teams should use this mapping table and the data files for cross-platform data comparison. It is also agreed that the same set of 12,091 data points should be used for inter-site comparison for the platform. However, individual manuscripts may extend the comparison to the entire microarray contents. Data analysis sites are encouraged to cross-check the data to ensure that no clerical errors are introduced.
 - GEH decided that no offset value should be added to its data; the offset value of 0.3 added to each data point in the distribution of `V2_norm_GEH` has been removed in the `uniform_MAQC_data.zip`.
 - Leming acknowledged the contributions of Rick and his groups in pushing forward the one-one mapping table.
2. The very first drafts of manuscripts have been distributed among manuscript teams on Mar-19-2006 (Leming):
 - Suggestion: If you want your ideas and favorite analysis methods to be considered for inclusion in a manuscript, please conduct your own data analysis, generate figures/tables, write texts, and then send them to the MS Team Leader for consideration.
 - Sending your feedback to MS Team Leaders by Mar-31.
 - Next deadline: Apr-10-2006 (2nd version for internal review by many contributing organizations).
3. Convention for fold change calculation (Leming):

All manuscript teams should follow the same convention for fold change calculations: B/A (not A/B); C/A; D/A; C/B; D/B; and D/C.
4. Consistency of terminologies for MAQC publications (Rich):

Janet Warrington suggested that MAQC manuscript teams would as much as possible adhere to those definitions and use of terms recognized by ISO and other authoritative bodies that are recognized by the clinical and research laboratory community. The CLSI

website has a very useful and user-friendly Harmonized Terminology Database that cross references terminology from a number of authoritative sources including ISO. The web address is <http://www.clsi.org>. It is always a good place to start. Thanks to Janet for the great suggestion.

5. CHI QPCR panel discussion, Mar-20-06 (Shawn Baker, Kathy Lee, Yuling Luo, Leming Shi, Jim Willey, and Paul Wolber): PowerPoint presentation slides have been posted at MAQC web site: <http://edkb.fda.gov/MAQC/>.

6. Others:

On March 16, 2006, the FDA unveiled Critical Path Opportunities List (<http://www.fda.gov/oc/initiatives/criticalpath/>) outlining blueprint to modernizing medical product development by 2010. Biomarker development and clinical trial design are greatest areas for impact. “*Standards for Microarray and Proteomics-Based Identification of Biomarkers*” was listed as the 2nd of the 76 opportunities.

Next Teleconference:

Thursday, April 6, 2006 (9 am PST / 11 am CST / 12 pm EST / 17:00 GMT)

USA Toll Free Number: **888-566-5020**; International caller: +1-210-795-9594

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