

Real-time PCR Data Markup Language

A new standard for archiving and exchanging real-time PCR data



Steve Lefever
On behalf of the RDML consortium



qPCR = golden standard for nucleic acids quantification Dedicated and precise instruments needed



Different software/output format for each instrument/manufacturer



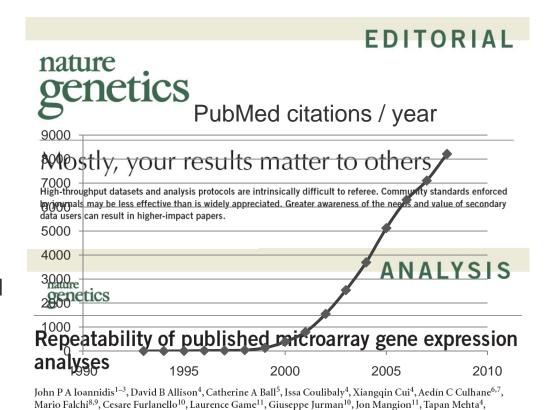
Limits possibility to exchange and reanalyse data







Genetics



Michael Nitzberg⁵, Grier P Page^{4,12}, Enrico Petretto^{11,13} & Vera van Noort¹⁴

► History of RDML



- Birth on September 1st 2005 Jan Hellemans
- 2005 2007 : Open discussion about RDML
- January 1st 2008 : start of the RDML consortium
- April 1st 2008 : RDML joins MIBBI
- January 12th 2009 : RDML paper accepted in Nucleic Acid Research

Nucleic Acids Research, 2009, 1–5 doi:10.1093/nar/gkp056

SURVEY AND SUMMARY

RDML: structured language and reporting guidelines for real-time quantitative PCR data

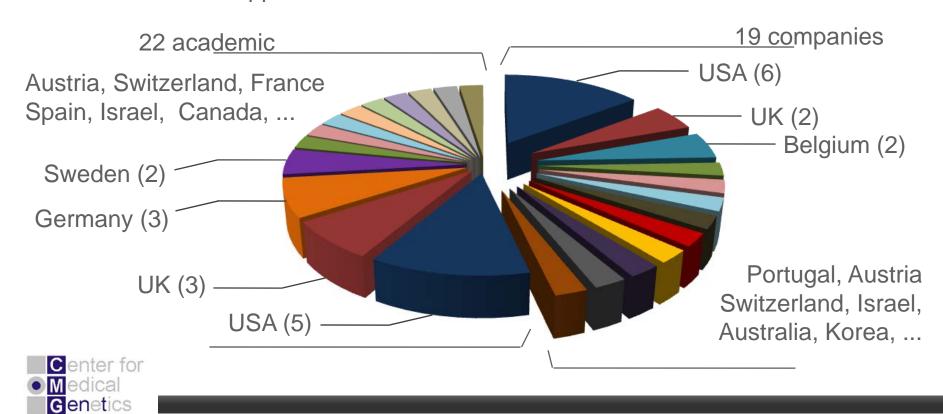
Steve Lefever¹, Jan Hellemans^{1,*}, Filip Pattyn¹, Daniel R. Przybylski², Chris Taylor³, René Geurts⁴, Andreas Untergasser⁴ and Jo Vandesompele¹, on behalf of the RDML consortium



► RDML consortium



- Develops and maintains the RDML data exchange format
- Key developer group, a member community and supporters
- 41 supporters and members from 20 different countries





 <u>M</u>inimum <u>Information for <u>B</u>iological and <u>B</u>iomedical <u>Investigations</u>
</u>

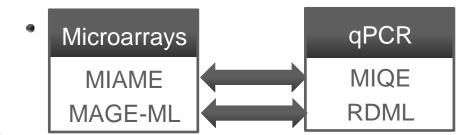


- http://www.mibbi.org
- Published in August 2008 by Nature Biotechnology



Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project

RDML adopted as standard for qPCR experiments





▶ What is RDML?



- RDML = Real-time PCR Data Markup Language
- Universal format to store and exchange qPCR data
- Structured
- Based on XML
- Platform independent
- Easy to extend
- Small RDML files

instrument software

TOK TOK

colleagues collaborators public repositories journals

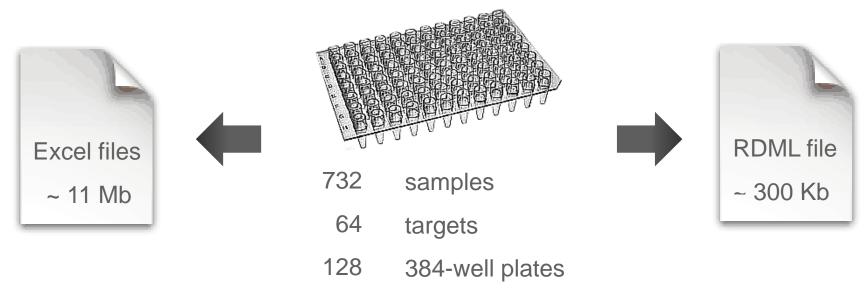
third party software databases



▶ What is RDML? ▶ File size reduction



- Vermeulen et al.
- Prognostic gene study in neuroblastoma







- e<u>X</u>tensible <u>M</u>arkup <u>L</u>anguage
- Language to store data in a structured manner
- Defines elements delimited by opening and closing tags
- Easily extensible

```
<gene>
     <symbol>actb</symbol>
     <function>muscle contraction</function>
     <location>chromosome 7: 5533308-5569941</location>
</gene>
```





List of Id's

List of experimenters

List of targets

List of samples

List of protocols

Documentation

Experiments

Runs

Reactions

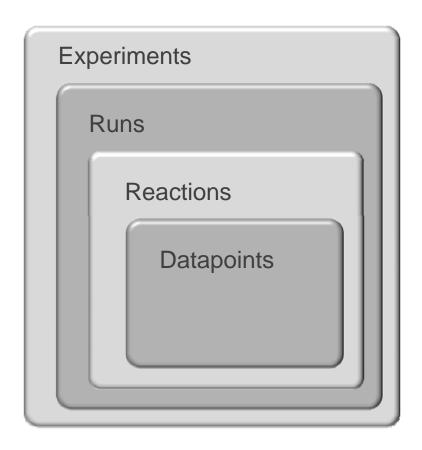
Datapoints

annotation —/ ___ qPCR data





- qPCR data
- Experiment annotation
- Multiple experiments per file
- Standard vocabulary (MIQE)
 - reaction
 - Cq







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 Accession numbers for online repositories or journals





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Contact information of experimenters





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- Target annotation
- Oligonucleotide sequences





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- Sample annotation
- cDNA synthesis





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Documentation

Any type of protocol





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Documentation

Additional information



▶ RDML supporting software





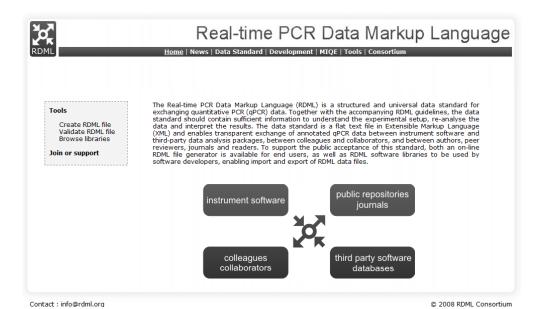
- · qbase Plus
- Under development:
- **Primer3Plus**
- RDML viewer and editor



More to come







- www.rdml.org
- Tool for creating RDML files
- Tool for converting RDML file to .csv files
- Libraries in Java, C, .NET and PHP



▶ RDML demonstration



- Online generation of an RDML file
- Importing the RDML file in qBasePlus for analysis
- Convert RDML file into .csv files



▶ Conclusion



- Data standard for qPCR data
- Universal and extensible
- Easy exchange of data
- Broad acceptance by community
- Submit data in RDML format to journals
- www.rdml.org







- The RDML consortium
- Jo Vandesompele
- Jan Hellemans
- Filip Pattyn
- Andreas Untergasser
- Daniel Przybylski

