

RDML

Real-time PCR Data Markup Language

Discussion forum

qPCR instruments

Applied Biosystems

- ABI5700
- ABI7000
- ABI7300
- ABI7500
- ABI7700
- ABI7900
- StepOne

Biogene

- InSyte

Bioneer

- Exicycler

BioTrove

- OpenArray NT Cyclor

Bio-Rad

- Opticon
- Opticon 2
- MiniOpticon
- Chromo4
- iCycler
- MyiQ
- iQ5

Cepheid

- SmartCycler
- GeneXpert

Corbett Research

- Rotor-Gene 2000
- Rotor-Gene 3000
- Rotor-Gene 6000

Eppendorf

- Mastercycler ep realplex

Fluidigm

- BioMark

Roche

- LightCycler 1.5
- LightCycler 2
- LightCycler 480

Stratagene

- Mx3000P
- Mx3005P
- Mx4000

Techne

- Quantica

qPCR software

Instrument software

Academic software

- BestKeeper
- DART-PCR
- geNorm
- Normfinder
- qBase
- qCalculator
- qPCR DAMS
- Q-Gene
- REST (# versions)

Biogazelle

- qBasePlus

Bio-Rad

- Gene expression macro (GENEX)

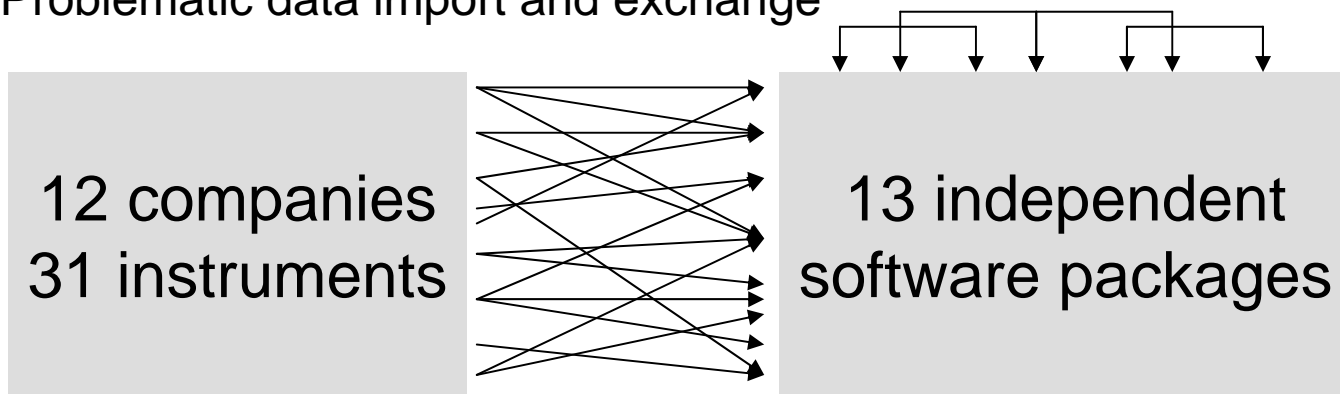
Multid

- GenEx

Metralabs

- SoFar

- **Stick to instrument software?**
 - Restricted to data from a single instrument
 - Limited data processing / visualization options
- **Data processing in spreadsheets?**
 - Time consuming & error prone
 - Knowledge on equation required
- **Use alternative software packages?**
 - Wider spectrum of calculation options & visualizations
 - Instrument independent
 - Problematic data import and exchange



qBase: best effort for data compatibility - exchange

■ Formats

- 15 – 20 formats supported
- Lacks support for at least 10 instrument formats
- No perfect support

■ Effort

- 2700 SLOC → 8 to 9 months of programming & debugging

■ Problems

- Based on interpretation (not specifications) of the different formats
- New instruments and data formats

Solution: universal qPCR data format

- Exchange of
 - Raw data
 - Run & well annotation
 - Calculation method and settings
 - Results
- Exchange between
 - Instrument software
 - Spreadsheets
 - Data analysis software
 - Data management software
 - Experimenters
 - Scientific journals
- Advantages
 - Time saving
 - Error prevention
 - Freedom of choice for
 - Instruments
 - Software
 - Collaborations
 - Peer review

RDML: Real-time PCR Data Markup Language

- First proposed
 - Freising 2005
- Supported by
 - T. Bar (LabonNet)
 - A. Forootan (MultiD)
 - M. Kubista (TATAA Biocenter)
 - M. Pfaffl (GeneQuantification Editor, TATAA Biocenter)
 - P. Scott Adams (Core facility director)
 - H. Srere (Bio-Rad)
 - # people in academia

RDML: Real-time PCR Data Markup Language

- Way ahead
 - Discuss RDML at the third international qPCR meeting (Freising 2007)
 - Publish the RDML specifications
 - Request / create / require support for RDML

RDML discussion topics

1. Scope?
2. Required or optional content?
3. Free text or predefined values?
4. Terminology?
5. How to obtain broad acceptance of this standard?
6. Continue development in RDML working group?

3 min pause to read proposal

1. Data export from instrument software
2. (1) + annotation
3. Experiment data: grouping of (2)
4. (3) + experiment annotation
5. (4) + analysis settings
6. (5) + results
7. (6) + statistical analyses

RDML variants for the different levels?

- What is the minimum required information?

- **Predefined values**
 - Benefit exchangeability
 - What if new values are required?

- Cq (quantification cycle)
 - Ct, Cp, TOP
- Target
 - Use target in stead of gene
 - Reference targets
 - Targets of interest
- Sample types
 - Sample of interest
 - Standard
 - Negative control
 - Positive control

- Convince users, editors and companies of benefits
- Create converters
- Update programs with RDML import / export capabilities
- Convince journals to request qPCR data
 - See MIAME

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<http://groups.yahoo.com/group/RDML-format/>

<http://medgen.ugent.be/rdml/>