Age- and sex-specific pediatric LMS-Percentiles for Laboratory Parameters enabled by Data mining

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Data Note

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Abstract

Background:

Various laboratory parameters routinely measured in pediatric practice covariate with sex and age. Conventional reference intervals are not suitable to account for this variation. Here we demonstrate construction of continuous LMS percentile curves from routine laboratory data. This allows adequate adjustment for both sex- and age-dependent covariation in childhood.

Material and Methods:

Anonymized routine blood test results requested by primary health care physicians were collected, outliers excluded and LMS-models generated in R.

Results:

Percentiles for several biomarkers derived from a regional population were established in the 'LMS' framework and provided here for comparison with established reference ranges, discussion and, potentially, clinical use.

Conclusion:

The reference framework 'LMS' is well-known from pediatric growth charts and can also be used in laboratory medicine.

Introduction

Pediatric growth charts are reference sets of continuous LMS-percentile curves⁽¹⁾ for a range of essential age- and sex-related variables, e.g. anthropometric height, weight, head-circumference, and body-mass index. Growth curves represent important tools for pediatricians to longitudinally monitor child development in health and disease and visually track developmental status of patients⁽²⁾. Various laboratory parameters routinely measured in pediatric practice also covariate with sex and age⁽³⁾. However, pediatric percentiles curves for common laboratory parameters rarely exist. Here we demonstrate construction of continuous LMS percentile curves from routine laboratory data and deposit the underlying LMS-models.

Material

Data was acquired as anonymized routine test results for pertinent biochemical markers that vary with age and/or sex in childhood and adolescence, requested by primary health care physicians. Ethical approval was obtained from the Western Health Regional Ethics Committee, Norway (REK-vest/265205).

Construction of reference curves

Duplicate identities were removed and the chronologically first result per individual was retained. Likely outliers were excluded(4). Reference percentiles were modelled using the LMS algorithm provided in the 'gamlss' package in R(5). Model conformity to normality within acceptable skewness (L), mean (M), coefficient of variation (S) and kurtosis (K) was evaluated by Q-tests. Residual distribution was evaluated by z-score histograms, worm plots and detrend Q-Q plots(6).

Results

LMS reference curves applied to $\log(\text{biomarker} \times 10^6)$ data are visualized in attachment 1

Model name	Biomarker	Gender	Sample size	Method	SI unit
SSHFCREATININEF	Creatinine	Female	11570	Roche Cobas, enzymatic	μmol/L
SSHFCREATININEM	Creatinine	Male	9844	Roche Cobas, enzymatic	μmol/L
SSHFTCF	Total cholesterol	Female	6309	Roche Cobas	mmol/L
SSHFTCM	Total cholesterol	Male	5134	Roche Cobas	mmol/L
SSHFTSHF	TSH	Female	17502	Roche Cobas	mIU/L
SSHFTSHM	TSH	Male	12783	Roche Cobas	mIU/L
SSHFFT3F	Free T3	Female		Roche Cobas	pmol/L
SSHFFT3M	Free T3	Male		Roche Cobas	pmol/L
SSHFFT4F	Free T4	Female	18213	Roche Cobas	pmol/L
SSHFFT4M	Free T4	Male	7362	Roche Cobas	pmol/L
SSHFUAF	Uric acid	Female	7519	Roche Cobas	μmol/L
SSHFUAM	Uric acid	Male	5646	Roche Cobas	μmol/L
SSHFLDLF	LDL cholesterol	Female	10668	Roche Cobas	mmol/L
SSHFLDLM	LDL cholesterol	Male	8692	Roche Cobas	mmol/L
SSHFHDLF	HDL cholesterol	Female	9296	Roche Cobas	mmol/L
SSHFHDLM	HDL cholesterol	Male	7426	Roche Cobas	mmol/L
SSHFALPF	Alkaline phosphatase	Female	12964	Roche Cobas	U/L
SSHFALPM	Alkaline phosphatase	Male	9879	Roche Cobas	U/L
SSHFTGF	Triglycerides	Female	8727	Roche Cobas	mmol/L
SSHFTGM	Triglycerides	Male	7623	Roche Cobas	mmol/L

The underlying L,M,S-for-age entries are specified in attachment 2.

The normality Q-tests are specified in attachment 3.

Declarations

Conflict of Interest:

References

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Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Attachment1LMSreferencecurves.zip](#)
- [Attachment2LMSentriesjson.zip](#)
- [Attachment3LMSQtest.zip](#)