

# Database of sensory characteristics of older persons and persons with disabilities

## Graphical presentation of the data according to search criteria entered

We have constructed the “Database of Sensory Characteristics of Older Persons and Persons with Disabilities,” which displays the sensory characteristics of vision, hearing, and touch, according to search criteria such as age and types of disability. The data were measured at AIST for target groups with a total number of more than 3,000 people. Since these data on characteristics have been adopted as Japanese Industrial Standards (JISs), the database serves as a tool for displaying JIS contents graphically that were described using equations and tables. By referring to the database, product designers can make products more accessible for various types of people including older persons and persons with disabilities. Japanese and English versions of the database have been released to the public on the Web (<http://scdb.db.aist.go.jp/?lng=en>) from August 19, 2013. The data can be accessed and used free of charge as long as they comply with the conditions of use.

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AIST TODAY Vol.14 No.1 p.14 (2014)

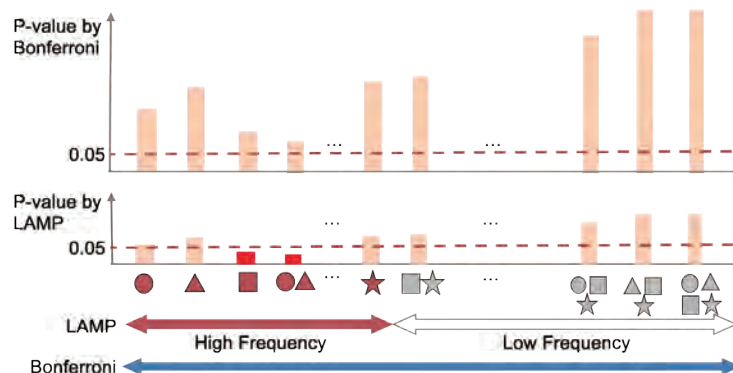
An example of database display:  
Estimation of minimum legible font size



# Novel statistical methods for discovery from big data

## Wide applicability in all experimental life sciences

More than three transcription factors often work together to enable cells to respond to various signals. The detection of combinatorial regulation by multiple transcription factors, however, is not only computationally nontrivial but also extremely unlikely because of multiple testing corrections. The exponential growth in the number of tests forces us to set a strict limit on the maximum arity. We developed a novel statistical test called LAMP (limitless-arity multiple testing procedure). LAMP counts the exact number of testable combinations and calibrates the Bonferroni factor to the smallest possible value. LAMP lists significant combinations without any limit, while the family-wise error rate is kept under the threshold. In the human breast cancer transcriptome, LAMP discovered statistically significant combinations of as many as eight binding motifs.



**Comparison between LAMP and the existing method**  
Combinatorial factors shown in red are regarded as discovery.

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AIST TODAY Vol.14 No.1 p.15 (2014)