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COMMENTARY

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MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment

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The need for metadata standards for microbe sampling in the built environment

The composition of indoor microbial communities has the potential to profoundly affect human health. A number of factors within a building or room can alter the microbial abundance and diversity, such as occupancy, temperature and humidity, which in turn impacts indoor air quality. Researchers Hospodsky et al. (2012); Kembel et al. (2012) and Dunn et al. (2013) are exploring the intersection of microbial ecology, building materials and architectural design to understand microbial diversity and abundance within a building. Metadata (data describing data) provides an essential complement to experimental data, helping to answer questions about its source, mode of collection and reliability. As the impact and prevalence of large-scale metagenomic surveys grow, so does the need for more complete and standards compliant metadata. While marine (Gilbert et al., 2012), soil and the human microbiome environments have representation in the standards being developed the built environment (BE) represents a unique context in need of standards development for the use in the study of microbial sequences. Metadata collection and interpretation have become vital to the genomics and metagenomics community to share information and integrate data across resources and within data repositories. The Genomic Standards Consortium (GSC, http://gensc.org; Field et al. (2011)) has developed widely accepted metadata MIxS (MIGS, MIMS, MIMARKS; Yilmaz et al. (2011)) standards for genomic, metagenomic and amplicon (for example, 16S rRNA) sequence data sets. These standards have been developed within a framework that is both modular and extensible. The MIxS-BE, as a minimal metadata standard, represents a unique extension to the GSC's MIxS standard as a rigorous and structured tool for the analysis of microbial ecosystems of the sequences and indoor

environment. The MIxS-BE package provides the BE community with a suggested list of parameters to record and report for each sequenced sample and to compare data across studies. The MIxS-BE standard incorporates the core set of required MIxS fields for a bacterial sequence along with a Built Environment (BE) package (http://gensc.org/index.php?title=MIx-S_extensions) comprised of a BE core, MIxS air environmental package terms, BE building properties and BE sample properties. The MIxS-BE package has been incorporated into the MIxS checklist and integrated into the QIIME (Caporaso et al., 2010), MoBeDAC and MG-RAST (Meyer et al., 2008) databases to foster metadata submission compliance across BE projects. Updates to the MIxS specification will be included in BioSample (Barrett *et al.*, 2012) as part of the annual MIxS release. Requests for additions or changes to the MIxS checklists can be directed to the GSC Developers mailing list: developers@gensc.org or by contacting Lynn Schriml or Elizabeth Glass.

Development of the MIxS-BE package has been an open and iterative process engaging the GSC community, the GSC's MIxS developers, stakeholders across the BE community including microbial ecologists, microbiologists, architects and engineers. The Microbiology of the Built Environment Alfred P. Sloan funded initiative established a metadata working group as part of the MoBeDAC, bringing together Sloan-funded researchers, architects, civil engineers, bioinformaticists and computational biologists to discuss the need and context for standards to describe the most relevant metadata to be collected for BE samples. Led by Elizabeth Glass and Lynn Schriml, the working group proposed the development of the BE-MIxS package to the GSC and gained the GSC's board approval to develop the standard. The working group initially identified a comprehensive list of metadata terms reported in BE literature. Based on feedback solicited from industry experts and microbial ecologists, the working group established a minimal set of metadata terms for the BE package environment samples with a subset of the MIxS-BE terms classified as M (Mandatory),
 Table 1
 MIxS-BE
 metadata
 package
 terms

MIxS-BE term

Carbon dioxide^a Ventilation type^a Organism count^a

BE core Surface material Surface-air contaminant Relative air humidity Absolute air humidity Surface humidity Air temperature Surface temperature Surface moisture pH Surface moisture Dew point Building occupancy type

- BE Building properties Indoor space (room type) Indoor surface Filter type Heating and cooling system type Substructure type Building setting Light type
- BE Sample properties Sample size sorting method Space typical state Typical occupant density Occupancy at sampling Occupant density at sampling

Terms, definitions, required or optional status (for reporting compliance) and syntax are presented at: MIxS project, (http://gensc.org/gc_wiki/images/7/70/Built_environment-metadata-termsv51.xls).

^aThe MIxS-BE package includes MIxS-air environmental package terms and the built environment core, building and sample property terms.

which indicates that the term has to be reported for the metadata to be considered compliant to the MIxS checklist. The MIxS-BE minimal set will be complemented by a MIxS-BE-Building package (under development) describing the larger set of building and room metadata pertinent to describing a BE sample (Table 1).

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References

- Barrett T, Clark K, Gevorgyan R, Gorelenkov V, Gribov E, Karsch-Mizrachi I *et al.* (2012). BioProject and Bio-Sample databases at NCBI: facilitating capture and organization of metadata. *Nucleic Acids Res* **40**: Database issue D57–D63.
- Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK *et al.* (2010). QIIME allows analysis of high-throughput community sequencing data. *Nat Methods* **7**: 335–336.
- Dunn RR, Fierer N, Henley JB, Leff JW, Menninger HL. (2013). Home life: factors structuring the bacterial diversity found within and between homes. *PLoS One* 8: e64133.
- Field D, Amaral-Zettler L, Cochrane G, Cole JR, Dawyndt P, Garrity GM *et al.* (2011). The Genomic Standards Consortium. *PLoS Biol* **9**: e1001088.
- Gilbert JA, Steele JA, Caporaso JG, Steinbrück L, Reeder J, Temperton B *et al.* (2012). Defining seasonal marine microbial community dynamics. *ISME J* **6**: 298–308.
- Hospodsky D, Qian J, Nazaroff WW, Yamamoto N, Bibby K, Rismani-Yazdi H *et al.* (2012). Human occupancy as a source of indoor airborne bacteria. *PLoS One* **7**: e34867.
- Kembel SW, Jones E, Kline J, Northcutt D, Stenson J, Womack AM *et al.* (2012). Architectural design influences the diversity and structure of the built environment microbiome. *ISME J* **6**: 1469–1479.
- Meyer F, Paarmann D, D'Souza M, Olson R, Glass EM, Kubal M *et al.* (2008). The metagenomics RAST server—a public resource for the automatic phylogenetic and functional analysis of metagenomes. *BMC Bioinformatics* **9**: 386.

Yilmaz P, Kottmann R, Field D, Knight R, Cole JR, Amaral-Zettler L *et al.* (2011). Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. *Nat Biotechnol* **29**: 415–420. This work is licensed under a Creative Commons Attribution 3.0 Unported License. To view a copy of this license, visit http://creativecommons.org/licenses/ by/3.0/