genomeRxiv: a microbial whole-genome database for classification, identification, and data sharing

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1. We need a stable, genome-based classification system for microbes

The mapping of traditional taxonomic nomenclature to the history revealed through genome analysis is not exact, leading to significant challenges:

Genomic disagreement with nomenclature
genome-based classifications do not always agree with published taxonomies [1]

Genome-based classifications resolve novel taxa
genome-based classifications produce highly-resolved taxa at levels that are not represented in prokaryotic taxonomy [2]

Inaccuracies in reference databases
a significant minority of genomes in public databases are misidentified [3]

Our goal is to build ***genomeRxiv***, a "preprint genome server" that provides:

A stable, taxonomy-independent classification scheme
a transparent, quantitative "co-ordinate" scheme in sequence space, with fine-grained resolution (LINs… see right)

Genome-based quantitative identification
precise, secure and confidential taxonomy-independent classification of submitted microbial genomes

Candidate diagnostic markers
practical molecular diagnostic tools targeted at precise groups of microbial genomes

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2. *genomeRxiv*

genomeRxiv will provide a service for rapid, quantitative classification of microbial genomes using **Life Identification Numbers (LINs)**, extending the existing **LINbase** service.

LINs work like map co-ordinates in sequence space. Degrees of genome sequence identity are marked with letters (e.g. A-T as in **Figure 1**; example in **Figure 2**), and numeric symbols assigned to indicate a particular grouping of genomes sharing at least that degree of identity with each other.

This string of numeric symbols precisely locates each genome in a region of sequence space. For example, in Figure 1 the LIN $0_A1_B0_C0_D0_E3_F$ circumscribes species *G1 s2*.

			70%	75%	80%	85%	90%	95%	96%	97%	98%	98.5%	99%	99.25%	99.5%	99.75%	99.9%	99.925%	99.95%	99.975%	99.99%	99.999%
Genus	Species	Strain	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
G1	S1	X1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G1	S2	X2	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G1	S2	X3	0	1	0	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0
G1	S3	X4	0	1	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G1	S3	X5	0	1	0	0	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0
G1	S3	X6	0	1	0	0	0	4	1	0	0	0	0	0	0	0	1	0	0	0	0	0

Figure 1. Each LIN position (A-T) represents an average nucleotide identity (ANI) threshold, ranging from 70% (A) to 99.999% (T). The more similar two genomes are, the further to the right their LINs match.

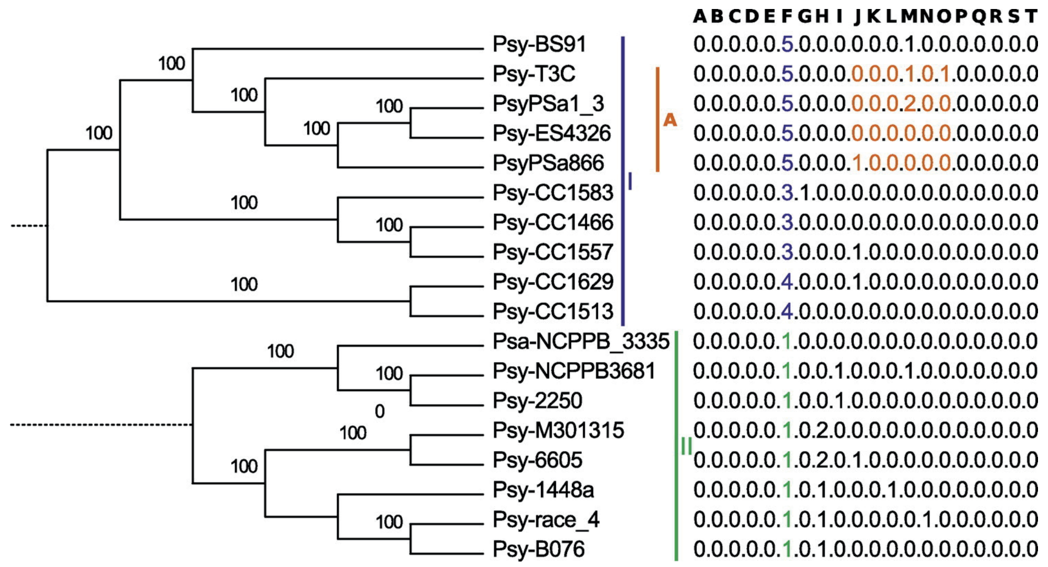

Figure 2. Two clades of *Pseudomonas syringae sensu lato*, showing assignment of LINs (from Vinatzer et al. (2017))

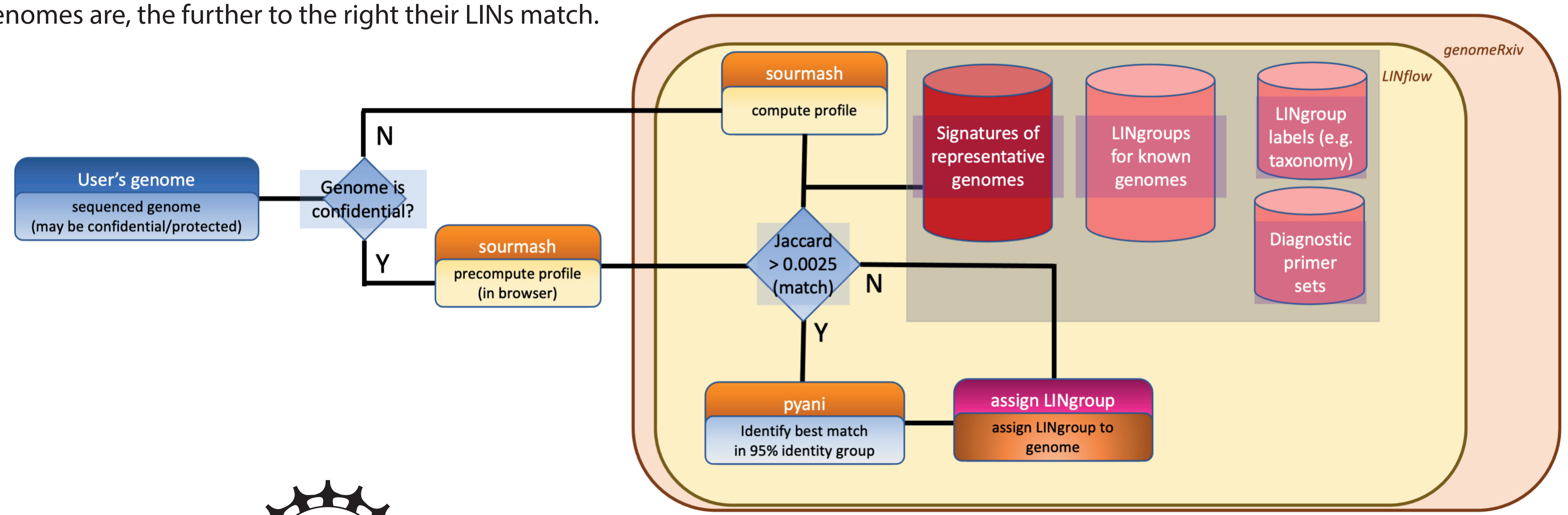

Figure 3. Flowchart of LIN assignment (**LINflow**). The user submits a sequenced genome, which is translated into a **sourmash** profile (in the browser if the genome is confidential). The profile is compared against a set of representative genome profiles. If a match is found, the best-matching genome is selected for ANI (**pyani**) comparison and a new LIN assigned; if not, a new LIN is assigned directly. Adapted from Tian *et al.* (2021)

3. More Information

The genomeRxiv project is at an early stage. We invite you to follow its development and learn more about the underlying technologies at the links below:

Vinatzer *et al.* (2017) *Phytopathology*
https://doi.org/10.1094/phyto-07-16-0252-r
Proposal for LINs

Tian *et al.* (2021) *PeerJ*
https://doi.org/10.1094/phyto-07-16-0252-r
LINflow computational pipeline

https://code.vt.edu/linbaseproject
LINbase repository

https://sourmash.readthedocs.io/en/latest/
sourmash documentation; MinHash-based classification

https://github.com/widdowquinn/pyani
pyani repository; ANI-based classification

https://github.com/widdowquinn/find_differential_primers
pdp repository; diagnostic primer prediction

References

[1] Pritchard *et al.* (2016) *Analytical Methods* doi:10.1039/c5ay02550h

[2] Rodriguez-R *et al.* (2018) *Nuc. Acids Res.* doi:10.1093/nar/gky467

[3] Varghese *et al.* (2015) *Nuc. Acids Res.* doi:10.1093/nar/gkv657