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Developing New Tools for the Old Tree of Life

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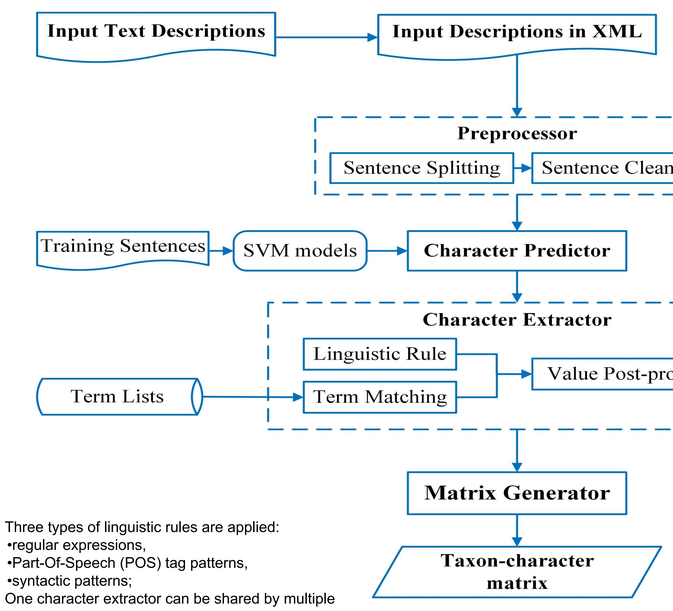
NSF AVAToL: Next Generation Phenomics for the Tree of Life
http://avatol.org/ngp/

Abstract

Millions of species reside in the Tree of Life, making the task of resolving the evolutionary origin of many organisms difficult. Biologists draw on genetic and phenotypic information to sort the Tree of Life, but the study can be slow and complex. Phenomic data (such as cell shape, metabolism and ecology), particularly for microorganisms, is often found in scientific publications and has little digital presence outside of being scanned into an online database. This has been aided by a new text mining computer program, MicroPIE (Microbial Phenomics Information Extractor), that sifts through relevant phenomic data and creates a matrix of key phenomic characters taken from the published descriptions. MicroPIE utilizes multiple natural language processing tools to extract data, along with the knowledge of microbiologists to help with developing and verifying the tools. One major challenge to building such a tool is the time it takes to collect and edit phenomic data for tens of thousands of sentences needed to develop a functioning program. We have helped to further the development of MicroPIE to identify new characteristics by providing sentences from published microbial descriptions. We also are creating a "Gold Standard" matrix (GSM) of phenomic information for 100 different bacteria that can then be compared to the MicroPIE output in order to test that MicroPIE has correctly identified and extracted phenomic information. So far MicroPIE has shown potential to aid in resolution of the microbial Tree of Life.

Development and System Architecture of MicroPIE Algorithm

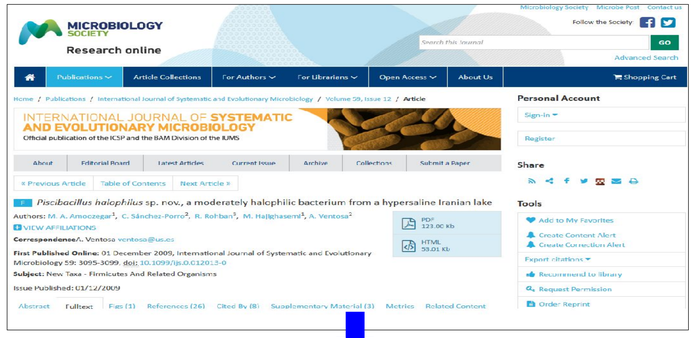


Three types of linguistic rules are applied:
- regular expressions,
- Part-Of-Speech (POS) tag patterns,
- syntactic patterns;

One character extractor can be shared by multiple extractors.

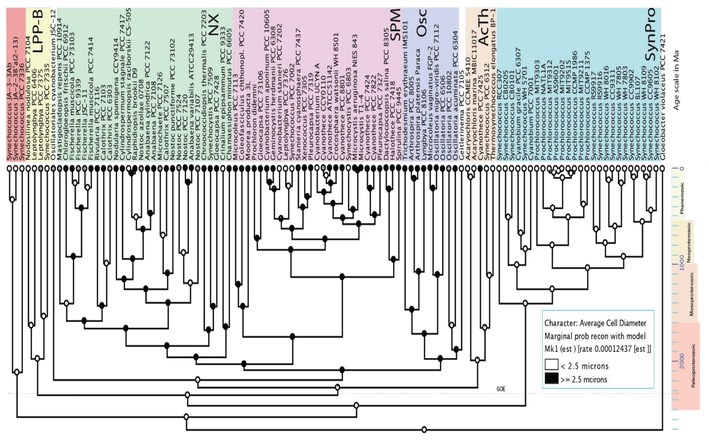
Visual Map of Workflow Used to Improve GSM v2 for MicroPIE

Example of Collecting and Formatting Publications for Use in MicroPIE



Author: M. A. Amoozegar, C. Sánchez-Porro, R. Rohban, M. Hajighasemi, A. Ventosa
Year: 2009
Title: *Piscibacillus halophilus* sp. nov., a moderately halophilic bacterium from a hypersaline Iranian lake
Journal (doi): 10.1099/ijs.0.012013-0
Genus name: Piscibacillus
Species name: Halophilus
Accession#: FM864227
Morphology: Cells are Gram-positive, motile rods (0.5–0.7×2.5–4.0 μm). Cells produce oval endospores terminally positioned within swollen sporangia. Colonies are circular, entire, smooth, cream in colour and 2 mm in diameter on 10% HM agar medium after 48 h incubation at 35 °C. Facultatively anaerobic. Moderately halophilic. The optimum NaCl concentration for growth is 10% (w/v), with a range of 1–20% (w/v) NaCl for growth. No growth occurs in the absence of NaCl. Growth is observed at 15–55 °C (optimum at 35 °C) and at pH 7.0–10.0 (optimum at pH 7.5). Catalase- and oxidase-positive. Indole and H2S are not produced. Gelatin, casein, aesculin, and Tweens 20, 40, 60 and 80 are hydrolysed. Starch and DNA are not hydrolysed. Nitrate is not reduced to nitrite. Acid is not produced from d-glucose, d-fructose, galactose, lactose, maltose, melibiose, d-mannose, trehalose, d-xylose or *myo*-inositol. Methyl red, Voges–Proskauer, urease, *β*-galactosidase, lysine and ornithine decarboxylase, arginine dihydrolase and phenylalanine deaminase tests are negative. The following compounds are not utilized as sole source of carbon and energy: d-fructose, galactose, d-glucose, lactose, maltose, d-mannose, melibiose, d-ribose, sucrose, glycerol, *myo*-inositol, alanine, arginine, asparagine, cysteine, glycine, leucine, lysine, methionine, proline and valine. Sensitive to carbenicillin (100 μg), nitrofurantoin (300 μg), tetracycline (30 μg) and rifampicin (5 μg). Resistant to amoxicillin (30 μg), gentamicin (30 μg), tobramycin (10 μg), kanamycin (30 μg) and polymyxin B (100 U). Polar lipids are phosphatidylglycerol and diphosphatidylglycerol as well as two minor phospholipids. The isoprenoid quinone is MK-7. The peptidoglycan type is A1γ, with *meso*-diaminopimelic acid as the diagnostic diamino acid. Cellular fatty acids are anteiso-C15:0, iso-C15:0, anteiso-C17:0, iso-C16:0, iso-C17:0, iso-C14:0, C16:1 *ω7 c*, C16:0, C16:1 *ω11 c* and summed feature 4 (iso-C17:1 and/or anteiso-C17:1). The DNA G+C content of the type strain is 37.5 mol% (*T*$_m$). The type strain, HS224 ^{T} (=CCM 7596 ^{T}=DSM 21633 ^{T}=JCM 15721 ^{T}=LMG 24786 ^{T}), was isolated from the hypersaline lake Howz-Soltan in Iran.

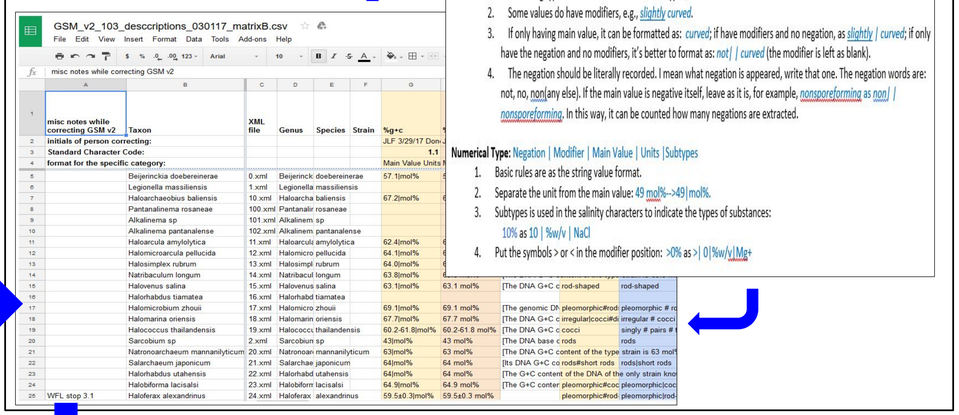
Example of Results From MircoPIE in Phenology Reclassification



Future Work

- Explore new methods for detecting extraction boundaries and for constructing linguistic rules automatically.
- Replace simple term lists with a new microbial ontology, MicrO (Blank et al. 2016).
- Expanding the variety of target characters for extraction.

Example of How Training Sentences were Corrected for Improving MicroPIE Algorithm



Progress Made on GSM for MicroPIE v1 and v2

Category Code	Category Label	Micropie V.1 Sentence Count	Minimal Number of Sentences Needed	Desired Number of Sentences	Micropie V.2 Sentence Count	Total Sentence Count
2.5	Cell relationships & aggregations	114	200	300	375	489
2.8	External features	136	200	300	190	326
2.12	Biofilm formation	4	100	200	4	4
2.13	Filterability	8	100	200	5	5
2.14	Lysis susceptibility	14	100	200	41	55
2.15	Cell division pattern & reproduction	12	100	200	24	36
3.11	Pressure preference	3	100	200	0	0
3.13	Magnesium requirement for growth	35	100	200	117	152
3.14	Vitamins/cofactors required for growth	164	300	500	97	261
3.17	Salinity preference	-	100	200	135	135
5.5	Film test result	24	100	200	3	27
5.6	Spot test result	17	100	200	0	0
6.1	Fermentation products	99	200	300	1464	1563
6.3	Methanogenesis products	53	100	200	0	53
6.4	Other metabolic product	169	300	500	762	931
8.1	Symbiotic relationship	1	100	200	8	9
8.3	Pathogenic	38	200	300	112	150
8.4	Disease caused	20	200	300	78	98
8.5	Pathogen target organ	21	200	300	67	88
8.6	Haemolytic&haemadsorption properties	76	200	300	147	223

References

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Cui H, 2012, CharaParser for fine-grained semantic annotation of organism morphological descriptions. Journal of American Society for Information Science and Technology 63(4): 738-754, doi:10.1002/asi.22618.

Vandamme P, Debruyne L, De Brandt E, Falsen E. Reclassification of Bacteroides ureolyticus as Campylobacter ureolyticus comb. nov., and emended description of the genus Campylobacter. Int J Syst Evol Microbiol. 2010; 60(9): 2016-22.

MicroPIE source code in GitHub (https://github.com/biosemantics/micropie2/tree/0.1.0).

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