

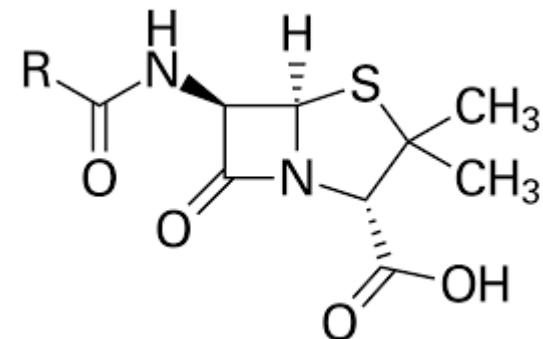
SMMole: Pipeline for searching biological properties of secondary metabolites based on their molecular structures

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PNP

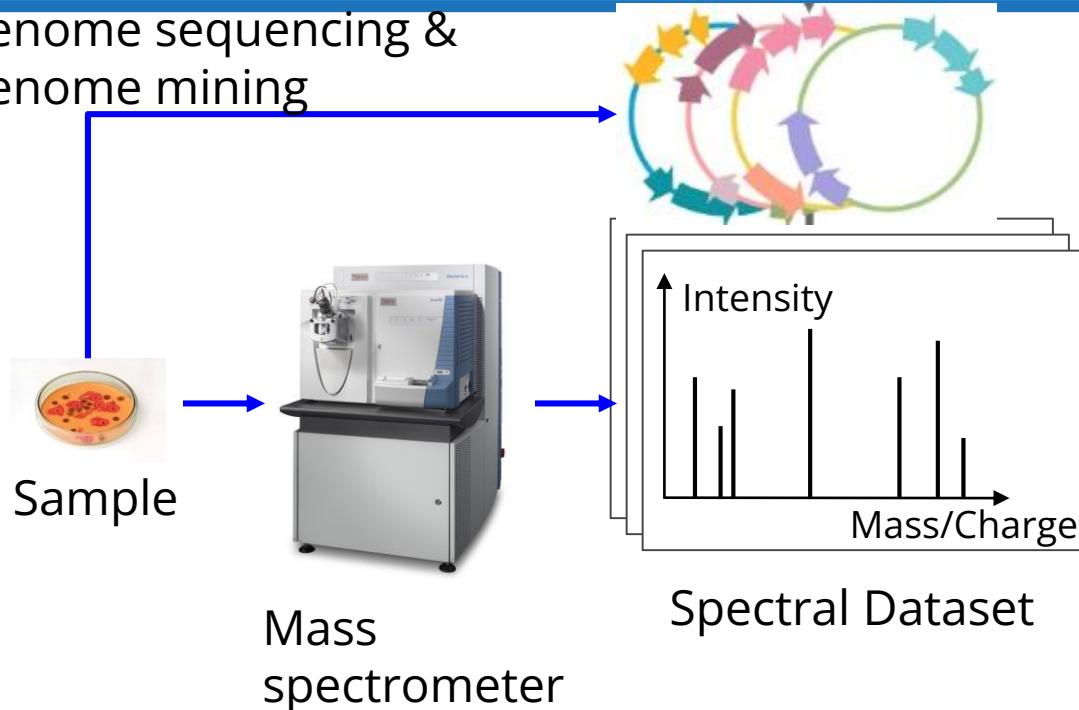
Peptidic Natural Products (PNPs):

- small bioactive peptidic molecules
- nonribosomal peptides (NRPs) and ribosomally synthesized and post-translationally modified peptides (RiPPs)
- promising compounds in the drug research (including antibiotics, antitumor agents, ...) (Dang & Süßmuth, 2017).



Genome-based MS search of PNPs

Genome sequencing &
Genome mining

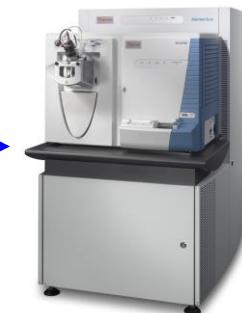


Genome-based MS search of PNPs

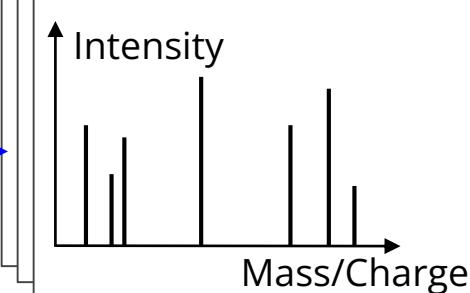
Genome sequencing &
Genome mining



Sample



Mass
spectrometer



Spectral Dataset

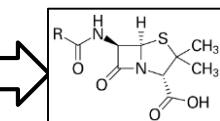
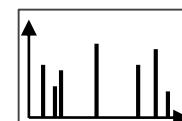
Structure prediction

Database of
putative PNPs



Many predicted
molecules

Identification



MetaMiner (Cao et al., 2019)

Current approaches & their limitations

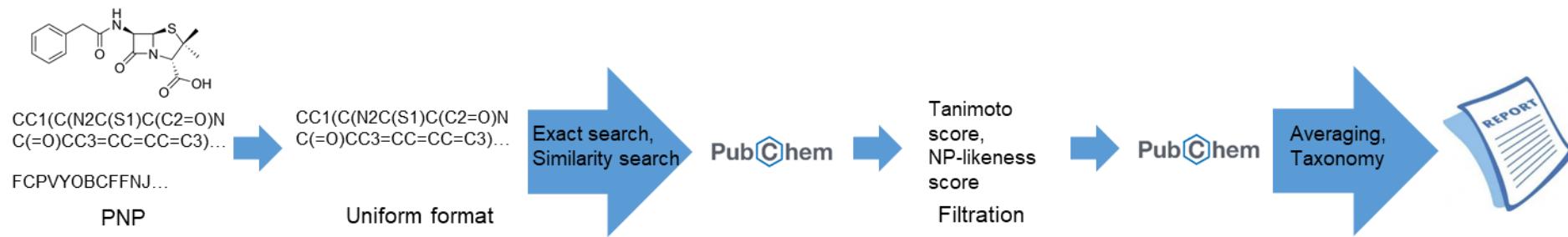
PASS (Filimonov et al., 2014)

- Commercial (or online only, one query per time, limited functionality)
- Should be retrained with new data available
- No taxonomy information

PubChem (Kim S et al., 2020)

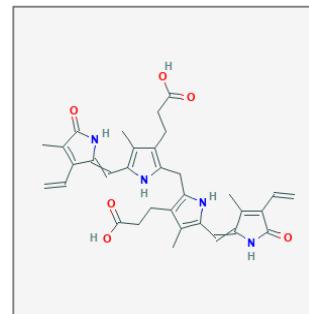
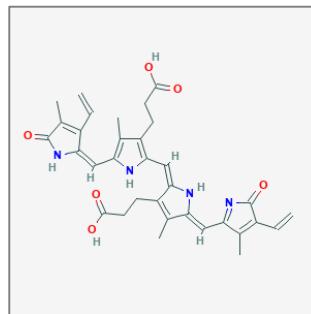
- Online only, thus not suitable for high-throughput analysis
- No predictions
- General purpose (both natural and synthetic compounds)

SMMole pipeline

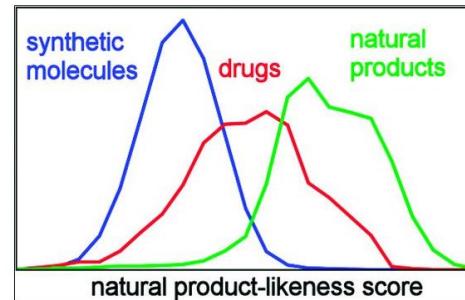


Python-based, with the use of

- RDKit
- PubChemPy
- Biopython
- requests



Tanimoto similarity (0.655)
(Kim et al., 2016)



NP-likeness
(Ertl et al., 2007)

Report example

EXACT match (Tanimoto == 100%)

Name	Azithromycin
Active (items):	310/4792
Tanimoto score	100.0 %
NP-likeness	1.85
Producer taxonomy	<i>Streptomyces lavendulae</i> (100.0 %)

SIMILAR compounds (100% > Tanimoto >= Threshold)

Name	Many hits (2)
Active (items):	809/10309 (min:110, max:699)
Tanimoto score	83.0 \pm 0.486 % (min:82.0 %, max:83.0 %)
NP-likeness	1.83 \pm 0.06 (min:1.77, max:1.89)
Producer taxonomy	<i>Streptomyces</i> (81.82 %)

Taxonomy processing

Producers of similar compounds:

Streptomyces hygroscopicus

Streptomyces lydicus

Streptomyces albidoflavus

Streptomyces platensis

Aeromicrobium erythreum

Predicted taxonomy:



Genus: *Streptomyces* (80%)

Results

- We tested SMMole on PNPs from MIBiG (Kautsar et al., 2019).

Total	Identified structure	Identified bioactivity	Running time (avg/total)
541	85.8 % (464)	55.8% (259 from 464)	4 min / 36 hours

- We plan to integrate SMMole with approaches to PNPs discovery: MetaMiner and NRPminer (Cao et al., 2019, Behsaz et al., 2021).
- SMMole output will help to prioritize *in silico* predicted PNPs for experimental validation and testing.

Thank you!

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