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Exploring the chemical space of post-translationally modified peptides in *Streptomyces* with machine learning

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Stellingen

propositions accompanying the thesis

Exploring the chemical space of post-translationally modified peptides in *Streptomyces* with machine learning

1. Machine learning can help solve biological problems, but its results cannot be blindly trusted (Chapter 3).
2. In order to find novel biochemistry, the boundaries laid down by high-confidence genome mining tools need to be stretched by more explorative methods (Chapter 2 and Chapter 3).
3. The discovery of a novel family of lanthipeptides supports the hypothesis that the chemical space of natural products is still far from exhausted (Chapter 4).
4. The fact that most BGCs need to be genetically engineered before their products can be detected, emphasizes the need for new methods to link BGCs to their products (Chapter 4 and Chapter 5).
5. RiPP genome mining should not be ruled by classifying RiPPs themselves, but rather by classifying their modifying enzymes.
6. Understanding the biological function of BGCs is just as important as identifying their products.
7. The dependence on large amounts of biological data creates a growing gap between experimental biologists and bioinformaticians.
8. The slow process of science is in strong contrast with how it is reported in the media.
9. The saying “A good chef can do it right, a great chef never does it wrong” does not apply to scientists.
10. The tendency to resolve stressful situations quickly can do more harm than good, as better solutions are found when we tolerate the stress and think more deeply about the problem (Based on “Creativity” by John Cleese).

12 mei 2021, Alexander Kloosterman