Metabolomics in community-acquired pneumonia: exploring metabolomics-based biomarkers for diagnosis and treatment response monitoring of community-acquired pneumonia

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Stellingen
Behorende bij het proefschrift

Metabolomics in community-acquired pneumonia
Exploring metabolomics-based biomarkers for diagnosis and treatment response monitoring of community-acquired pneumonia

1. Increasing the number of metabolites in a predictive model does not necessarily increase the performance of the model. *Chapter 2*

2. Exploratory analysis is a valuable first step to associate metabolic perturbations to immune processes. *Chapter 3*

3. Only if we understand how metabolites vary within a patient, between patients, and during disease, effective longitudinal biomarkers can be developed. *Chapter 4*

4. Network analysis can support the interpretation of immunometabolomics data and guide the design of prospective immunometabolomics studies. *Chapter 5*

5. The development of a clinically applicable biomarker assay requires multidisciplinary collaboration between patients, analysts, physicians, engineers, statisticians, and immunobiologists. *Inspired by Pinu et al., Metabolites, 2019.*

6. A healthy control group is not a necessity for developing a specific biomarker assay in hospitalized patients. *Inspired by Slupsky et al., Journal of Proteome Research, 2009.*

7. Clinical assays should include only the essential metabolites that provide valuable information to accomplish short turnaround times, minimal costs and ease of interpretation. *Inspired by Van der Laan et al., Analytical Chemistry, 2020*.

8. Sharing of samples, clinical data, and metabolomics data via biobanks and databases, is essential to speed up discoveries in the field of metabolic response to infectious diseases. *Inspired by Witting, Proteomics, 2023.*

9. We can't control the wind, but we can adjust the sails. *Unknown*

10. I can do things you cannot, you can do things I cannot; together we can do great things. *Unknown*

11. No Day But Today. *Rent*

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Leiden, 17 september 2024