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Type: **Oral presentation**

## **Modeling and predicting the overlap of B- and T-cell receptor repertoires in healthy and SARS-CoV-2 infected individuals**

*mercredi 2 novembre 2022 10:00 (15 minutes)*

Adaptive immunity's success relies on the extraordinary diversity of protein receptors on B and T cell membranes. Despite this diversity, the existence of public receptors shared by many individuals gives hope for developing population wide vaccines and therapeutics. Yet many of these public receptors are shared by chance. We present a statistical approach, defined in terms of a probabilistic V(D)J recombination model enhanced by a selection factor, that describes repertoire diversity and predicts with high accuracy the spectrum of repertoire overlap in healthy individuals. The model underestimates sharing between repertoires of individuals infected with SARS-CoV-2, suggesting strong antigen-driven convergent selection. We exploit this discrepancy to identify COVID-associated receptors, which we validate against datasets of receptors with known viral specificity. We study their properties in terms of sequence features and network organization, and use them to design an accurate diagnosis tool for predicting SARS-CoV-2 status from repertoire data.

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**Classification de Session:** Oral Presentations (first in the morning)