## Complex Neoantigen Prediction in Cancers: Leveraging Deep Learning to Unravel Tumour-Immune Interactions

## Introduction:

Cancer, a complex and multifaceted disease, poses a significant global health burden. Immunotherapy, harnessing the body's immune system to fight cancer, has emerged as a promising treatment option. However, its efficacy remains limited by incomplete understanding of tumour-immune interactions and challenges in identifying patients who will respond. Neoantigens, peptides arising from somatic mutations unique to cancer cells, are crucial targets for the immune system. Identifying and prioritizing immunologically relevant neoantigens is key to personalizing immunotherapy and improving patient outcomes.

Currently, neoantigen prediction relies on traditional methods with limitations in capturing complex mutations and personalized HLA binding affinities. Additionally, integrating diverse data types like NGS omics and patient-specific HLA information remains a challenge. Recent advances in deep learning offer powerful tools to address these limitations. Deep learning models can:

* Learn complex patterns: They can analyse vast NGS data sets, including genomic, transcriptomic, and HLA information, to identify novel neoantigens arising from diverse mutations.
* Personalize predictions: rThey can learn individual HLA repertoires and protein structures for accurate and patient-specific HLA binding affinity predictions.
* Integrate diverse data: They can seamlessly integrate various data types, providing a holistic view of the tumour-immune landscape and unlocking hidden insights into neoantigen presentation and immune recognition.

However, current deep learning approaches face challenges, including limited data availability, model interpretability, and clinical translation.

## Objectives:

This project aims to develop a deep learning-powered bioinformatic pipeline for comprehensive neoantigen prediction and prioritization, addressing the limitations of current approaches. We will:

* Develop a robust deep learning model: This model will integrate diverse NGS omics data and personalize HLA binding affinity predictions.
* Validate predicted neoantigens: We will experimentally validate the predicted neoantigens in vitro and in vivo using established immunological assays.
* Identify neoantigen signatures: We will analyse the association between predicted neoantigens and immunotherapy response in a diverse patient cohort.
* Translate findings into clinical practice: We will develop user-friendly tools for clinicians to incorporate deep learning predictions into treatment decision-making.

## Significance:

This project has the potential to:

* Unveil the hidden landscape of neoantigens: This will deepen our understanding of tumour-immune interactions and lead to the discovery of novel immunotherapeutic targets.
* Personalize cancer immunotherapy: By identifying immunologically relevant neoantigens for each patient, we can maximize treatment efficacy and minimize side effects.
* Develop next-generation immunotherapies: Precisely targeted neoantigen vaccines and immune cell therapies can be developed based on deep learning-derived insights.
* Bridge the gap between AI and clinical application: We will demonstrate the feasibility of translating deep learning models into robust clinical tools for personalized patient care.

## Conclusion:

This project holds immense promise for revolutionizing cancer treatment through personalized immunotherapy. By building predictive bioinformatics pipelines unlock the secrets of neoantigens, we can empower the immune system to fight cancer more effectively and offer new hope for patients.