**University of Leicester**

**MRC AIM Studentship Project 2025-6 entry.**

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| **Additional Supervisor** |  |

**Industrial involvement.** Nonacus Ltd

**Section 2 – *Project Information***

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| **Project Title** | iCase: Dissecting disparities in response to immunotherapies in under-represented patients with head and neck cancer by integrative omics and machine learning |
| **Project Summary**  |
| This MRC iCASE studentship has three main aims: first, to explore the differences in genetic mutations, human papillomavirus (HPV) subtypes and microsatellite instability (MSI) that influence how under-represented populations respond to immunotherapy; second, to investigate whether the oral and gut microbiomes affect these responses; and third, to develop machine learning models to predict relapse in head and neck cancer patients using diagnostic images. This research is important and exciting because oral cancer disproportionately impacts South Asian communities, yet we lack a clear understanding of the biological factors driving these disparities. By integrating genetic, microbial, and clinical data, this project aims to provide insights that could lead to more personalized treatment strategies and improve outcomes for under-represented patients. Throughout this project, the student will gain valuable technical skills, including whole exome sequencing, targeted sequencing, microbiome analysis, and machine learning techniques. They will also spend time at Nonacus Ltd, learning to work with advanced bioinformatics tools and contributing to innovative approaches in cancer research. This multifaceted training will prepare the student for a successful career in biomedical research, with the potential to make a significant impact on public health and clinical practices. |
| **References** |
|  1. Siegel, R.L., A.N. Giaquinto, and A. Jemal, *Cancer statistics, 2024.* CA Cancer J Clin, 2024. **74**(1): p. 12-49.2. Patil, N., et al., *Oral Cavity Cancers: Ethnic Differences in Radiotherapy Outcomes in a Majority South Asian Leicester Community.* Clin Oncol (R Coll Radiol), 2024. **36**(5): p. 300-306.3. Huang, J., et al., *Effects of microbiota on anticancer drugs: Current knowledge and potential applications.* EBioMedicine, 2022. **83**: p. 104197.4. Verrou, K.M., G.A. Pavlopoulos, and P. Moulos, *Protocol for unbiased, consolidated variant calling from whole exome sequencing data.* STAR Protoc, 2022. **3**(2): p. 101418.5. Johnson, J.S., et al., *Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis.* Nat Commun, 2019. **10**(1): p. 5029. |