

Discussing Transformations Grant

Amy Hurford

April 23, 2024

2026 Transformation Competition

<https://www.sshrc-crsh.gc.ca/funding-financement/nfrf-fnfr/transformation/2026/competition-concours-eng.aspx?hsid=a9eccc7e-87ea-490c-a2fd-d768903d342d>

Funding opportunity description for the New Frontiers in Research Fund: 2026 Transformation Competition

First Nations - more specifically, if anyone knows about any reference that can help us to understand their health priorities, it would be a great.

Iqbal - At FNHA we support 204 First Nations communities in BC - perhaps we can help. a key priority for FNHA is the return of data back to First Nations communities - this is broader than infectious diseases and provides endemic health profiles to communities/sub-regions.

Mike: I agree with Nate, despite i am one of the developer. Nate, are you involve with the odin2 group? <https://mrc-ide.github.io/odin2/>

Nate: Thanks -- Although we have some common threads, we have are not involved in odin2.

Our ABM approach is based on a from-the-ground-up investment on the mathematical foundations of ABMs, which allows some similar benefits to odin2 (e.g., DSLs and visualizability, hybrid models), but also a wide variety of other benefits in terms of modularity, flexibility, support for mathematical analysis, etc.

James said that new models will be needed after COVID...

Julien: Continuing James' argument: understanding non-equilibrium situations and models without DFE is important in the endemic regimes...

Shokoofeh: I completely agree with James that the prerequisite to modelling is to understand the communities and characteristics. Maybe first step is to design a strategy around that.

Lisa: said GBV could have a place in this funding. There are SIR models for GBV too - there are many instances when the GBV and infectious disease modelling are riding parallel paths - especially in small jurisdictions.

Nate: Agreed - like you, I have a strong interest and heavy involvement in GBV/IPV modeling. It did come up as an issue with our communicable disease modeling in a remote indigenous community.