

**Opportunity Title:** Individual-Scale Contact Tracing of Infectious Diseases Through Next-Generation Sequencing

**Opportunity Reference Code:** ICPD-2021-12

**Organization:** Office of the Director of National Intelligence (ODNI)

**Reference Code:** ICPD-2021-12

**How to Apply:** Create and release your Profile on Zintellect – Postdoctoral applicants must create an account and complete a profile in the on-line application system. **Please note: your resume/CV may not exceed 2 pages.**

**Complete your application** – Enter the rest of the information required for the IC Postdoc Program Research Opportunity. The application itself contains detailed instructions for each one of these components: availability, citizenship, transcripts, dissertation abstract, publication and presentation plan, and information about your Research Advisor co-applicant.

Additional information about the IC Postdoctoral Research Fellowship Program is available on the program website located at: <https://orise.orau.gov/icpostdoc/index.html>.

If you have questions, send an email to [ICPostdoc@orau.org](mailto:ICPostdoc@orau.org). Please include the reference code for this opportunity in your email.

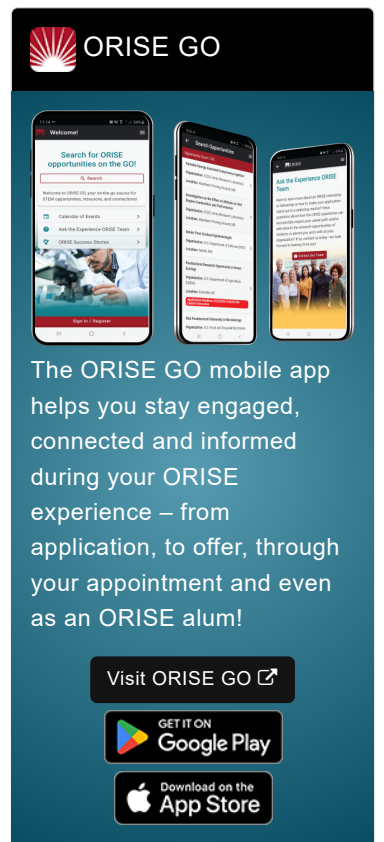
**Application Deadline:** 2/26/2021 6:00:00 PM Eastern Time Zone

**Description:** Research Topic Description, including Problem Statement:

Near real-time whole-genome sequencing of emerging pathogens has become possible in the past decade through the combination of high-throughput, next-generation sequencing combined with low-cost and easy access cloud computing and storage. This new global capability to collect and share massive amounts of pathogen data has been effectively demonstrated with the COVID-19 outbreak. Within the first two weeks of the outbreak, multiple whole-genomes of the virus were available online. In the 10 months since, thousands of viral genomes have been sequenced and made publicly available. This massive quantity of genetic data has enabled and driven global research activities at a pace never before realized during a pandemic. This availability of data has also led to new capabilities to track virus transmission and movement at a country and regional scale. Tools, such as NextStrain, have demonstrated the ability to compare different genomes and map mutations, enabling the prediction of viral species movement among countries and continents. Although many of these modeling processes are effective at regional or country scales, they often fail to accurately model individual-to-individual transmission because of the limited number and transient state of mutations associated with this type of transmission. The goal of research associated with this topic should focus on improved understanding of these individual-to-individual mutations across numerous individuals and the bioinformatics and software tools for modeling these changes.


**Example Approaches:**


As referenced in the topic paragraph, NextStrain and similar approaches have leveraged data predominately from clinical human samples. Although these clinical samples align with the public health need, they are not ideal for a controlled research activity within the IC Postdoctoral Research Program because of the numerous uncontrolled variables associated with such samples, increased costs, and personally identifiable information/institutional review board (PII/IRB) requirements often associated with collecting or storing these type of samples. Additionally, approaches and models should be extensible outside of just transmission within individuals of the same species to include other intra-species and inter-species transmission modeling. As such, some alternative approaches to study this phenomenon would include models leveraging laboratory transmission studies for well-controlled environments or samples collected from




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zoonotic or domestic animals.

**Relevance to the Intelligence Community:**

Retrospective analysis of genomic data associated with infectious spread has provided insight toward attribution and timeline. For example, a limited number of criminal cases have used molecular analysis of HIV to corroborate the intentional spread from one individual to another of the virus. Building on this retrospective and individualistic approach, approaches that can dive deeper than a regional, or even city, level could better inform the Intelligence Community (IC) of potential transmission mechanisms (natural or intentional spread), transmission rates (super spreader events), and, potentially, transmission routes (air, ground, or sea). Advances aligning to some or all of these information spaces, through real time analysis, would improve the IC's biosecurity and biodefense stance when dealing with future biological events.

**Key Words:** Infectious disease, contract tracing, next-generation sequencing, forensics, individual-to-individual transmission

**Qualifications** **Postdoc Eligibility**

- U.S. citizens only
- Ph.D. in a relevant field must be completed before beginning the appointment and within five years of the application deadline
- Proposal must be associated with an accredited U.S. university, college, or U.S. government laboratory
- Eligible candidates may only receive one award from the IC Postdoctoral Research Fellowship Program

**Research Advisor Eligibility**

- Must be an employee of an accredited U.S. university, college or U.S. government laboratory
- Are not required to be U.S. citizens

**Eligibility Requirements**

- **Citizenship:** U.S. Citizen Only
- **Degree:** Doctoral Degree.

- **Discipline(s):**
  - **Chemistry and Materials Sciences** ([12](#))
  - **Communications and Graphics Design** ([2](#))
  - **Computer, Information, and Data Sciences** ([17](#))
  - **Earth and Geosciences** ([21](#))
  - **Engineering** ([27](#))
  - **Environmental and Marine Sciences** ([14](#))
  - **Life Health and Medical Sciences** ([45](#))
  - **Mathematics and Statistics** ([10](#))
  - **Other Non-Science & Engineering** ([2](#))
  - **Physics** ([16](#))
  - **Science & Engineering-related** ([1](#))
  - **Social and Behavioral Sciences** ([27](#))