

Improved Annotation of Sequences of Concern to Better Understand Biorisk in Engineered Microbes

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Problem Statement

As synthetic DNA sequences for microbial engineering become easier to obtain, the risk of an accidental or deliberate generation of a microbial threat increases. Effective screening requires recognition of potentially hazardous sequences.

Working Toward a Solution

- We developed open-source software, SeqScreen, to screen sequences for those with hazardous functions: sequences of concern (SoCs)
- SeqScreen requires that sequences that cause problems be recognized and classified.
- How are hazardous sequences best understood?

Microbial Pathogens for Humans¹⁻³

How many microbial pathogens for humans are there? Probably fewer than 1600:

- ~600 fungi,
- ~600 bacteria,
- 250 RNA viruses
- 50 DNA viruses
- 60 protozoa

How Do SoCs Contribute to Disease?

Damaging SoCs

- Cytotoxic
- Degrade Tissue
- Disable Organ
- Induce Inflammation

Immune-Subverting SoCs

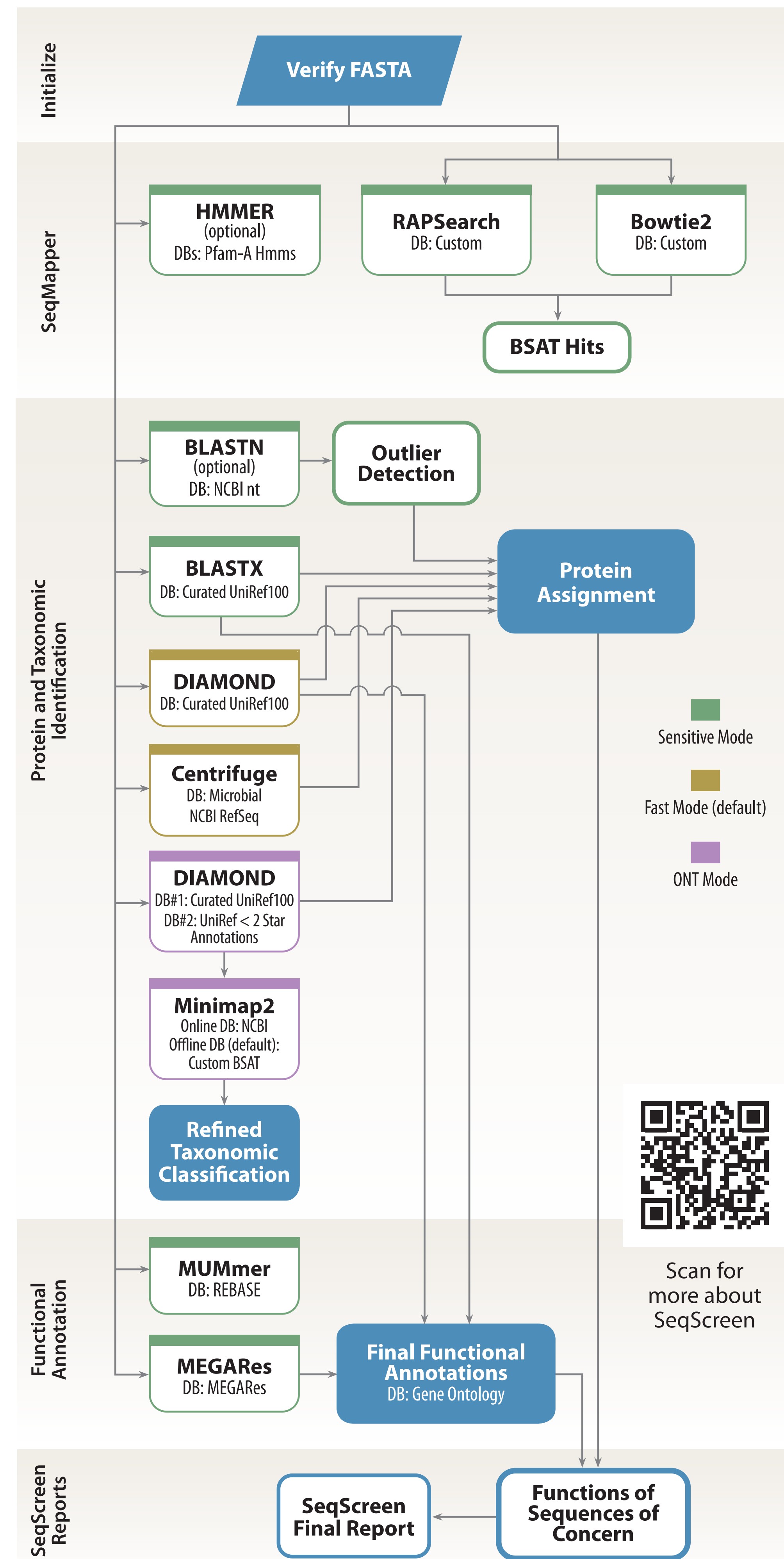
- Suppress host immune signaling by disrupting:
 - JAK-STAT
 - MAPK
 - NFκB
 - RIG-I
 - Protein kinase R
 - STING
 - TNF receptor-associated factors
 - Toll-like receptor binding/activation
- Resist host phagocytosis
- Resist host complement-killing (serum resistance)
- Resist host antimicrobial peptide
- Resist host oxidative killing
- Counter host immunoglobulin
- Defeat host chemokine or cytokine
- Inhibit host antigen presentation
- Immunomodulation

Other Direct-Acting SoCs

- Adherence to host cell
- Dissemination in host
- Host cell invasion
- Movement in host cell
- Niche-creation in host cell

We have annotated functions of sequences of concern [FunSoCs] from 105 bacterial, 58 viral, 7 protozoal, and 4 fungal species pathogenic for humans.

SeqScreen Workflows



A Dataset of SoCs Annotated by Function Could Bring Clarity to Dual-Use Research of Concern (DURC) for Researchers, Regulators, and Funding Agencies

Function of Sequence of Concern (FunSoC)	Case 1 – SoC transferred to other pathogen or Case 2 – SoC altered for enhancement of original pathogen	Case 3 – SoC transferred to nonpathogen
Damaging	• Could enhance the harmful consequences of the agent	• Might enable the nonpathogen to have harmful consequences
Immune-Subverting	• Enhances the harmful consequences of the agent • Disrupts immunity or the effectiveness of an immunization against the agent • Alters the host range or tropism of the agent • Enhances the susceptibility of a host population to the agent	• Might enable the nonpathogen to have harmful consequences • Might enable the nonpathogen to infect novel hosts • Might enhance the susceptibility of a host population to the agent
Attachment Protein/ Adhesin	• Alters the host range or tropism of the agent • Enhances the susceptibility of a host population to the agent	• Probably none
Fusion Protein/Invasin	• Alters the host range or tropism of the agent • Enhances the susceptibility of a host population to the agent	• Probably none
Dissemination	• Enhances the harmful consequences of the agent • Increases the transmissibility or the ability to disseminate the agent • Enhances the susceptibility of a host population to the agent	• Probably none

Acknowledgements & References

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- References**
1. Woolhouse M, Gaunt E. (2007) Ecological origins of novel human pathogens. *Crit Rev Microbiol* 33:231–242. doi: 10.1080/10408410701647560.
 2. Brown GD, Denning DW, Levitz SM. (2012) Tackling human fungal infections. *Science* 336:647. doi: 10.1126/science.1222236.
 3. Woolhouse MEJ, Brierley L. (2018) Epidemiological characteristics of human-infective RNA viruses. *Sci Data* 5:180017. doi: 10.1038/sdata.2018.17.
 4. Godbold, GD, Kappell, AD, LeSassier, DS, Treangen, TJ, and Ternus, KL (2022) Categorizing Sequences of Concern by Function To Better Assess Mechanisms of Microbial Pathogenesis. *Infect Immun* 90, e0033421. doi: 10.1128/IAI.00334-21.
 5. Balaji, A, Kille, B, Kappell, AD, Godbold GD, Diep, M, Elworth RAL, Qian, Z, Albin, D, Nasko, DJ, Shah, N, Pop, M, Segarra S, Ternus, KL, Treangen TJ (2022) SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. *Genome Biol* 23: 133. doi: 10.1186/s13059-022-02695-x.

Work in Progress

We are involved in reforming the Gene Ontology (GO) terms relating to host-symbiont interactions via the Multiorganism Working Group. This will provide a greater comprehension of these processes for both humans and machines.