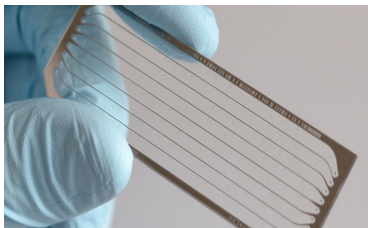




Photo: Nogas1974/CC-BY-SA-4.0 The picture has been mirrored

Bioinformatics - seeing the unseen

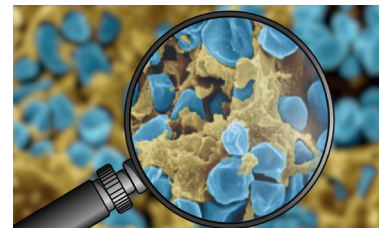
Are you curious about...



...the latest sequencing technologies?



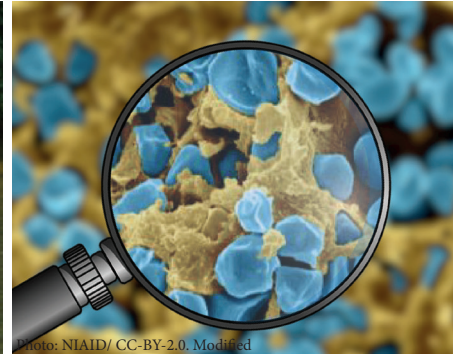
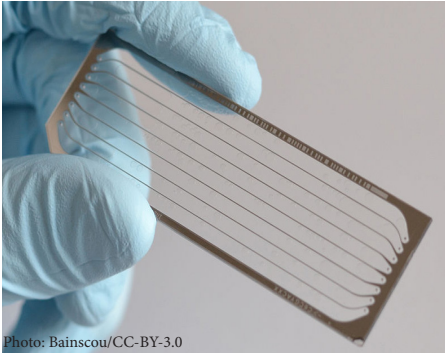
...the species content and source of your samples?



...microbial forensics?

Contact FOI's experts in bioinformatics for a free project consultation

We support you in...



- Handling and interpretation of NGS data
- Marker design and high-throughput genotyping
- Community characterization of complex samples e.g. contaminated water, soil and air samples
- Bayesian methods for data analyses and evidence evaluation
- Statistic design, analysis and interpretation
- Automated pipelines for data analyses

...and offer

- Sequencing with the latest technologies
- Real time on-site sequencing
- Expertise consultation in microbial ecology, microbial epidemiology, and population genetics of microorganisms

Selected publications

Genomic analyses of *Francisella tularensis* strains confirm disease transmission from drinking water sources, Turkey, 2008, 2009 and 2012. *Euro Surveill.* 2015;20:21136

Scaffolding of a bacterial genome using MinION nanopore sequencing. *Sci Rep.* 5, 11996, 2015

Chemometrics comes to court : evidence evaluation of chem-bio threat agent attacks. *J Chemometr.* 2015;29(5):267-276

The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. *Nucleic Acids Res.* 2012;40:D1313-7

Landscape epidemiology of tularemia outbreaks in Sweden. *Emerg Infect Dis.* 2009; 15(12):1937-47

A real-time PCR array for hierarchical identification of *Francisella* isolates. *PLoS One.* 2009;4(12):14

The complete genome sequence of *Francisella tularensis*, the causative agent of tularemia. *Nat Genet.* 2005;37(2):153-9

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The commitment to quality and confidentiality is standard professional practice at FOI

For more information, please contact CBRN Defence and Security, Umeå, Sweden

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