AI and machine learning in biostatistical research: example projects and IT requirements

Valeria Vitelli
Oslo Center for Biostatistics and Epidemiology (OCBE)
Department of Biostatistics, University of Oslo

September 6, 2018

Outline

Oslo Center for Biostatistics and Epidemiology (OCBE)

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- people at OCBE deal with methodological research in all areas of biostatistics & machine learning;

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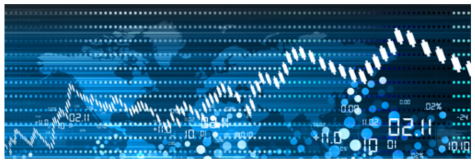

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A joint centre with

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With funding from

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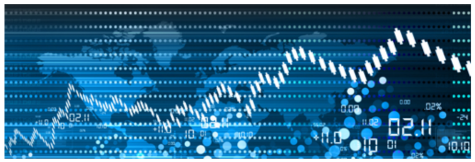

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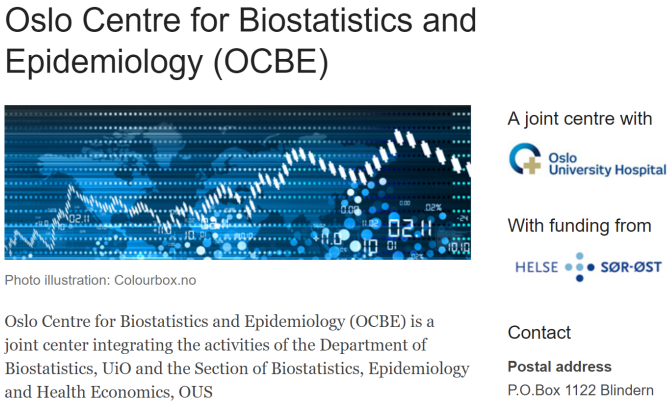

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- the advising activity at OCBE is directed towards all areas of medicine and health related research, from clinical and epidemiological research, to molecular biology and other basic medical sciences.

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- **Probabilistic Inference Lab (PIL):** more later....

OCBE in a nutshell: **teaching**

- **PhD courses.** Introduction to infectious disease modelling; Quantitative biology, or mathematics is biology's next microscope; Prediction (in Molecular Biology); Introduction to statistics and bioinformatics for the analysis of large-scale biological data; Population-based Association Analysis; Introduction to genetic epidemiology; Videregående statistikk: Analyse av repeterte/korrelerte kategoriske data; Analyse av repeterte / korrelerte målinger; New statistical methods for causal inference; Videregående kurs i epidemiologiske metoder.
- **PhD-courses for students at UiO only.** Introductory course to the medical PhD program, INTRO II; Introductory course in statistics; Logistic regression, survival analysis and Cox-regression.
- **Courses for the professional study programme for medicine.**
- **Courses in the Master's Programme in Clinical Nutrition.**
- **Courses in the Master's Programme in International Community Health.**

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What is our advising activity?

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`https://www.med.uio.no/imb/english/research/centres/ocbe/advising/`

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In particular, Bayesian methods embed prior information & available data in a unified framework: neat approach to include strong biological knowledge into the model, which is then modified / updated according to the data.

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AI @ OCBE – IT use

Typical requirements on IT (hardware and software) for many of our projects:

- memory for huge datasets: clinical registries, genomic, study cohorts;
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Some statistics from a recent survey...

- **software use:**
  80% R, 20% Matlab, 25% C++, 28% Phyton, SPSS and STATA
- **open-source packages production:** 20% often, 30% rarely or never, the rest does not apply
- **server use:** 64% run analyses on a server (increasing!) specifically, of those using a server: 80% use abel, 67% use TSD, 27% use med-biostat
- **sensitive data:** 52% of OCBE staff (increasing!) encounters this issue

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*One major issue with using the ibm-frigessi is that it is in the TSD secure environment, which means that the Internet is not reachable from the server. This has implications for software availability (R packages, for instance).

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- we (typically) don't need licensed software.

Many thanks for your attention!

Questions?