# ELMED219-2022

Onsdag Jan. 5, 2022

Kursets plattformer: hva, hvordan og hvorfor?

Alexander S. Lundervold (HVL)







## ELMED219

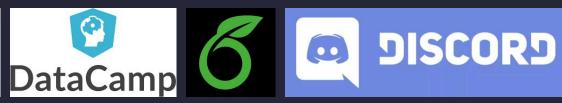


















#### https://mitt.uib.no/courses/33274



1

Dashbord



Văr 2022

Hjem

Kunngiøringer

Moduler Videoseminar

Oppgaver

Personer

Emner

888 Kalende

Meldinger

Historikk ?



#### Siste kunngjøringer



#### Velkommen til ELMED219!

Godt nytt år! ELMED219 starter med egenaktivitet mandag 3. janua...

← Svar

Postet på:

30. des. 2021 i 17.06

Postet på:

#### Digital undervisning i januar

På grunn av smittesituasjonen i Bergen og landet for øvrig, er det b...

17. des. 2021 i 10.17

Kurset tilhører Institutt for biomedisin e og er assosiert med Institutt for datateknologi, elektroteknologi og realfag e, Høgskulen på Vestlandet, og Mohn Medical Imaging and Visualization Centre e.







I løpet av kurset får du innblikk i beregningsorientert tankegang, maskinlæring og kunstig intelligens, og en forståelse for pros et cons for AI i fremtidens medisin. Det blir gitt en guidet tur gjennom noen biomedisinske og kliniske anvendelser av matematiske og statistiske modelleringsteknikker, samt prinsipper for utvalgte sensorer og måleinstrumenter i forskning og klinisk praksis.

Vi møter konsepter som big data, data-analyse, maskinlæring, og kunstig intelligens (AI), med eksempler fra persontilpasset og prediktiv medisin. Du vil ta i bruk metoder og verktøy fra numerisk programmering, dataanalyse og «scientific computing» for medisinske anvendelser, og lære om viktigheten av open science, deling av data, og reproduserbar forskning.

Tentativ timeplan finner du her & (og her &).

Gå til modulen Gjør deg klar og deretter til kursets GitHub-repositorium e for å komme i gang!

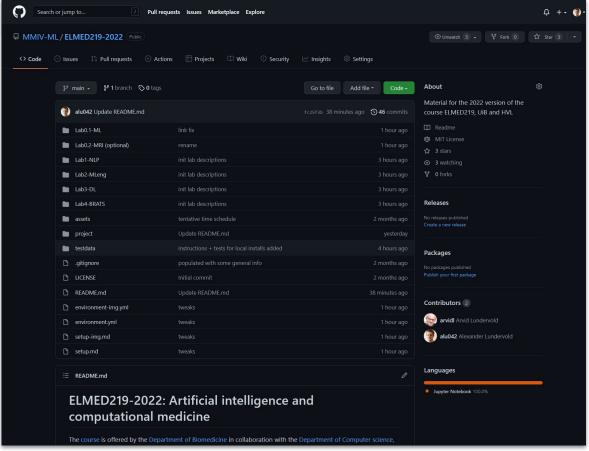


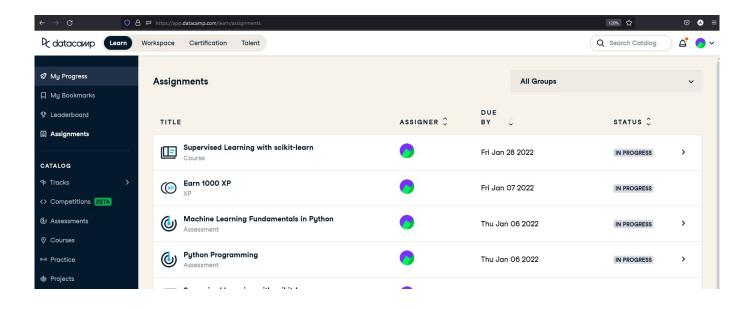


6. jan. i 8.15 [ELMED219] Seminar 11. jan. i 8.15 [ELMED219] Seminar 13. jan. i 8.15

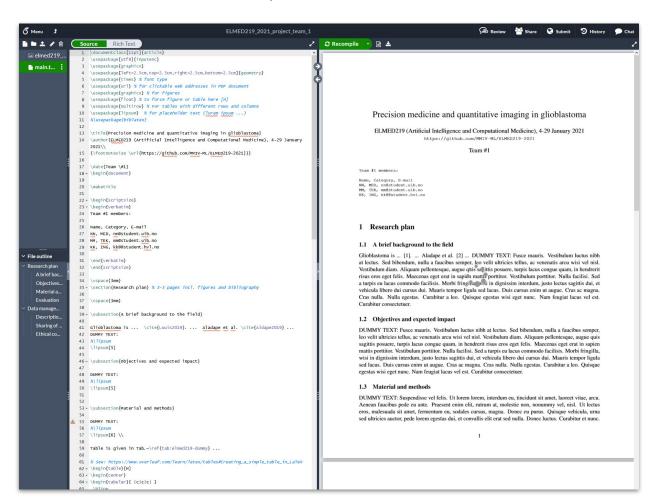


#### https://github.com/MMIV-ML/ELMED219-2022



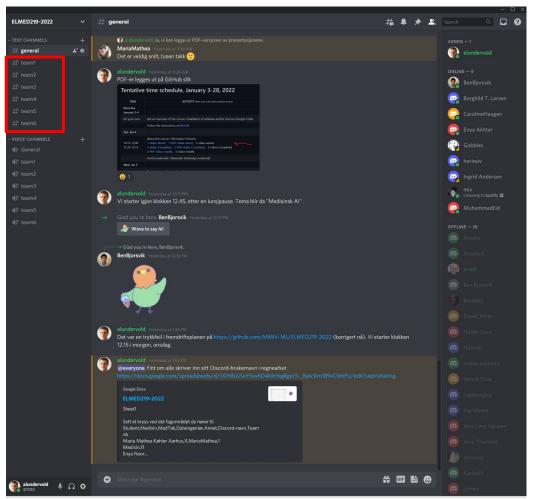


#### https://www.overleaf.com

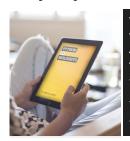




#### https://discord.gg/3DCbM8aW45



## • Why Python?



# **Programming for Biologists**

Teaching biologists the tools they need to use computers to do cool science

- 1) Easy to Learn and Use
- 2) Mature and Supportive Python Community
- 3) Support from Renowned Corporate Sponsors
- 4) Hundreds of Python Libraries and Frameworks
- 5) Versatility, Efficiency, Reliability, and Speed
- 6) Big data, Machine Learning and Cloud Computing
- 7) First-choice Language
- 8) The Flexibility of Python Language
- 9) Use of python in academics
- 10) Automation

http://www.programmingforbiologists.org/about/why-python

https://www.upgrad.com/blog/reasons-why-python-popular-with-developers

### Why <u>Jupyter</u> notebooks?



Interactive notebooks: Sharing the code

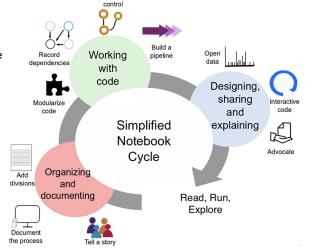
## • Why GitHub?

Github is like facebook for programmers. Everyone's on there. You can look at what they're working on and easily peruse their code and make suggestions or changes.

It's really open source. "Open source" is not so open if you can't easily study it. With github, all of the code is easily inspected, as is its entire history.

Github lowers the barriers to collaboration. [link]

Jupyter notebooks provide an environment where you can freely combine human-readable narrative with computer-readable code.



Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks  $[\mbox{link}\,]$ 

#### https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6920002

Journal of the Medical Library Association, v. 1–89
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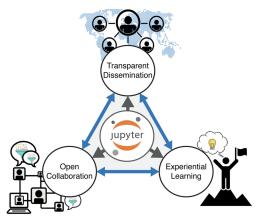
 J Med Libr Assoc.
 2020 Jan; 108(1): 29–35.
 PMCID: PMC6920002

 Published online 2020 Jan 1. doi: 10.5195/jmla.2020.819
 PMID: 31897049

Why do biomedical researchers learn to program? An exploratory investigation

Ariel Deardorff

We use the Python language because it now pervades virtually every domain of the biosciences, from sequence-based bioinformatics and molecular evolution to phylogenomics, systems biology, structural biology, and beyond. [link]



... their interactive and easily deployable framework can drive experiential learning opportunities for computational novices to develop their own skills and better understand metabolomics data analysis [ link ]