What should be the characteristics of online bioinformatic platforms in LifeWatch ERIC?



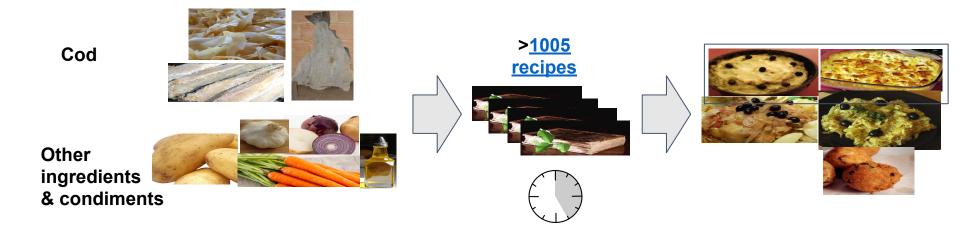


What should be the characteristics of online metabarcoding bioinformatic analysis platforms in LifeWatch ERIC?

Shared notes/whiteboard: https://tinyurl.com/s4y3zxo



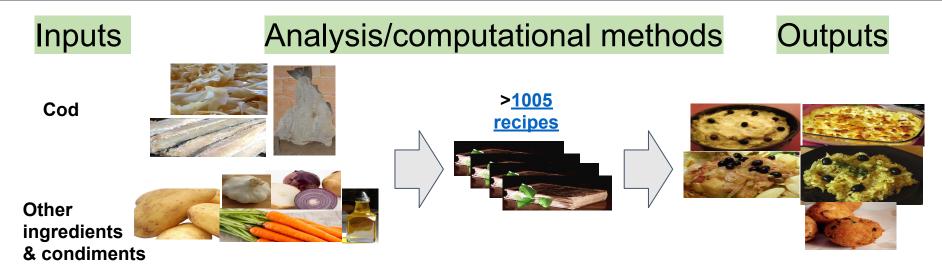






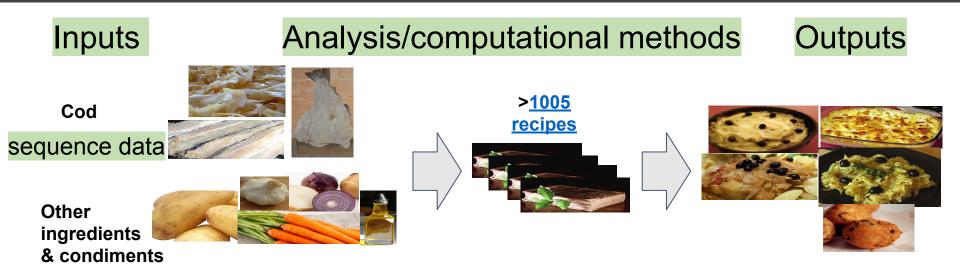


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Reference database Metadata

. . .



Main Topics

- Metabarcoding analysis pipelines
 - Inputs
 - Analysis methods/pipelines
 - Outputs
 - Data sharing
- Standardization!Standardization!...



Presentation

Integration of metabarcoding bioinformatic pipelines





• Inputs

- Sequence data
 - Support heterogeneous sources?
 - Different sequencing platforms
 - Different protocols
 - File format?
 - E.g., fastq(.gz)? BAM? CRAM? Others?

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• Inputs

EnvMetaGe

- Reference databases
 Which ones?
 - Public only? Genbank, ...
 - Semi-public or private? Bold,...

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- Custom databases
- Generic vs specific?

vurl.com/s4

■ File formats?

- Inputs
 - Metadata?
 - File formats?

EnvMetaGehttps://tinyurl.com/s4y3

- Which ontologies?
- Minimum data requirements?
 - Use/expand existing standards?
 <u>MIxS</u>

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 What characteristics should the analysis protocols have?





- What components should the analysis protocols include?
- Can we agree on a set of tools/pipelines? How to achieve this?
- How many parameters would the users be able to change?





- Outputs
 - What should contain and what format?
 E.g. OTU/ASV table
 - Web reports?
 - Available for a time period? Downloaded?...





- Data sharing policy
 - Input data
 - Output data
 - Uploaded data and results
 Private/Public/Embargo





• Next steps?





Coffee break





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