#### **Outline**



What I've learned after 5 years of trying to automate Koopmans functionals





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... but what have I learned throughout this process?



Well not quite



but the intervening years have not been kind – see permit photos)

# Interfacing with AiiDA



What I needed to do

- isolate into steps
- functional programming

# **Common Workflow Language**









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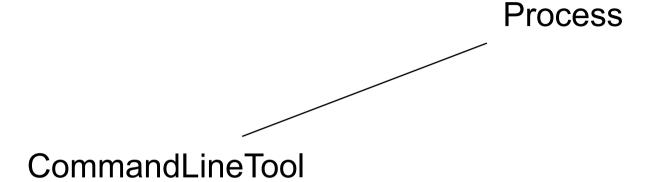


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- introduced in 2014; version 1.2 released in 2020
- mostly used by bioinformatics community

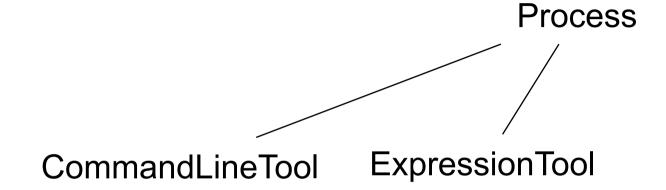


#### **Process**

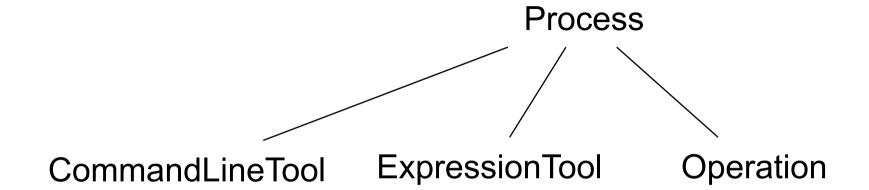






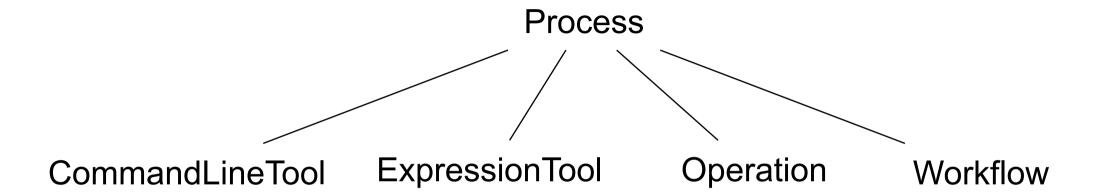






#### CommandLineTool





### **ExpressionTool**



```
echo.cwl
cwlVersion: v1.2
class: CommandLineTool
baseCommand: echo
inputs:
  message:
    type: string
    default: "Hello World"
    inputBinding:
      position: 1
outputs: []
```

#### Workflow



```
uppercase.cwl
cwlVersion: v1.2
class: ExpressionTool
requirements:
  InlineJavascriptRequirement: {}
inputs:
  message: string
outputs:
  uppercase message: string
expression:
```

#### Workflow



```
${ return {"uppercase_message":
inputs.message.toUpperCase()}; }
```



```
echo uppercase.cwl
cwlVersion: v1.2
class: Workflow
requirements:
  InlineJavascriptRequirement: {}
inputs:
  message: string
outputs:
  out:
```



```
type: string
    outputSource: uppercase/uppercase message
steps:
  echo:
    run: echo.cwl
    in:
      message: message
    out: [out]
  uppercase:
    run: uppercase.cwl
    in:
```



```
message:
```

source: echo/out

out: [uppercase\_message]



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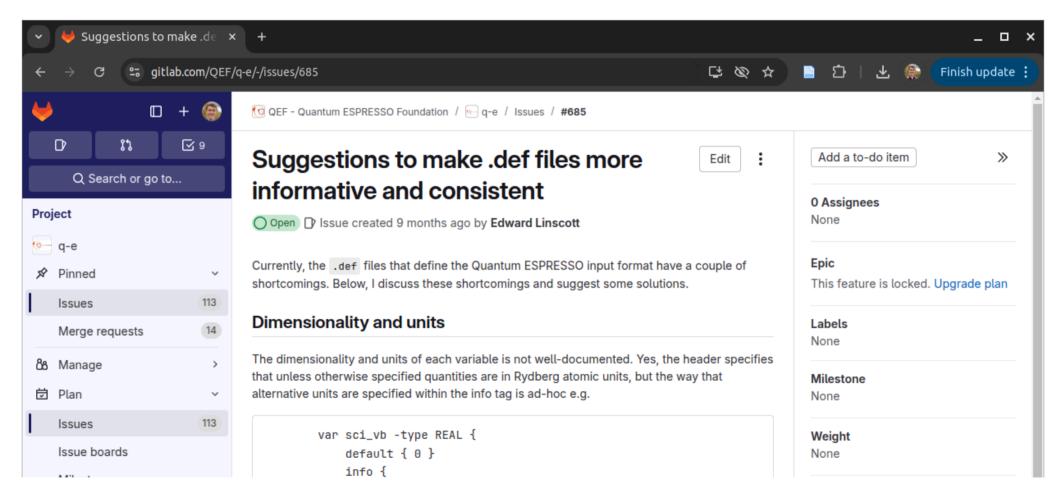
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  - rigorous schemas require willingness from the community

### ... willingness from the community?





#### References



