

## Abstract:

We propose a human and machine-readable plant growth protocol to improve experimental replicability and reproducibility in plant science. The protocol builds on the ICCEG guidelines for measuring and reporting parameters in growth chambers and tissue culture and allows for more complex growth protocols including dynamic setpoints over the course of a plant life cycle, radiation information in the form of spectral plots, and a unique identifier (UID) to share protocol setpoints and recorded experimental data through an accessible repository such as FAIRsharing. This protocol can be used for routine plant growth, more formal phenotyping experiments, and in controlled environment agriculture as a “plant growth recipe.” The protocol is open-source to allow community development, and extensible to allow for the evolution of the protocol as technologies and user preferences evolve over time.

## A Protocol Summary:

- Human- and machine-readable document format
- Describe dynamic and complex setpoints and recorded data
- Findable, Accessible, Interoperable, Reusable (FAIR) [1]
- Open-source and extensible
- Improve reproducibility in plant science

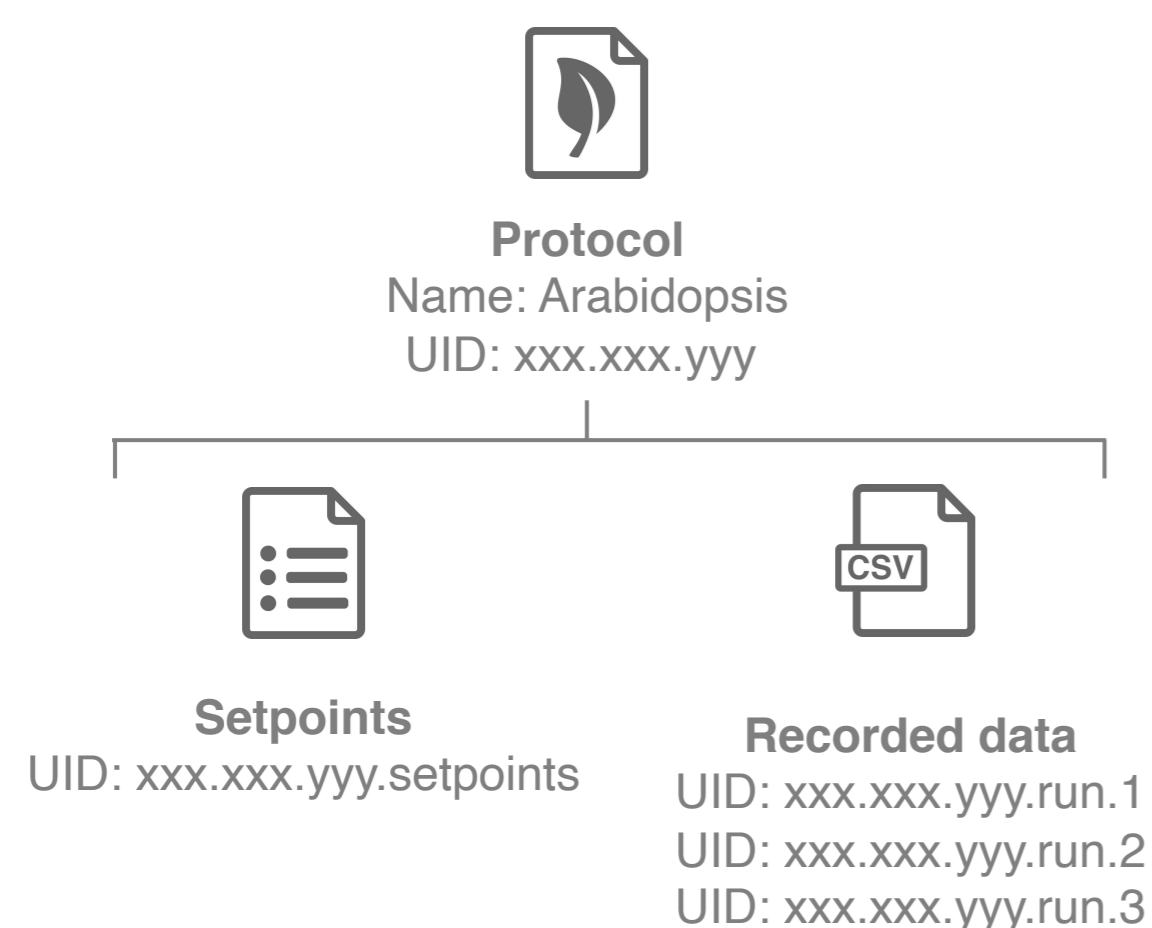
## B Inspiration (guidelines):

- Langhans and Tibbitts (eds) (1997) **Plant Growth Chamber Handbook**
- ICCEG (2004) *Minimum Guidelines for Measuring and Reporting Environmental Parameters for Experiments on Plants in Growth Rooms and Chambers*
- ICCEG (2008) *Guidelines for Measuring and Reporting Environmental Parameters for Experiments in Plant Tissue Culture Facilities*
- Both et al (2015) *Guidelines for measuring and reporting environmental parameters for experiments in greenhouses*. **Plant Methods 13**

## C Inspiration (design specifications):

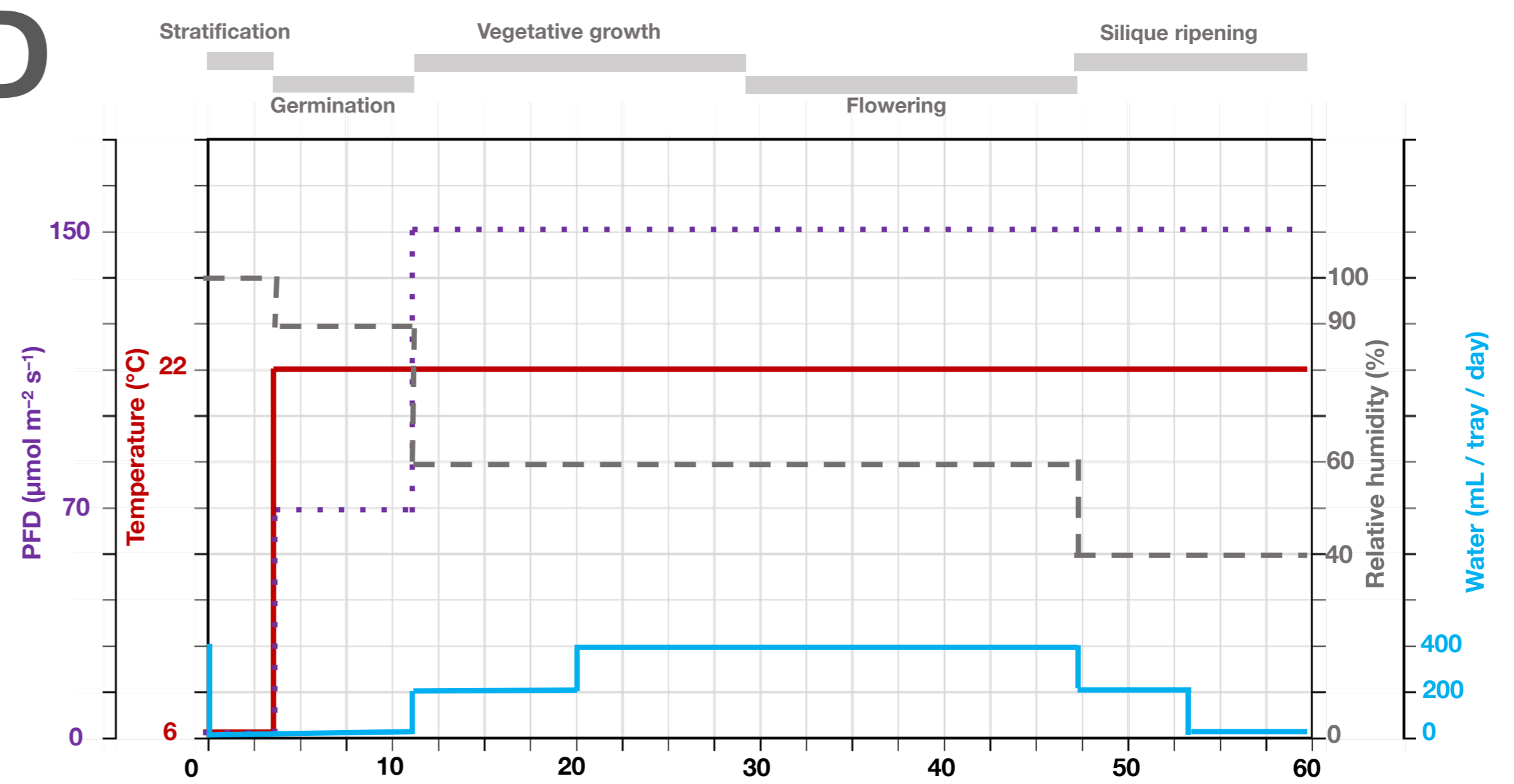
- Philosophy, parameters, units, nomenclature, etc.
  - ICCEG, community
- File formats and standards
  - FASTA (nucleotide and amino acids)
- Unique identifiers and open data
  - MIAME (Minimum Information About a Microarray Experiment) [2]
  - MINSEQE (Minimum Information About a Next-generation Sequencing Experiment) [3]
  - MIAPPE (Minimum Information About a Plant Phenotyping Experiment) [4]

## F



**F. Example protocol file structure.** A protocol file should contain a setpoints file (as in E.), and recorded data from when those setpoints are run in an experiment. The protocol, setpoints, and recorded data should all have related UIDs.

## D



**D. Example dynamic Arabidopsis plant growth protocol.** A 60 day Arabidopsis life-cycle split into five growth periods with differing setpoints. Showing only daytime setpoints for simplicity.

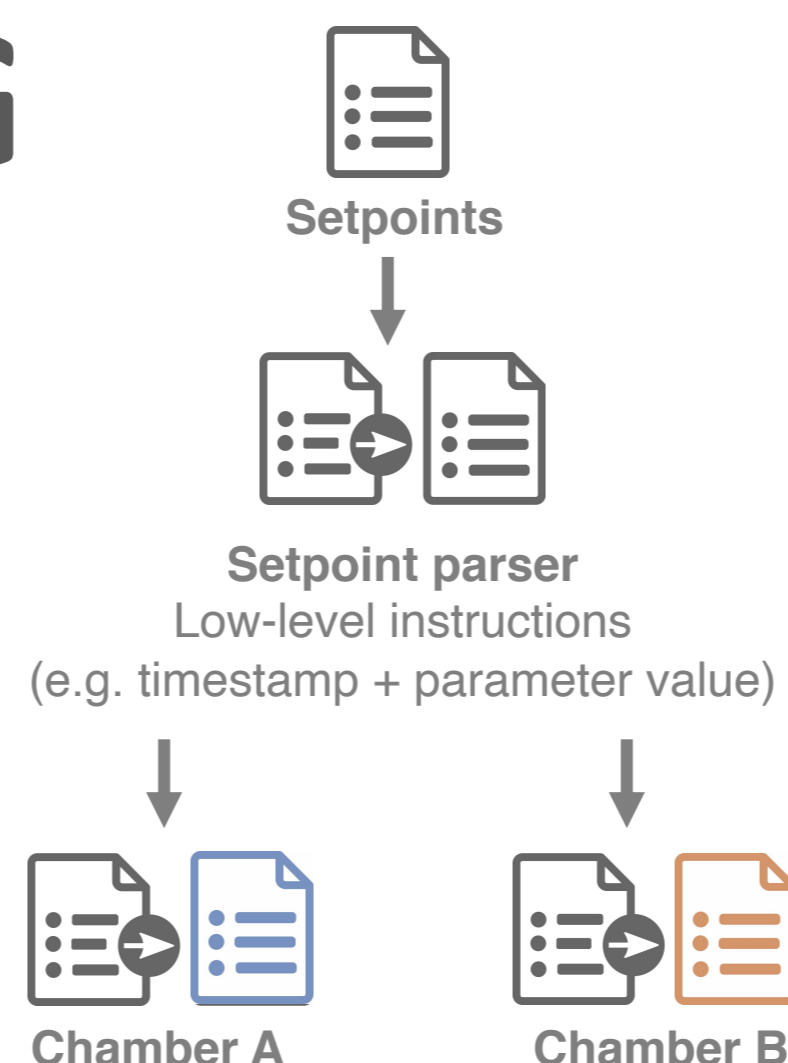
## E

```

1 [protocol]
2 name = "Arabidopsis"
3 uid = "xxx.xxx.yyy"
4 date = 2020-02-01
5 [[setpoints]]
6 day = 0
7 pfd = 0
8 temp = 6
9 humid = 100
10 water = 100
11 [[setpoints]]
12 day = 1
13 water = 0
14 [[setpoints]]
15 day = 10
16 pfd = 150
17 humid = 60
18 water = 50
19 [[setpoints]]
20 day = 20
21 water = 100
22 [[setpoints]]
23 day = 48
24 humid = 40
25 water = 50
26 [[setpoints]]
27 day = 53
28 water = 0
    
```

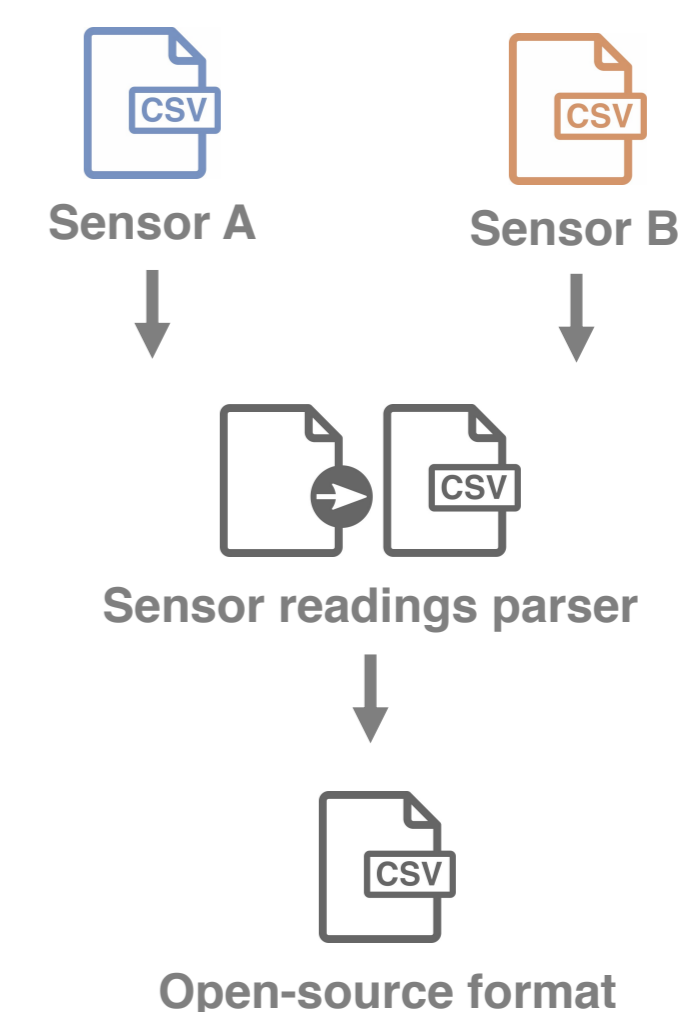
**E. Example plant growth protocol setpoint code.** An example setpoints file describes the dynamic 60 day plant growth protocol shown in D., using only 28 lines of code.

## G



**G. Interoperable.** A setpoint parser can be written to take setpoints in the open-source format and convert them to low-level instructions suitable for different chamber control systems.

## H



**H. Accessible.** A sensor readings parser can be written to sensor readings from different sensors and convert them to the open-source data format.

### Acknowledgements:

Stephen Rolfe (University of Sheffield); Henry Bookey, John Macarthur, Vasili Savitski (Fraunhofer Centre for Applied Photonics); Chris Nelson, Adam Ormerod (Stockbridge Technology Centre)

### References:

[1] Sansone et al (2019) **Nature biotechnology 37** [2] Brazma et al (2001) **Nature Genetics 29**  
[3] <http://fged.org/projects/minseqe/> [4] Ćwiek-Kupczyńska et al (2016) **Plant Methods 12**