For defining Sequences and Regimens, we have decided to use YAML.

References to sub-sequences can be done with their names.

Examples of Sequences and Regimens:

The ID of regimens and sequences, which is defined by the FarmBot when it receives it, will be written to file automatically.

YAML to define sequences with or without loops: Example of a YAML file: CSV: my\_map.csv other\_files: ["yaml\_file1", "yaml\_file2"] # This field is optional, the program will always look in its own file first. name\_set\_by\_user\_1: kind: "sequence" ID: <<created and set automatically by the app>> color: "gray" actions: [TO\_PLANT: "my\_favorite\_plant", WAIT: "1000", MOVE\_ABS: {x: 0, y: 0, z: 0, x\_off: 0, y\_off: 0, z\_off: 0, speed: 100}] name\_set\_by\_user\_2: kind: "sequence" ID: <<created and set automatically by the app>> color: "grav" group: ["11", "funny name"] # iterate over all members of this group type: ["broccoli", "onion"] # iterate over all members of this type actions: [TO\_SELF, SEQ: "water\_stuff\_sequence"] YAML Regimens: name\_set\_by\_user\_3: kind: "regimen" ID: <<created and set automatically by the app>> color: "green" schedule: [{name: "sequence\_name1", days: [1,2,5], time: "23:00"}, {name: "sequence name2", days: [11,12,15], time: "21:00"}] ,,,,,, The following are the keywords and formats we defined for single FarmBot commands such as Move\_Absolute and Write\_Pin. MOVE\_ABS: {x: 0, y: 0, z: 0, x\_off: 0, y\_off: 0, z\_off: 0, speed: 100} MOVE\_REL: {x: 0, y: 0, z: 0, speed: 100} IF : {cond: <<see below>>, then: , else: }

MESSAGE: {text: <<note: {{x/y/z}} is a special tag>>, type: "success/warning/busy/error/info"}

cond: "x = 0 AND y > 0 OR PIN 1 < 0 OR PIN A14 = UNKNOWN"

FIND HOME: [x,y,z]

WAIT: "time in milliseconds"

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READ_PIN : {pin : "<<number>>", label: "", mode : "D/A"}
WRITE_PIN : {pin : "<<number>>", value: "ON/OFF", mode : "D/A"}
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TO\_SELF # Go to the current plant in a loop

TO\_PLANT # go to a plant with this (unique) name, this saves typing in coordinates by hand if you have a special plant.

SEQ # get a sub-sequence