Name: ⸻

Date: ⸻

Collaborators: ⸻

(If applicable, the collaborators submit their individually written assignments together)

Question:	1	2	3	4	Total
Points:	10	20	30	10	70
Score:					

Instructor/grader comments:

1. (10 points) Before starting coding for this assignment:

   - ssh to your virtual machine

   - Create a directory, e.g. **hw06**.

   - Change to that directory.

   - Start Julia, switch to the package mode, and activate your project. Install the packages that you use for the assignment: `IJulia`, `PyPlot`, `SparseArrays`, `Random`, `Printf`. Exit Julia.

   - Create an empty `README.md` file.

   - Copy `.gitignore` file to your working directory.

   - Use jupyter notebook interface to write the code for this homework assignment.

2. (20 points) The correct way to determine the fractal dimension of dendrite clusters is to repeat the dla calculations multiple times and determine the best least squares fit for the dependence of $\log(m)$ vs $\log(r)$, where m is the number of molecules in the cluster and r is its characteristic size.

   As the first step in that process, conduct the calculations of the dla cluster growth 10 times and plot all graphs on the same figure.

   - Use the code `dla.ipynb` that we discussed in class, as a template for this assignment. Copy the notebook to your homework project directory, e.g. by typing at the command prompt

     `cp ../diffusion-limited-aggregation-lec19/dla.ipynb hw06p2.ipynb`

     Start ijulia and delete the markdown cells at the top of the notebook - they are not relevant to the homework assignment.

   - Keep the same rng seed, the 'dish' size and the number of molecules as defined in the template.

   - Disable animation by assigning `animate = false`.

   - Allocate the working storage as follows:

   ```
   nclust = 10
   rads = zeros(m, nclust)
   ```

   - Your main calculation loop may look as follows:

```
for i = 1:nclust
    dish, _ = dish_init(K, m)
    println(i)  # monitor calculation progress
    rr = @view rads[:,i]
    grow_cluster!(dish, basevecs, rr, m, animate, anistep)
end
```

- The part of your plotting code may look as follows:

```
nmin = 1000
nmols = nmin:m
loglog(rads[nmols,1], nmols, marker=".", markersize=0.5,
    linestyle="none", label="numerical experiment",
    color="black")
for i = 2:nclust
    loglog(rads[nmols,i], nmols, marker=".",
        markersize=0.5, linestyle="none")
end

beta = <your value here>

loglog(rads[nmols,1], 4*rads[nmols,1] .^ beta,
    label="fit "*L"n \sim r^{%$beta}", linestyle="dashed")
```

Provide the legend, grid, title, axes labels for each of your graphs.

- Describe in your README file whether the averaging over multiple code runs has significantly changed your result for the fractal dimension.

3. (30 points) Investigate whether the expansion of possible diffusion directions from the set (N, E, S, W) to (N, NE, E, SE, S, SW, W, NW) changes the fractal dimension of dendrite clusters.

   - Use the code dla.ipynb that we discussed in class, as a template for this assignment. Copy the notebook to your homework project directory, e.g. by typing at the command prompt

     ```
     cp ../diffusion-limited-aggregation-lec19/dla.ipynb hw06p3.ipynb
     ```

     Start ijulia and delete the markdown cells at the top of the notebook - they are not relevant to the homework assignment.

- Keep the same rng seed, the 'dish' size and the number of molecules as defined in the template.

- Modify `basevecs` variable as requested

- Run the calculations once. Do not switch off the animation.

- Describe your conclusions in your README file.

4. (10 points)

    1. On the GitLab: Create an empty GitLab project called **hw06** (name it exactly as shown).

    2. On the VM: Clean the cells of your jupyter notebook and save the notebook. Delete unneeded notebooks if you created ones (e.g. `Untitled.ipynb`). Initialize a git repository for your project. Check your notebook(s), Project.toml and Manifest.toml, an empty README.md file, and your .gitignore file into the repository. Provide a meaningful commit message. Push the content of your git repository to GitLab hw06 project.

    3. On the GitLab: Edit README.md file to add content as requested in the assignments.

    4. On the VM: Pull the README.md file to your local git repository (`git pull`).

    5. On the GitLab: Share the project with the instructor (GitLab user name p2200_23f_in) and grant him **Reporter** privileges.