
David Moore takes you on a quick tour of the Neighbour-Sensing program

When you first start the program the screen shown in Fig. 1 appears. This is largely made up of data space (which is three-dimensional, of course), in the centre of which is a red dot representing the first hyphal tip (= fungus spore). The mycelium will grow from this point. Around the data space are various controls.

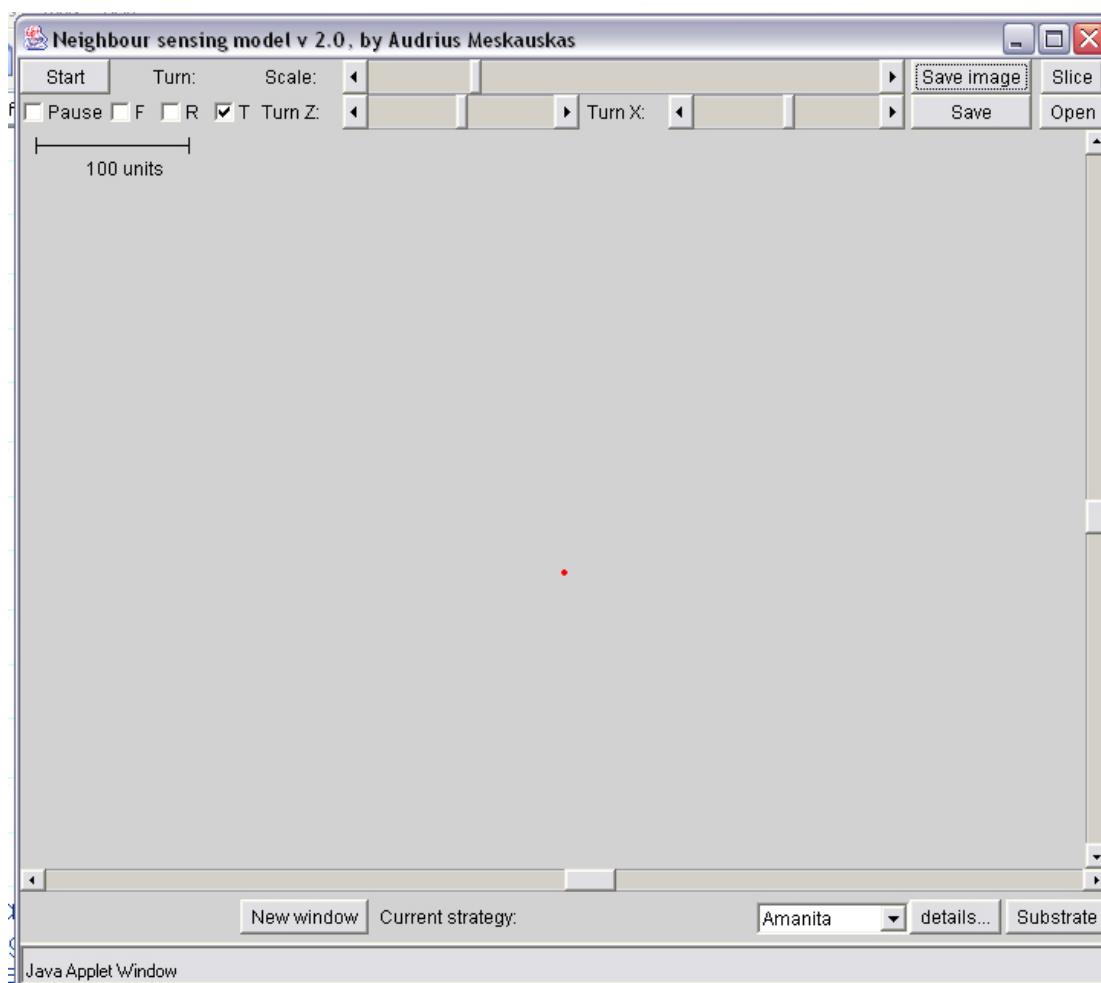


Fig. 1. The opening screen of the Neighbour-Sensing program.

At top left is the **Start** button – mouseclick on this to “press” it and the program starts to “grow” the mycelium. When a mycelium is growing the name of this button changes to “Start New”. Sliders on the right hand and bottom sides serve to position your view-point.



You can stop the growth at any time by clicking on the **Pause** check-box. **IMPORTANT** – to resume your experiment, click again on the Pause check-box to remove the check-mark. If

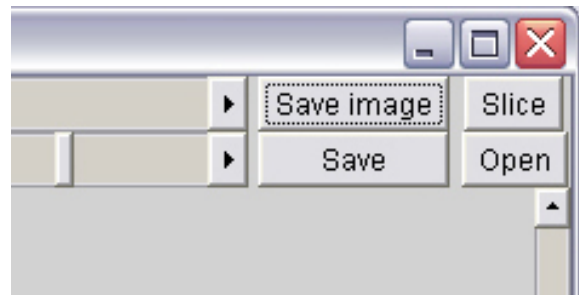
you press Start New it will do just that - start a new mycelium; it will not resume growth of the existing one.

Alongside the Pause check-box are check-boxes labelled **F**, **R**, and **T**. These control display modes of the image of your mycelium.

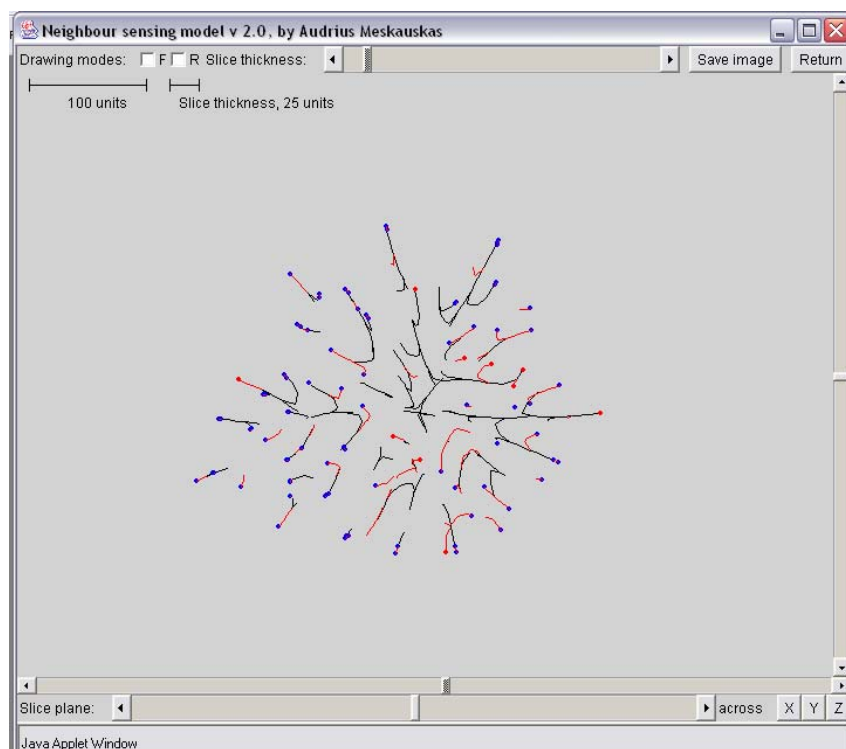
- **T** highlights the hyphal tips and colour codes them (red = not growing this iteration, blue = actively growing);
- **F** draws-in the vectors acting on each hyphal tip;
- when **R** is unchecked, hyphae that are no longer growing (because they have primary and secondary branches already) are shown in black, and sections that are in active growth are shown red, but when **R** is checked, colour coding is on the basis of distance from the start point (= essentially on the basis of hyphal age); in this case green represents sections close to initial point, and red which is very far from the initial point.

The main slider control at the top of the screen controls the **Scale** of your view; minimum magnification on left, maximum magnification on right (and the 100 length unit scale bar changes accordingly). Beneath Scale are rotation slider controls: **Turn Z** rotates your mycelium around an axis which is vertical with respect to the observer, **Turn X** rotates it around the horizontal axis.

At top right you have the standard Window controls, minimise, maximise and close. The program controls “Save image”, “Save” and “Open” are disabled in this Internet implementation of the program (it’s a security matter, preventing Internet programs accessing your computer’s file structure). But **Slice** works.



Press the **Slice** button and this view of a slice of your mycelium appears:



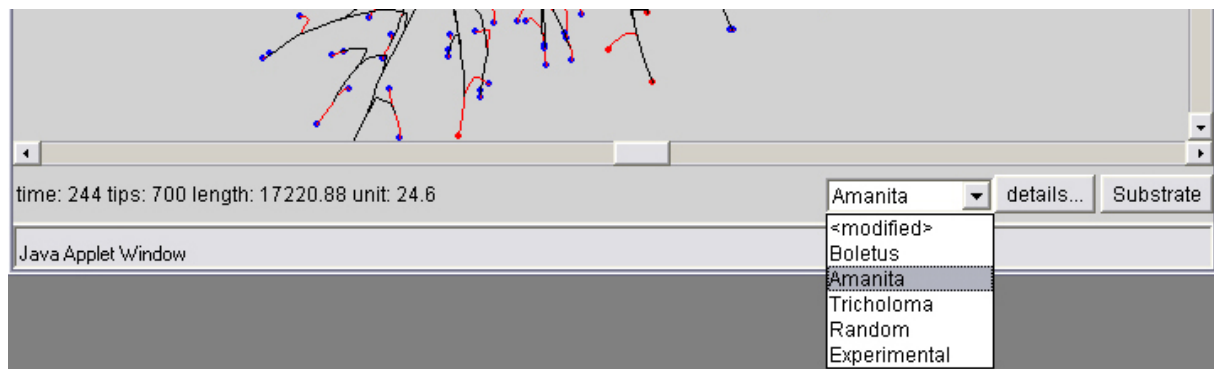
Controls along the top enable you to set **Slice thickness**, and to Return to the main screen (again “Save image” is disabled by Internet delivery).



And at the bottom of the screen is a **Slice plane** slider that positions the slice, and three press-buttons that allow you to decide whether to slice across **X**, **Y** or **Z** planes.



Now, let's turn our attention to the bottom of the main screen.



On the left is a set of basic statistics for your current mycelium – **time** of growth (= number of iterations of the program); number of hyphal **tips**; the total **length** of hyphae; and the current value of the hyphal growth **unit**.

In the right-hand corner are controls and indicators that enable you to choose the main parameters of the mycelium you will grow.

First is a **drop-down menu** that lists some ready-made parameter sets. They are called **Boletus**, **Amanita**, **Tricholoma** and **Random** – but you'll have to read our papers to find out why!

Press the **details** button and the main parameter dialog appears (Fig. 2). This screen allows you to input the characteristics that you want your mycelium to possess.

You can decide whether autotropism is operative, whether tip growth depends on the hyphal density field or on the number of neighbouring hyphal tips.

You can decide whether branching depends on any of these features, too. And when you are happy with your settings, you can **Return to simulation**, using the right-most button at the top of the screen and from that point on the growth simulation will use the parameters you have just set.

Once more, “Load parameters” and “Save parameters” are disabled by Internet delivery.

You can carry out experiments by varying these settings. Remember to visit the page where Liam McNulty describes some of the experiments that he has done.

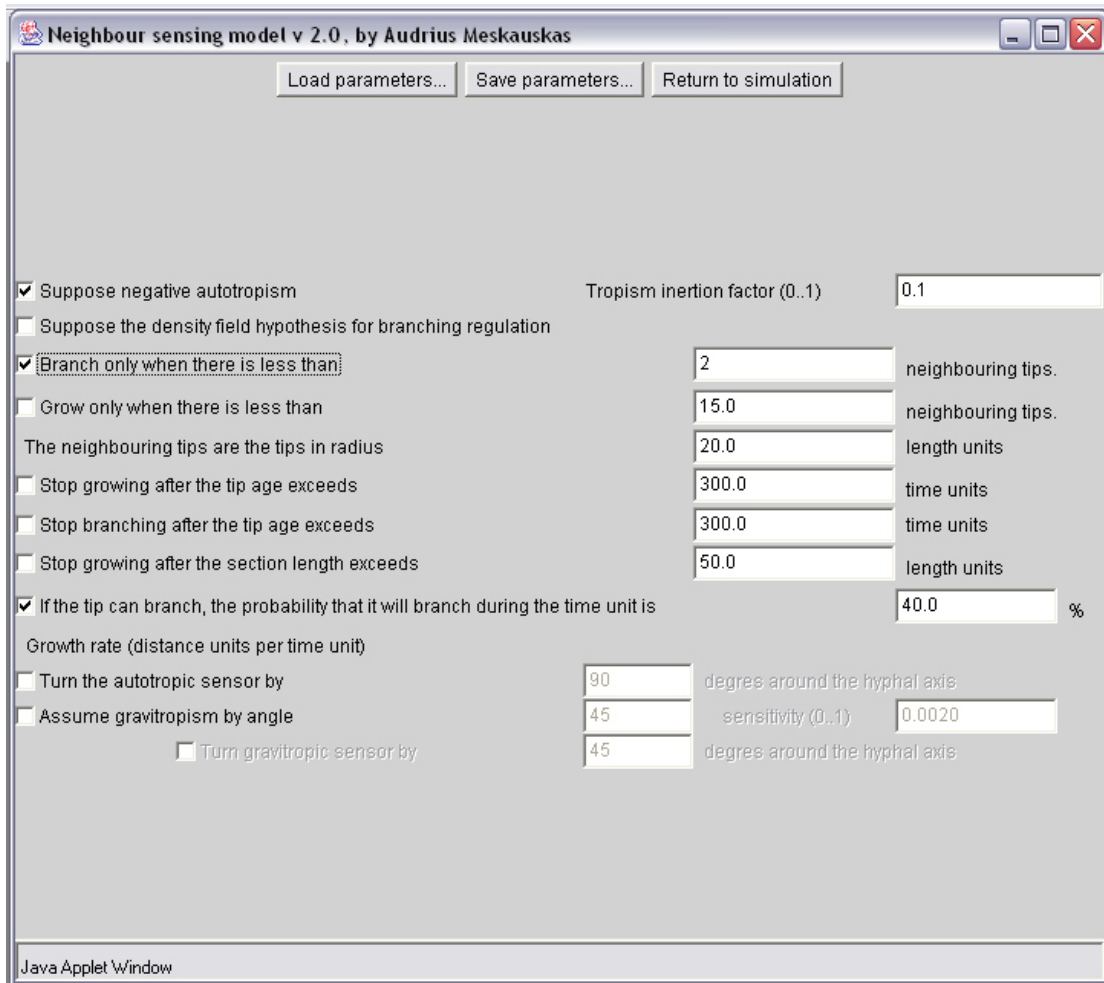
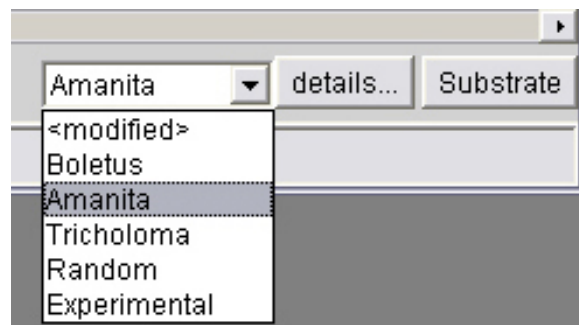


Fig. 2. The main parameter dialog screen.

The final button at bottom right of the main screen is labelled **Substrate**, and this enables you to add substrates and inhibitors to the data space occupied by your mycelium.



Press **Substrate** and the dialogue screen that appears permits you to decide the characteristics of your substrate(s).

In this program substrates attract hyphal tips (= positive tropism) and you can set the level of attractiveness, and you can also reverse it to a negative tropism (to create an inhibitor). Substrates are spherical volumes of the data space, and you can determine their **Size**. They can be placed at randomised co-ordinates suggested by the program, or you can **Position** them yourself by making appropriate entries in the boxes for **X**, **Y** and **Z** co-ordinates (position 0, 0, 0 is where the first hyphal tip is placed by the program to start a simulation).

Add a substrate

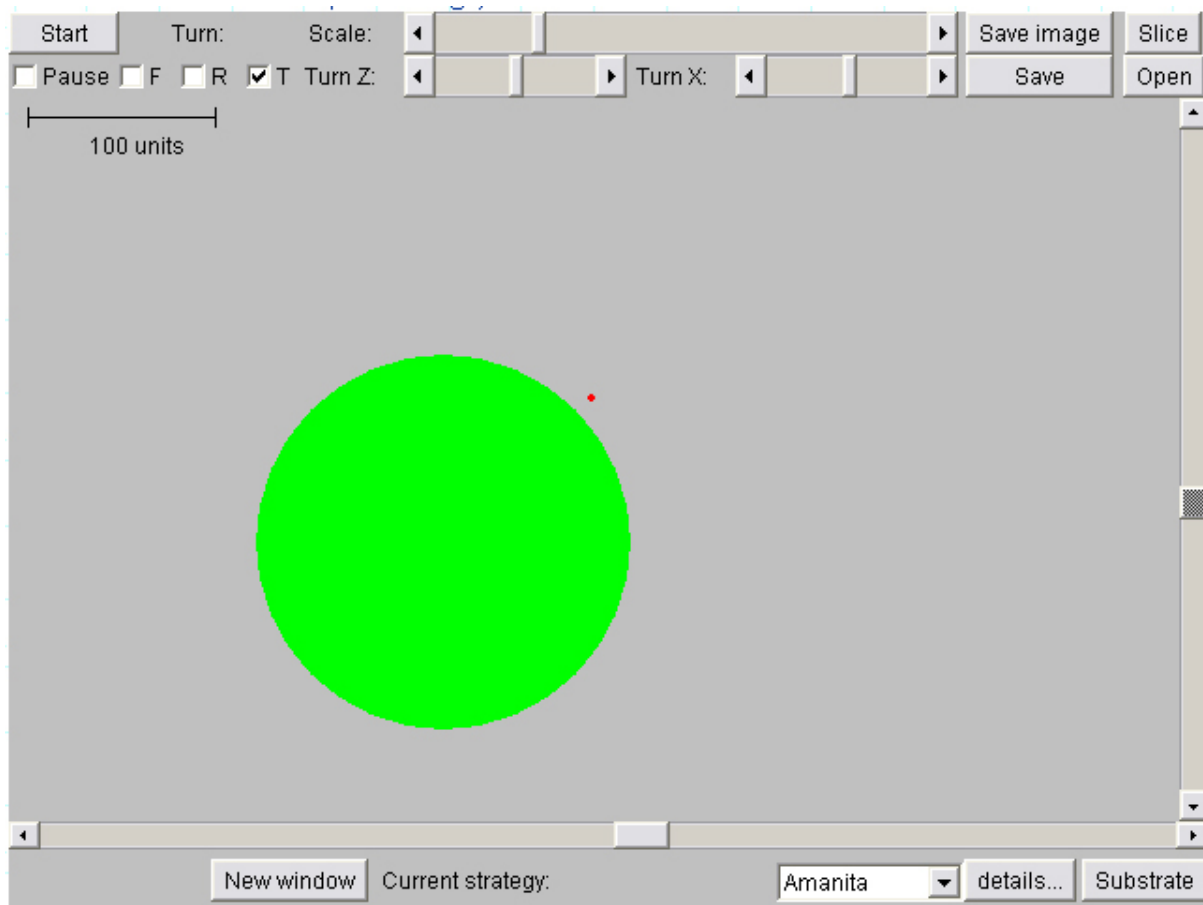
Size Position X Y Z

Negative tropism ("inhibitory substrate")

Attractiveness times more than a single hyphal tip

You can add several substrates to the surroundings of the mycelia

When you **Add substrate** and **Return** to the simulation, the substrate will appear as a green circle in your field of view.



Inhibitors are coloured pink. You can add any number and any combination of substrates and inhibitors.

Now, why don't you try the program for yourself?