Symbiotic Associations

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ABSTRACT

Soil contamination poses a series of important health issues, following years of neglect, constant industrialization, and unsustainable agriculture. It is estimated that 30% of the total cultivated soil in the world will convert to degraded land by 2020 (Rashid et al. 2016). Finding suitable treatment technologies to clean up contaminated water and soil is not trivial, and although technological solutions are sought, many are both resource-expensive and potentially equally unsustainable in long term. Bacteria and fungi have proved efficient in contributing to the bioavailability of nutrients and in aggregating formation in degraded soils (Rashid et al. 2016).

Our research aims to explore the possible implementation of physical computing, computational analysis, and digital fabrication techniques in the design and optimization of an efficient soil remediation strategy using mycelium. The study presented here is a first step towards an overarching methodology for the development of an automated soil decontamination process, using an optimized bio-cell fungus seed that can be remotely populated using aerial transportation. The presented study focuses on the development of a methodology for capturing and modeling the growth of the mycelium fungus using photogrammetry-based 3D scanning and computational analysis techniques.

1 Point cloud analysis.

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2 3D printed module for multiple apparatus.

INTRODUCTION

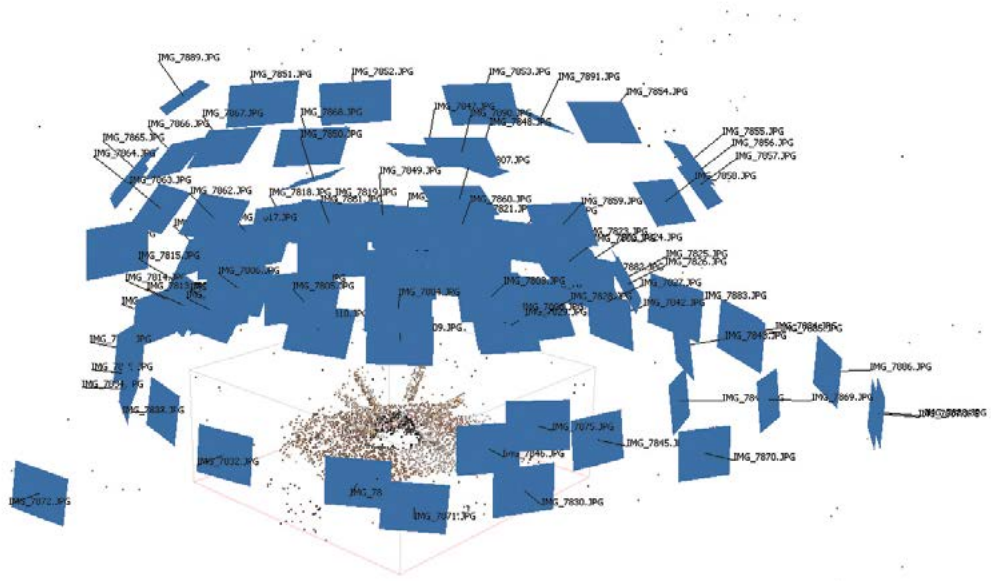
Soil contamination, also referred to as land pollution, is the degradation or destruction of the earth's surface, specifically soil, through xenobiotic (non-biological) chemicals or other substances, typically as a byproduct of human activities. Soil, being a porous and permeable mixture of unconsolidated mineral and rock fragments, acts naturally as a filter that allows the free flow of water through the pores and spaces between its particles. Land pollution thus poses a series of important health issues that have become prominent in recent years, following years of neglect, constant industrialization, and unsustainable agriculture. It is estimated that 30% of the total cultivated soil in the world will convert to degraded land by 2020 (Rashid et al. 2016). It is argued that the impacts of land degradation not only pose a serious challenge to sustainable development, but may also amplify the underlying social and political weaknesses which can contribute to global security threats (Barbut 2016).

Therefore, there is an evident need for proactive solutions for the reduction of land degradation, such as the promotion of sustainable land management and the restoration of degraded soils. Finding suitable treatment technologies to clean up contaminated water and soil is not trivial, and although technological solutions are sought many are both resource-expensive and potentially equally unsustainable in long term.

Bacteria and fungi have proved efficient in contributing to the bioavailability of nutrients and in aggregating formation in degraded soils (Rashid et al. 2016). Bacterial and fungal inocula have the potential to reinstate the degraded land's fertility by mobilizing key nutrients to the crop plants while remediating the soil's structure and improving its aggregation and stability.

In our effort to develop cost-effective procedures for cleaning up contaminated water and soil, our research focuses on studying the potential processes of using decontaminating agents—such as the mycelium fungus—to reinstate the degraded soil. Overall, our aim is to explore the implementation of physical computing, computational analysis, and digital fabrication for the design and optimization of an efficient soil remediation strategy using mycelium. The study presented in this paper is a first step towards an overarching methodology for the development of an automated soil decontamination process, using an optimized bio-cell fungus seed that can be remotely populated using aerial transportation. The study focuses solely on developing a methodology for capturing and modeling the growth of the mycelium fungus using the aforementioned technologies.

Many mathematical models of fungal growth and function have been and are currently being developed across different disciplines, including biotechnology (Ashley et al. 1990), soil science (Boddy et al. 2000), chemistry (Galli et al. 2008), mycology (Davidson et al. 2011) and biology (Lin et al. 2016), among others. We have found these models difficult to implement in our research and not focused on the aspect in we are most interested; namely, capturing the three-dimensional growth patterns of fungal growth. Our study is structured around data collection from either single or multiple apparatuses to detect



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3 Point cloud construction after 3D scanning process.

4 Data extraction. Parsing point cloud results.

5 Apparatus 01. Where strings are parsed according to their length.

the mycelium's growth in 3D. The digitally fabricated apparatuses, which contain a substratum and the inoculated mycelium fungus, aim to provide an initial experimentation test-bed for the further development of a bio-cell, which is the basis for the automated soil decontamination process.

To detect the growth pattern of mycelium, we have developed three-dimensional imaging and computational techniques to capture and analyze the growth process. In order to acquire the three-dimensional form of the mycelium growth, we have used photogrammetry-based 3D scanning. Different 3D scanning techniques have been previously used for detecting the growth of fungi (Senthilkumar 2016) and other biological organisms (Vilena 2010). In our study, we focus on affordable and accessible technology with an adequate level of accuracy. Further to the 3D imaging acquisition, computational analysis of the three-dimensional data is employed to iteratively detect the growth of mycelium.

Previous research on biological growth analysis in architecture has mainly focused on the development of design methodologies and morphogenetic computation. Growth modeling has been employed for structural optimization (Klemmt 2014, Itsuka 2014), morphological strategies (Klemmt and Bollinger 2015), and more commonly, for developing design methodologies and frameworks for generative design (Biloria and Chang 2012; Ahmar et al. 2013; Teixeira 2015). Biological fabrication techniques, similar to the ones envisioned under the overarching research goals of this study, have also been investigated (Araya et al. 2012), albeit in a completely different context and with a focus on producing physical design components. Thus, we can assume that this study is breaking new ground in the development of a fungal growth model under the scope of an automated soil decontamination process and within the context of architectural research.

METHODS

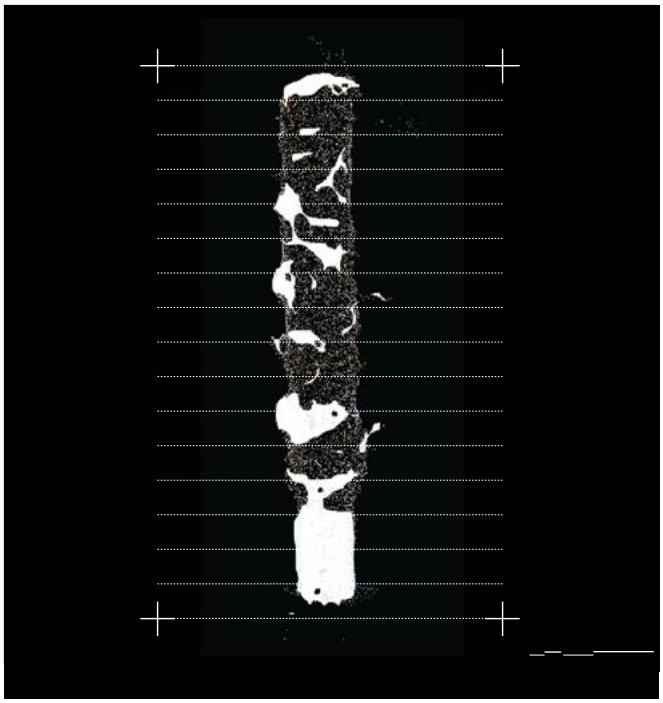
The study is structured in different parts, organized among analog and computational operations. The first part is focused on the design of a digitally fabricated apparatus for the observation of the mycelium growth. The next step is the generation of a 3D point cloud of this apparatus from a series of captured images using photogrammetry-based 3D scanning software (Agisoft PhotoScan). Following the 3D reconstruction process, the analysis of the 3D point cloud is done by parsing the data based on a specified color range in Rhinoceros 3D using Grasshopper. The computational analysis is then concluded by applying an octree subdivision to the parsed cloud in order to extract the main vectors that define the growing directions of the mycelium. The following part of the paper focuses on a detailed description of each part mentioned above. In order to establish an optimal process for the study, we tested different apparatuses with the intention to define the best method for data collection.

Apparatus

During the study, we developed several types of apparatus, each based on a combination of digital fabrication techniques and approaches to overcome the various challenges. The first apparatus was a 3D printed hexaedra structure with four faces capped with laser-cut metacrilatic plates. Between those faces, a grid of thin strings was inserted to provide a continuous surface, distributed in multiple directions where the mycelium could possibly grow. This first apparatus posed several difficulties for

3D scanning, as the spacing was very narrow and the strong symmetry of the structure generated significant noise in the point cloud. This led to the development of a few iterations of more linearly distributed grids. Overall, during the whole study, we designed a number of apparatuses, each with a specific observation focus, and tested different substrates and grid structures.

The main substrate consisted of straw, which was infused with a mix of water and honey to add complex sugars as a nutrient base for the mycelium. This substrate was inoculated with grain spawn of *Pleurotus ostreatus* (oyster mushroom), at a ratio of about 20% of the total substrate mass. The inoculation took place around a Bunsen burner gas flame to ensure a sterile working environment. Colonization of the different substrates was complete after 2 to 3 weeks, and produced mushrooms 5 weeks after inoculation. In some cases, we added plastic from 3D printing material in order to observe the possible decomposition of the material by the mycelium. For the digital fabrication process, the machines used were commercial 3D printers and laser cutters.



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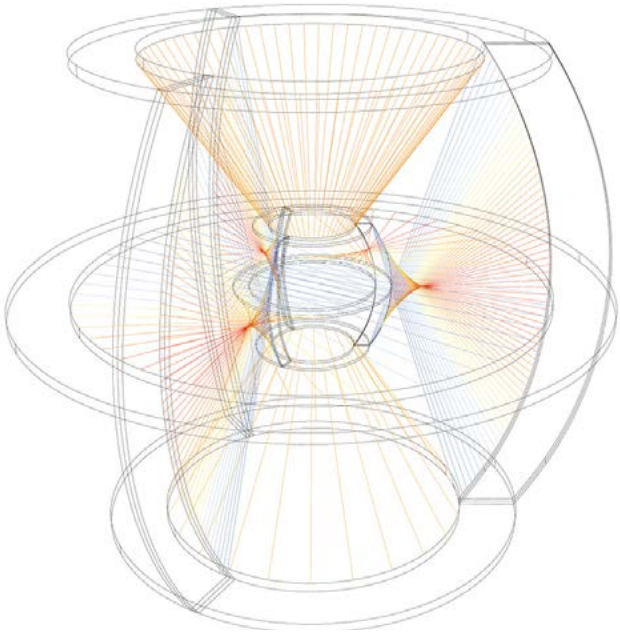
3D Scanning

With regards to the photogrammetry process, the collection of images was performed using a Nikon D3200 with a resolution of 25 megapixels and a fixed prime 50 mm lens. The analysis and reconstruction of the 3D point cloud was performed solely within PhotoScan, photogrammetry software which processes digital images to generate 3D point clouds.

The images used can be arbitrary, both in terms of positions as well as exposure or focal length—although a constant focal length was proven to give better results—thus the software is efficient in both controlled and uncontrolled conditions, which was ideal for our study. Other scanning frameworks were tested, mainly based on infrared depth sensors, but due to both the scanning inaccuracy as well as their outdoor performance limitations, they did not prove adequate for the purposes of the study. Image alignment and 3D point cloud reconstruction, which are fully automated processes in PhotoScan, were implemented in the study with adequately accurate results in both outdoor and indoor conditions. In order to get precise results for the level of accuracy needed for our analysis, around 30 to 50 pictures were used for every reconstruction iteration. Between building dense clouds and generating meshes, the processing time of reconstruction was on average 30 minutes, Once the cloud was generated, the entire process shifted to Rhinoceros 3D / Grasshopper.



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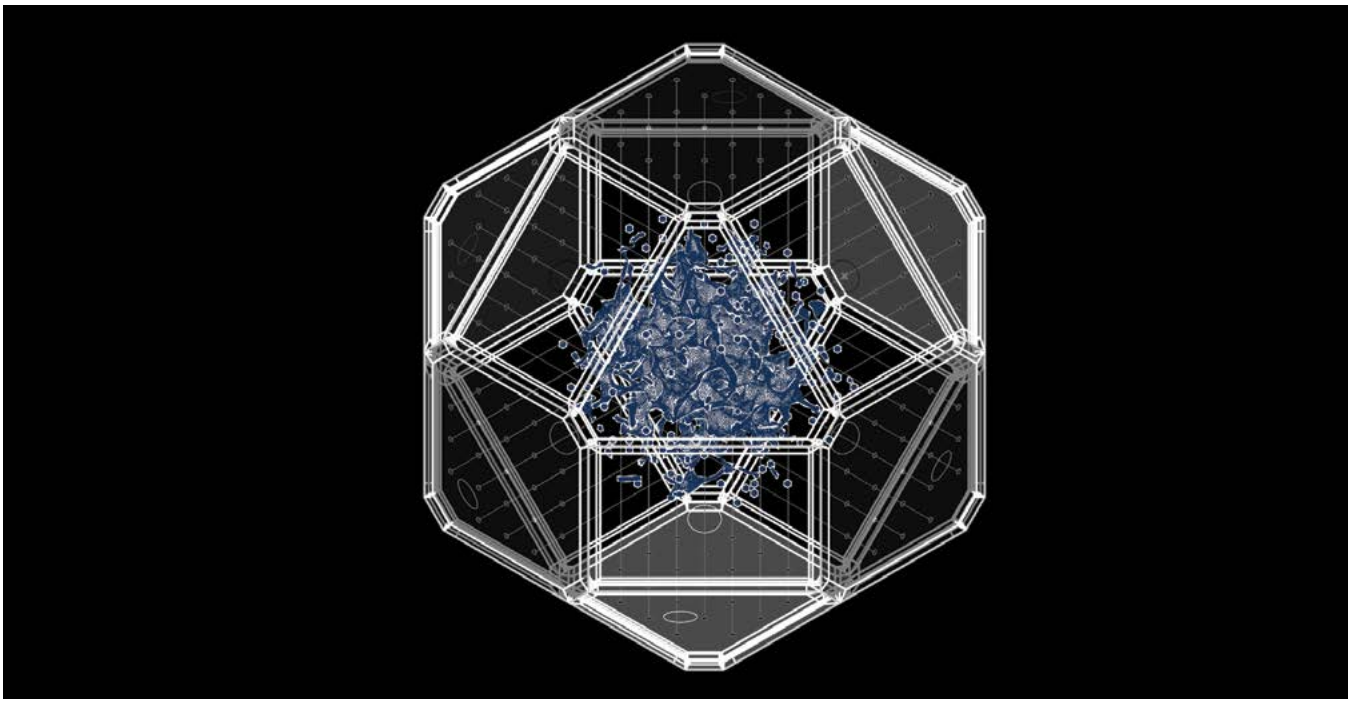
Growth Analysis

In Grasshopper, the main tool used was the Volvox library, developed as a part of the DURAARK project at the Center for



6 Apparatus 00. Designed to host different cameras to detect bio growth.

Information Technology and Architecture (CITA) by Henrik Leander Evers and Mateusz Zwierzycki. Volvox is a point cloud library which enables the creation, editing, and analysis of point cloud data. The library allows direct import of the formats which are exported from PhotoScan. Volvox allowed us to work with a large amount of points and perform multiple operations regardless of the quantity of data stored in each file. To detect the mycelium growth, a color range that corresponds to the mycelium was defined in Grasshopper. The point cloud is then clustered in 3D space by converting each band from RGB values to XYZ coordinates, and the range converted to a bounding box to select the growth points from the entire list. The final output is a list of boolean values which are used to cull the data from the point cloud. The entire point cloud list is also used in an octree subdivision, which organizes all points in the main eight quads of the 3D space recursively, by subdividing according to a minimum set of points that each cube can contain. Finally, from the overall amount of cubes generated for each quad in 3D space, we extract the main vectors representing the main growing direction of the mycelium.

The intention of this study is to perform this operation iteratively in order to generate a time-based growth model for the mycelium. At each time step, the growth can be scanned, reconstructed, and analyzed, thus creating an overlapping series of growth snapshots. This series will then be used to draw conclusions about the growth patterns of mycelium and to produce a growth model for our purposes.

RESULTS AND FUTURE WORK

Data acquisition

The study went through several apparatuses and different data collection methods, which resulted in a large amount of processed data. This data collection demonstrated substantial incremental improvements for each of the methods employed. From each single observation, we collected more than 50 pictures, generating a parse cloud of 56.000 points in PhotoScan, which was converted to a dense point cloud of more than 1.6 million points. Using the Volvox library, this point cloud was processed in Grasshopper, where we were able to parse the number of points associated with mycelium, translating percentage and growth direction into vectors. Collecting this information is crucial for our future work, which aims to generate a growth model that will allow us to predict the behavioral patterns for the organisms and which can be used to inform multiple design strategies.

Although our iterative experimentation has proven our initial hypothesis of detecting a growth pattern through our methodology, our experiments faced several difficulties in data collection, mainly related to the structure and accessibility of the camera in the internal part, and the ability of PhotoScan to reconstruct 3D point clouds in narrow and symmetric environments. One of the main pitfalls of the software is that it relies heavily on the pixel count of the acquired images. This makes the automation of the process cumbersome, as it relies on costly and

difficult-to-automate acquisition methods, such as high-definition DSLR cameras, to collect the image data.

Future work

At this stage, this initial study shows the potential of the method, but it has yet to be optimized by automating many of the steps, which are currently seen as separate entities. Specifically, the image acquisition could be automated with a robotic arm rotating around the apparatus. The 3D point cloud reconstruction could also be optimized by culling all information related to parts of the picture outside the apparatus. Although this operation is possible in PhotoScan, the method allowed in the software is not automatable, since it relies on manual correction of the pictures. For the computational methods implemented in Grasshopper, an interface needs to be developed which can store and allow access to all the information generated during the process. This interface can be open and accessible online to promote collaboration with other researchers developing similar studies. Automated image uploading and a data visualization service would enable an initial study of the overlapping analyses generated.

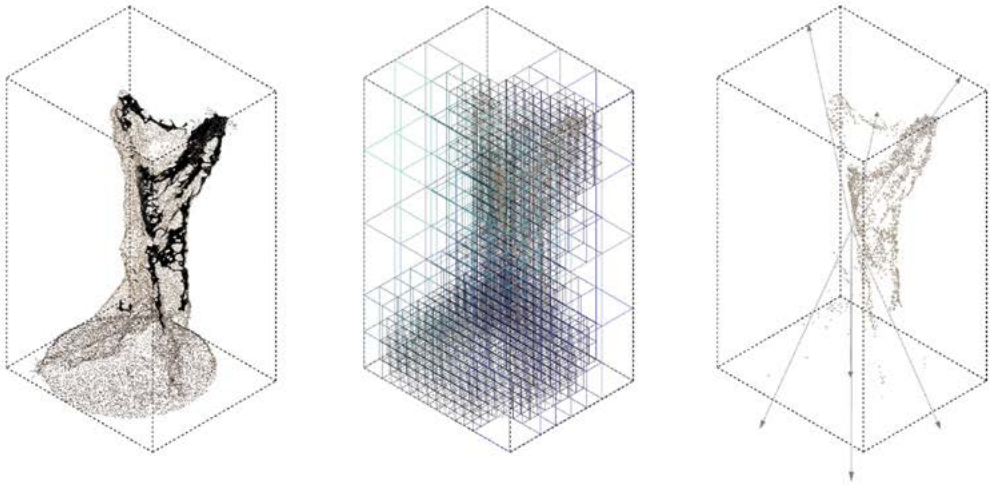
CONCLUSIONS

In this study, we presented a first step towards a methodology for the development of an automated soil decontamination process. The overarching research aims to produce an optimized bio-cell fungus seed that can be remotely populated using aerial transportation. This first step has proven that with the employment of appropriate technologies and computational techniques, we are able to get initial results of the growth pattern detection of mycelium. Although technical challenges still remain, we consider the initial results promising for future work and aim to continue developing this methodology further.

Significant further steps need to be taken, including the automation of the capturing and analysis process, and the development of accompanying appropriate interfaces for the dissemination of the work to a wider research audience. Nevertheless, we expect future developments to yield more interesting results and a more robust growth detection process, which will be the basis for the further development of the overall research goals. Moreover, this methodology can also be used to inform other studies associated not only with mycelium, but to similar image-based observations of living organisms.

The end goal of our research is to test the impact of mycelium growth on contaminated soil. Our next generation of apparatuses will focus on monitoring mycoremediation by adding data from pH sensors, humidity sensors, and thermal cameras to the dataset presented in this paper. The future work of this study is part of an overarching research effort to merge computational methods and traditional apparatuses for the observation of biological reactions. The results obtained by the overall process aims to converge to the development of a series of bio-cells—small hosts that can host both the mycelium and the substratum.

7 Preparation of the substrate.



8 Parsing point cloud, recursive sampling and growth orientation.

These bio-cells can then be involved in a wider aerial robotic research project involving drones, and focused on empowering reforestation and food production on dry or contaminated lands

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IMAGE CREDITS

Figures 1,3,4,5: (Sollazzo, 2016)
Figure 6: (Klein-Agbo-Ola, 2016)
Figure 2,7: (Postma. 2016)
Figure 8: (Sollazzo-Baseta, 2016)

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