

DNA Origami

Investigating the potential of different programs

Kingsdale Foundation school

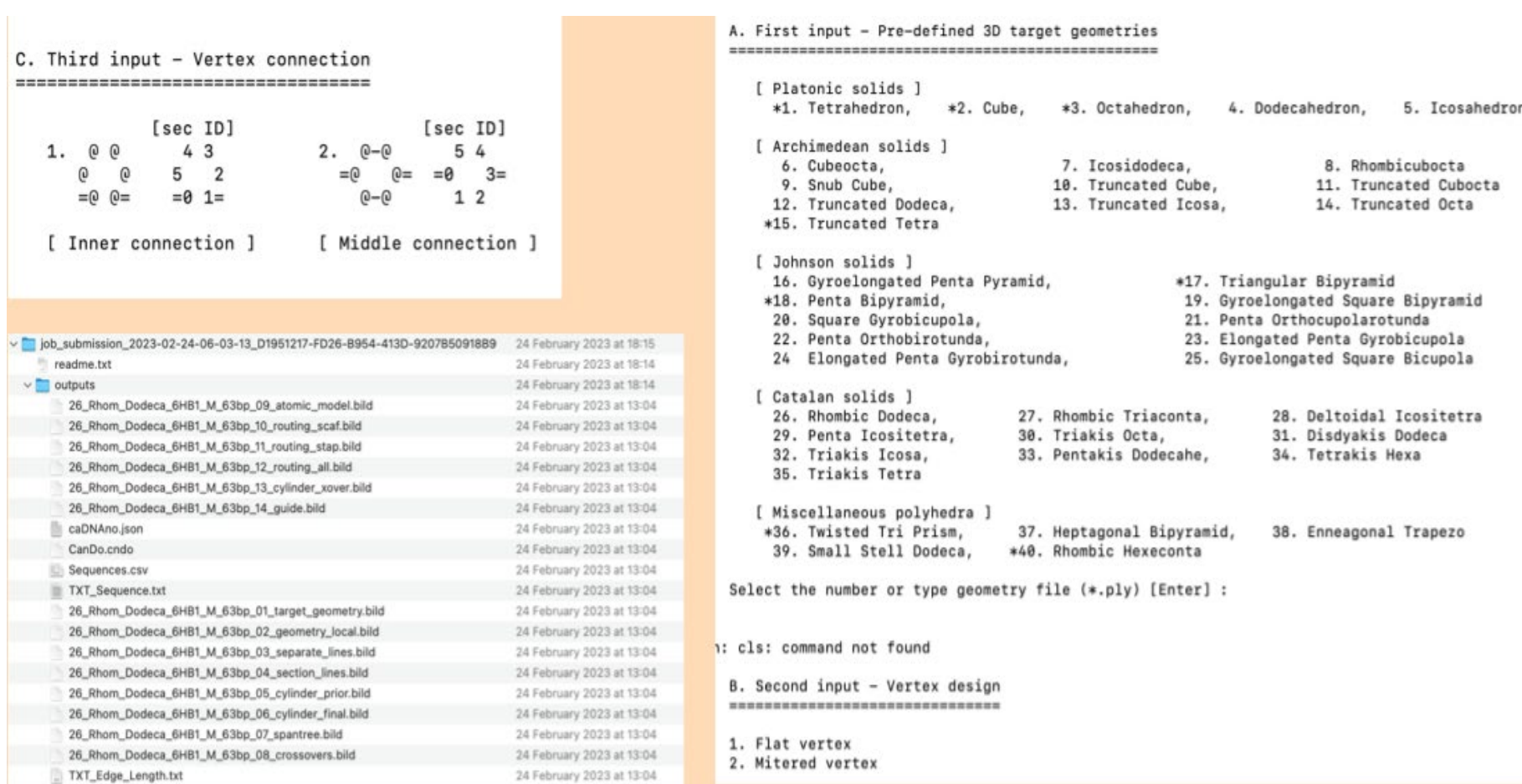
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Summary

During this project we have been investigating the opportunities that the field of DNA origami creates, we decided to further investigate the software that was used, scaDNAo, looking further into the possibilities of how the software could be made simpler and more efficient to use and also looked into using other programs like TALOS and Cando for structuring three-dimensional shapes.

Research aims

Firstly, we tried using python script to attempt to make the DNA origami software scaDNAo more efficient to use and to create larger structures faster with significantly less room for human error by automating some of the more lengthy processes. This was to be done by creating a computer programme that could format and insert two-dimensional shapes that are needed within the model, omitting large amounts of the manual, repetitive aspects of the scaDNAo software. This could be useful as on top of this being a far more time effective method, it would be far simpler to use and largely minimises the possibility for human error causing issues in the DNA structures. Secondly, we also decided to look further into the different programs used in creating DNA origami templates. One program was Talos which could be used to create sequences for the DNA bases of three-dimensional templates.



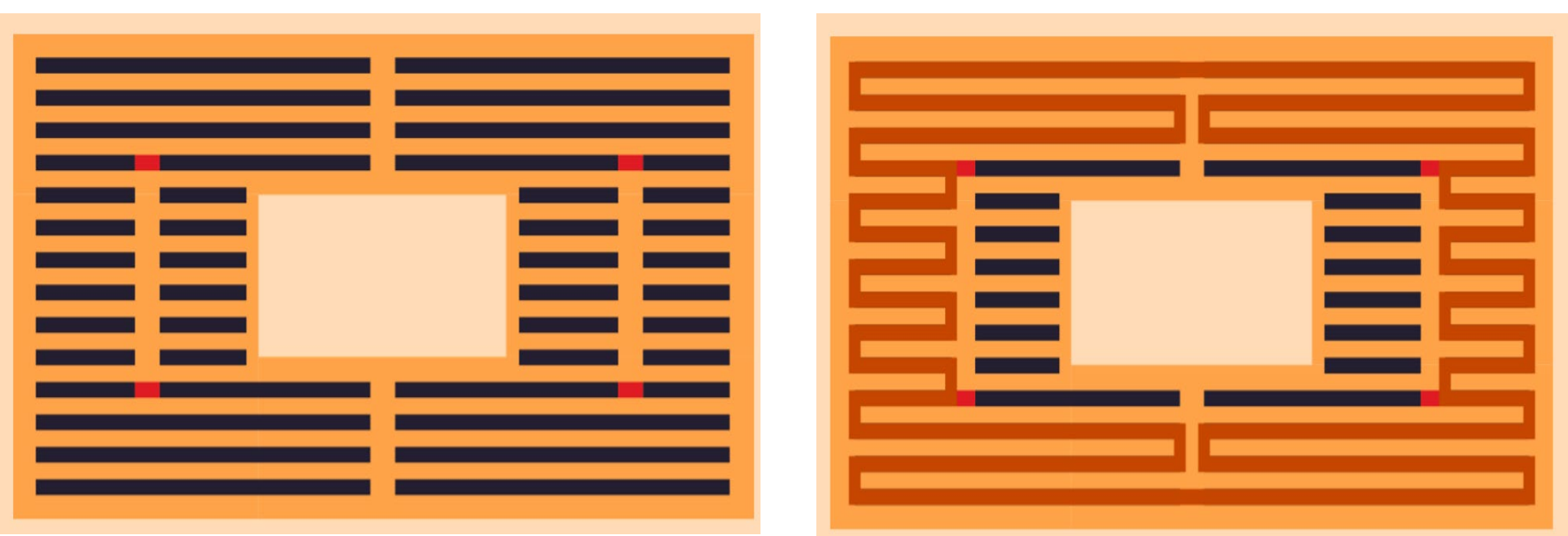
Talos' terminal format

Talos allows us to create parameters in which to generate a shape including vertex connection and vertex design. These are for a template of a cylinder made up of hexagonal frames.

Results of our research

Talos proved to be very effective for the sequencing and designing of three-dimensional shapes but its interface was significantly more complex than many other programs and was difficult to use. In the picture above you can see some of what we did on the software.

The program that we created from the scaDNAo python API had some success creating two-dimensional templates while still having some issues. The initial algorithm that we made, an outline of how it worked below, worked in creating some shapes but was not a very clear algorithm causing some incorrect routes. It also only worked in forming vertically symmetrical shapes with no holes in which is very limiting in terms of what it could be used for.



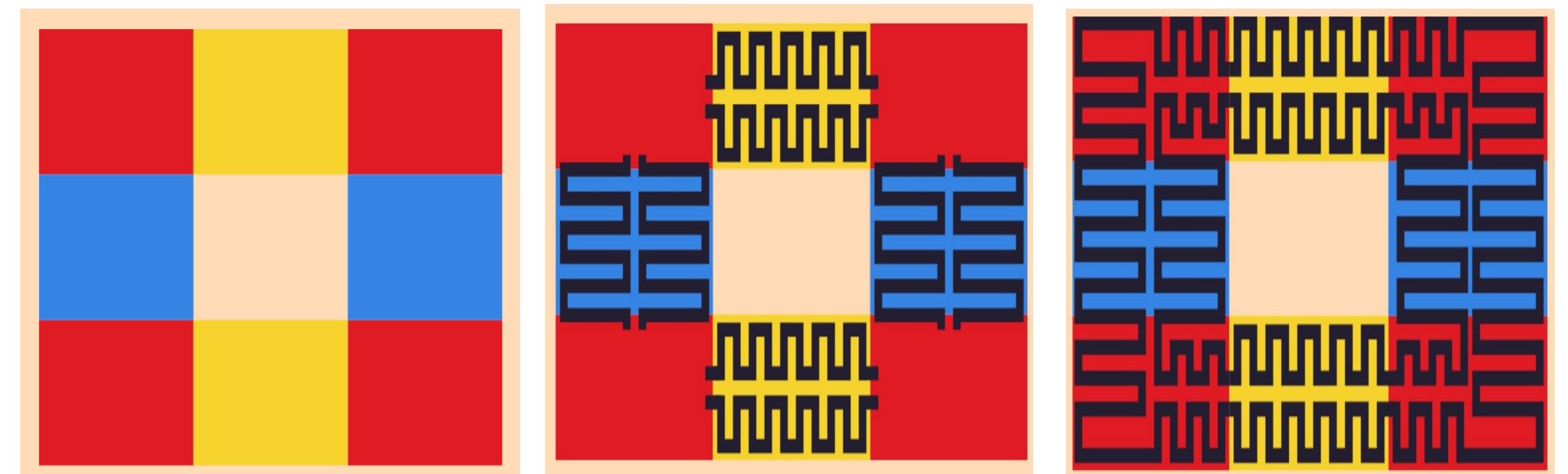
Filling and splitting

First the algorithm fills the area of the shape – in this case a rectangle with a hole – and then splits the rows appropriately so they can be turned into a functional scaffold.

Linking and staples

The program then links and staples together the strands to form the completed scaffold. As you can see a problem with this is the centre is not attached to the rest of the shape, this seems to occur in most shapes with holes.

As a result of the previously mentioned problems with the algorithm, we made a second model of the program that may be able to confront many of the issues faced by the first. The new algorithm changed this by splitting the shape into separate parts to be computed separately and then put together to form the scaffold, this is seen below. The new algorithm worked much better at handling various different types of shapes and created fewer errors; however we are yet to test how structurally sound these computer-generated scaffolds are and are currently limited to two-dimensional shapes.



Sectioning

First the shape is split up into sections; in this case horizontal, corner and vertical squares.

Separate computing

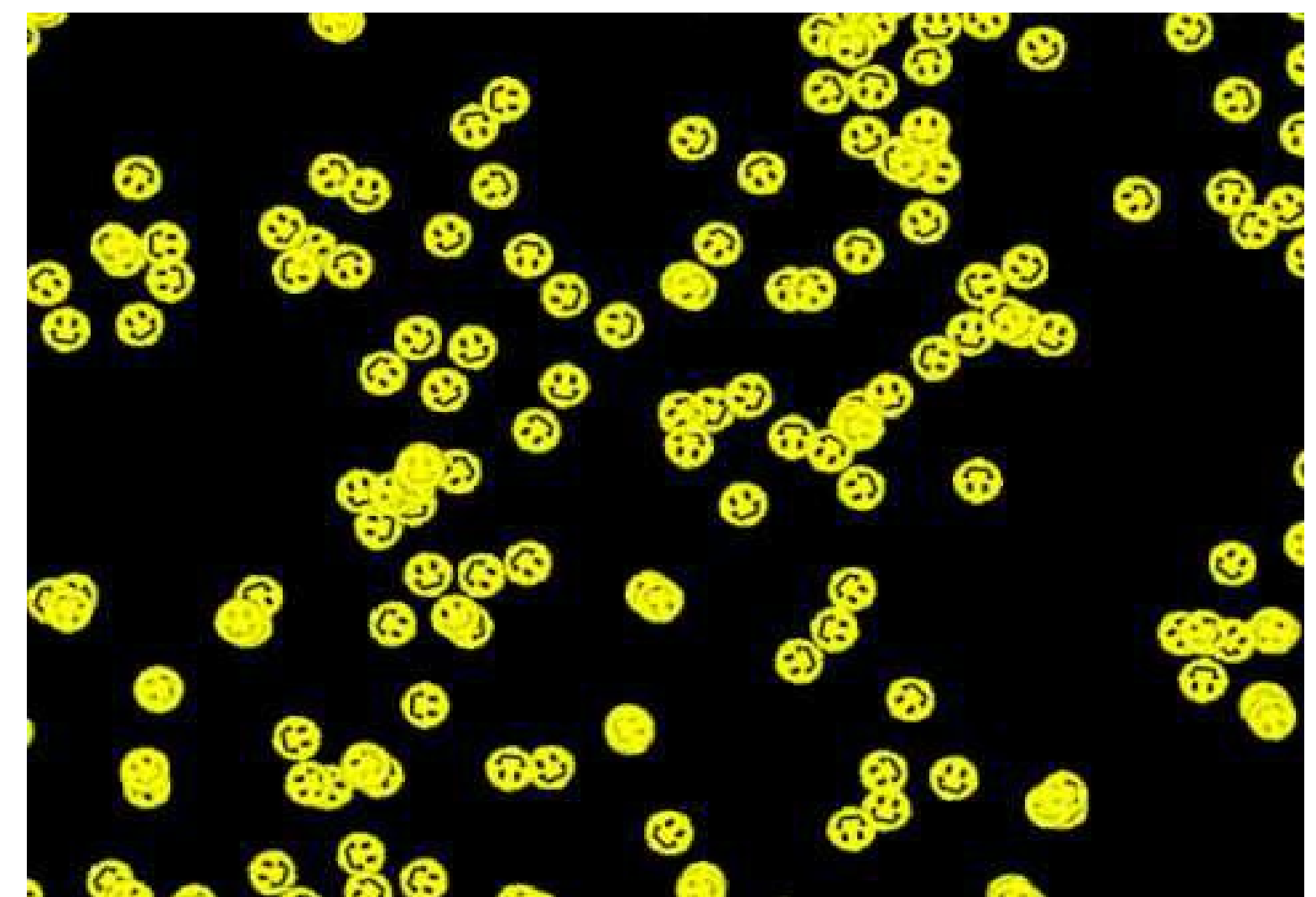
The separate sections are individually computed so they can be attached together.

Combining the chunks

lastly all of these pieces are combined, you can see here that the inner ring is not attached to the outer one, this could be fixed with staples but is not automated yet

Experimental method

As of now, we have not attempted to create our own DNA origami structures with the materials given to us through the Henry Braggs institute and IRIS. We will be creating smiley face shapes out of the DNA that should hopefully all going well turn out similar to the picture below. We should finish the process by July so we can send the results to be scanned and find out how it worked. We will be practicing and learning skills like pipetting and using a centrifuge.



Analysis & conclusion

Overall, we would say that continuing and further automation of DNA origami is a valuable endeavour and a very important one if these methods begin to see mainstream adoption. We hope that through our project we have helped demonstrate the large range of possibilities that can be provided by further automation to the field. Computer sequencing of three-dimensional shapes and creating two-dimensional scaffolds can greatly boost efficiency and accuracy of making these structures overall.