## **DEVELOPER** DOCUMENTATION

# INTRALATTICE

CORE MODULES

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This documentation was written for version 0.7.5

#### **AUDIENCE**

This is the developer documentation, and serves as a guide for people who want to contribute to the INTRALATTICE project, or are simply curious about the underlying algorithms. This document assumes you know what you have working knowledge of the INTRALATTICE core components. That is to say, you are familiar with the User Documentation.

### THE GITHUB REPOSITORY

This project is happily hosted on GitHub. Feel free to fork from

https://github.com/dnkrtz/intralattice/

## **SUPPORT**

If you have any issues, or want to report a bug, please contact <a href="mailto:support@intralattice.com">support@intralattice.com</a>

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#### **BACKGROUND**

The freedom of form enabled by 3D printing has allowed engineers to integrate new orders of complexity into their designs. The goal of this research was to develop a set of CAD tools for generating solid lattice structures within a design space. The software would be used to:

- Reduce volume/weight while maintaining structural integrity.
  - Increase surface area as a means of maximizing heat transfer.
  - Generate porosity in bone scaffolds and implants.
  - Serve as a platform for design optimization.

In doing so, it should always output a watertight mesh suited for 3D printing. The lack of flexibility of current software solutions was the driving force behind this project. We wanted to develop a flexible platform more conducive to research, which would allow us to explore and experiment with lattice design at a deeper level. The obvious first step was to decide in which environment we would develop our system. Rhinoceros is known to be very open ended, having its own engine for interpreting scripts (Python, C# and VB), and a powerful plugin SDK ( RhinoCommon ). Rhinoceros' Grasshopper addon is an algorithmic modeling tool widely used in architecture which provides an ideal interface for systematic design. In this visual interface, parameters and function components are combined sequentially to carry out the design of 3D models. By developing a set of custom components for Grasshopper, we established a modular workflow for lattice design.

That being said, if you are not familiar with Grasshopper, you are highly encouraged to have a look at the latest <u>Grasshopper Primer</u>, to bring you up to speed.

#### **DEVELOPMENT TEAM**

#### McGill Additive Design & Manufacturing Laboratory

**Aidan Kurtz** + Lead developer of the CORE modules.

+ Documentation, website, video tutorials.

+ GitHub repository management. Email: aidan.kurtz@mail.mcgill.ca

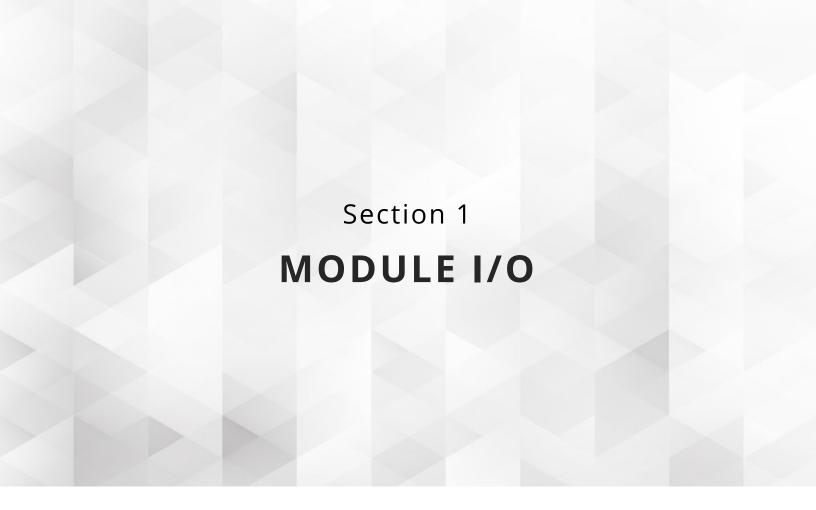
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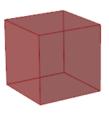




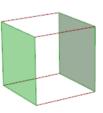
#### 2.1 CELL MODULE

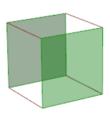
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A **valid unit cell** has the following property: opposing faces of the bounding box are identical. That is to say, opposing faces must have mirror nodes. To understand this, you can simply imagine appending the cell in each direction. In order to ensure continuity, opposing faces need to have the same nodes.









#### 2.2 FRAME MODULE

The frame algorithms all work in three steps. First, the cell topology input is formatted to a specific data structure. Second, the node grid is generated. Finally, the topology is mapped to this grid.

#### 2.2.1 DATA STRUCTURE

The first concept to introduce is the **UVW cell grid**. This is implemented in a <u>data tree structure</u>, where each unit cell in the lattice has a unique path (u,v,w). This format makes cell adjacency information intrinsic, since we know which cells are neighbouring a specific cell based on data paths alone. Expanding on the UVW concept, each cell can potentially have many nodes, and so we extend the data tree with an extra set of children, in the form of the **UVWI node grid**, which serves as our data structure for the lattice nodes. In other words, each node has a unique data path (u,v,w,i). This allows us to very quickly map relationships to this node grid, creating a lattice. To avoid creating duplicate nodes (and struts), we use the **UnitCell** Object Class to represent the unit cell topology.

Let's have a look at these fields progressively, building up the data as we do in the algorithm. The process of breaking down the topology into a malleable format involves 4 steps, summarized below.

**The first step** is to fix any intersection issues, by splitting all lines which intersect each other; the intersection points are in fact nodes, which need to be defined.

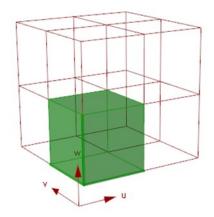
The second step starts building the UnitCell object. The list of lines is converted to a list of unique nodes (i.e. Nodes), and lines between these nodes are stored in two parallel lists, which each have their own purposes:

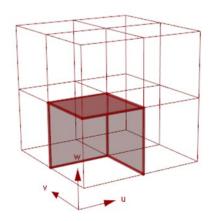
- List of node index pairs (i.e. NodePairs)
- List of node adjacency lists (i.e. NodeNeighbours)

**The third step** simply normalizes the unit cell. The cell is scaled to unit size (i.e. 1x1x1 bounding box), and moved to the origin (i.e. minimum corner at origin). To do this, the cell.Nodes values are modified.

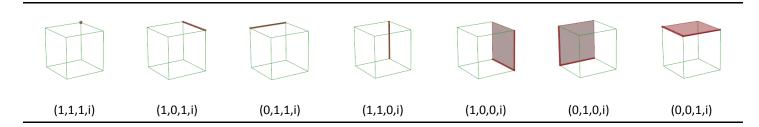
The fourth step involves computing the relative tree paths. To understand what this means, let's consider how the topology can be represented efficiently. Within a lattice, cells will always have neighbours, and so we need a way to make sure neighbours can share their interface nodes and struts, without creating duplicates. To do this, we state that <u>nodes and struts</u> lying on the positive faces of the unit cell boundary box, as well as all edges coincident with these faces, belong to neighbouring cells.

To better understand the concept of **relative paths**, consider the following illustrations. The green area is the current cell. The red area is the positive boundary of the cell – nodes lying in this area belong to neighbouring cells, so we must define their relative path in the tree.





To determine the relative path, we perform the following node location checks, in an else-if fashion. The relative paths corresponding to each case is shown below the image. The 'i' index will be determined based on the assumption that opposing faces are identical (cell is valid).



All other nodes have a relative path of (0,0,0,i), meaning they belong to the current cell. To determine the 'i' index for nodes which do not belong to the current cell, we rely on the assumption that opposing faces have identical nodes (cell is valid). Therefore, the Cell module must ensure the validity of the cell before passing it to the frame component.

In any case, by the end of this process, we have a valid UnitCell object, ready to be mapped to the design space.

#### 2.2.2 NODE MAPPING

Once the unit cell is translated to a UnitCell object, we are ready to map the grid of nodes to the design space. There are different ways of doing this. Let's first consider the simplest example possible: a box lattice, which is a uniform tessellation of unit cells in 3 orthogonal directions (i.e. 3D Cartesian).

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#### **NODE MAPPING — CONFORM**

#### 2.2.2 STRUT MAPPING

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#### STRUT MAPPING — CONFORM

#### 2.2 MESH MODULE

Based on Exoskeleton by David Stasiuk.

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## 3.0 CREATING USER OBJECTS (.GHO)

Grasshopper "User Objects" are essentially encapsulated Grasshopper algorithms, or black-box components. This is a great feature that allows you to quickly test algorithms and create prototype components.

# 3.1 CREATING ASSEMBLIES (.GHA)

Grasshopper assemblies are custom components written in C# with the RhinoCommon SDK.

