

ICFP Programming Contest 2018

Task Description (Full)

Thank you for purchasing a Deluxe Nanobot Matter Manipulation System (NMMS). Enclosed you will find one matter subspace pad and one fission/fusion-capable nanobot. Simply position an optional source object on the matter space pad, load an appropriate trace, place the nanobot at the origin of the pad, power on the system, and watch the nanobot begin construction, deconstruction, or reconstruction.

In comparison to the Standard Nanobot Matter Manipulation System, the Deluxe Nanobot Matter Manipulation System:

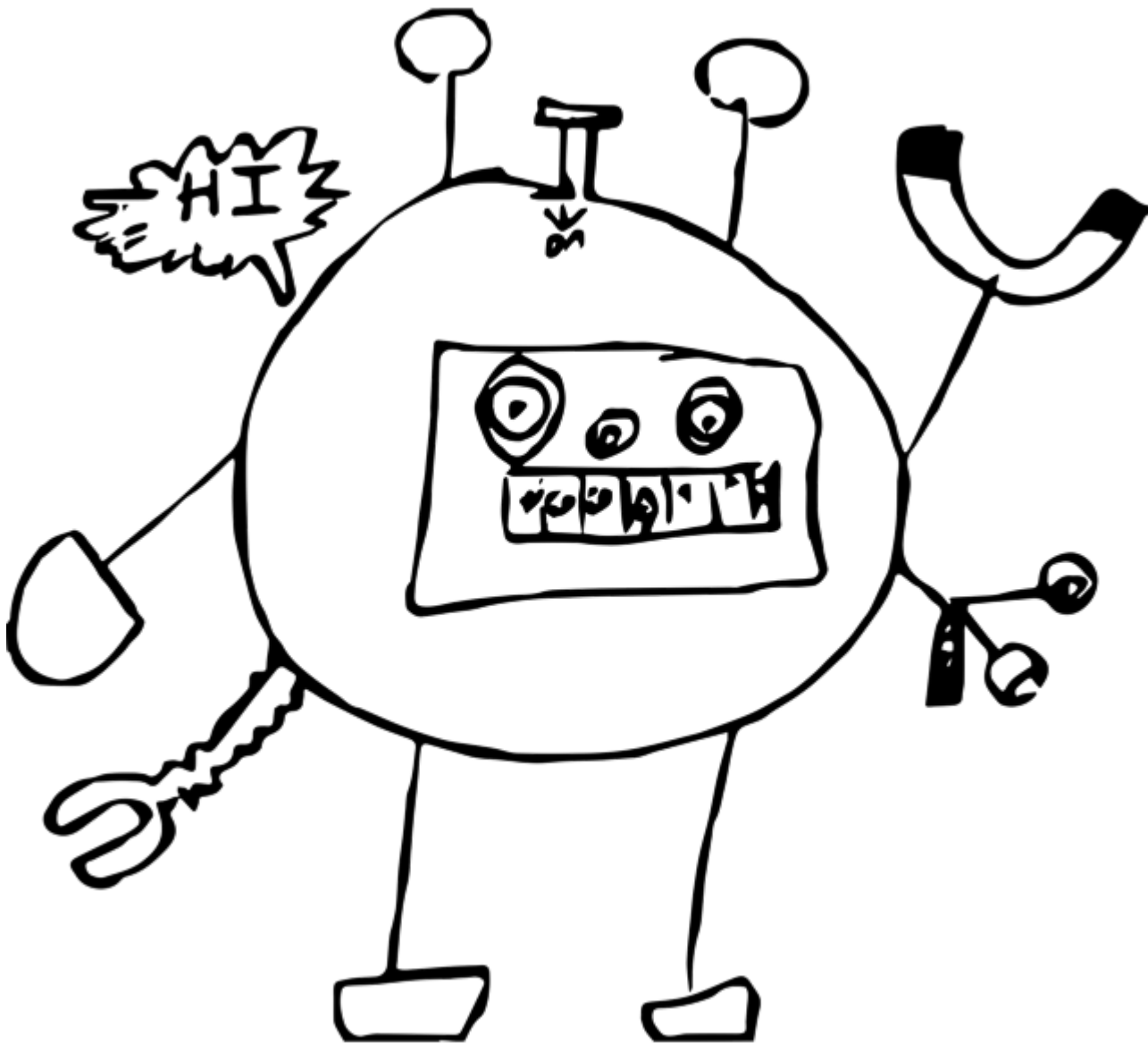
- Supports destroying matter in addition to creating matter; thus, your Deluxe Nanobot Matter Manipulation System can be used to construct target objects, destruct source objects, and reconstruct a source object into a target object.
- Has three new nanobot commands: *Void*, *GFill*, and *GVoid*
 - The *Void* command allows a nanobot to destroy matter in a voxel.
 - The *GFill* and *GVoid* commands allow a group of nanobots to create or destroy matter in a region.
- Initializes the nanobot with 39 seeds.

As an early adopter, please understand the shortage of freely available nanobot traces. Although your Deluxe Nanobot Matter Manipulation System ships with default nanobot traces for constructing, destructing, and reconstructing target models, they are extremely energy inefficient. We hope that you will enjoy generating your own nanobot traces and will contribute energy efficient ones back to the community.

Synopsis

Generate nanobot traces to construct, deconstruct, and reconstruct target 3D objects while minimizing energy used.

Nanobot Matter Manipulation System Overview



The initial nanobot is affectionately known as the Build-a-Tron 4000.

The Nanobot Matter Manipulation System is a breakthrough technology that enables a new form of 3D printing. The matter subspace pad utilizes advances in subspace physics to facilitate the light-weight conversion of energy to matter and vice versa. During execution, the pad generates a (global) resonant subspace field that establishes a matrix of voxels in which matter can be created and destroyed. The field holds matter at its fixed position in the matrix; under low harmonics, all matter must be part of a connected component that rests on the floor (“grounded”), while, under high harmonics, matter is unconstrained (“floating”). For precision construction, nanobots are used to focus the resonant subspace field during energy-matter conversion, either creating matter within a voxel or destroying matter within a voxel. Nanobots are able to move through empty voxels of the matrix; utilizing a local high-harmonics resonant subspace field, a nanobot’s position is unconstrained (“floating”). Nanobots are able to undergo fission (to fork off another nanobot) and fusion (to join with another nanobot).

Construction always begins and ends with a single nanobot at the origin of the matter subspace pad and proceeds in discrete time steps. Each time step, the pad generates a synchronous time-step signal that coordinates the actions of the nanobots. In response to the time-step signal, each active nanobot performs a single command. Commands include moving, swapping harmonics, creating and destroying matter, and undergoing fission and

fusion. All commands take effect simultaneously at the end of the time step. In general, it is an error if the commands of different nanobots interfere or have conflicting updates to the state of the system.

Each time step that the matter subspace pad is active has an energy cost, which depends on the volume of the space in which the resonant subspace field is being generated and the global harmonics. Similarly, each time step that a nanobot is active has an energy cost that depends on the command being performed.

Details

Coordinate System

The (global) resonant subspace field of the matter subspace pad establishes a cubical matrix (Cartesian grid) in finite three-dimensional Euclidean space, where each voxel of the matrix corresponds to a cubical volume of space. With respect to an observer, the x-axis extends from left to right, the y-axis extends from bottom to top, and the z-axis extends from near to far.

Resolutions

A **resolution** R specifies the number of voxels of the matrix along the x-, y-, and z-axes, where R is an integer and satisfies $0 < R \leq 250$.

Coordinates

A **coordinate** c specifies a particular voxel of the matrix and is written (x, y, z) , where x , y , and z are non-negative integers. For a matrix with resolution R , coordinate $(0, 0, 0)$ corresponds to the left, bottom, near voxel of the matrix and coordinate $(R - 1, R - 1, R - 1)$ corresponds to the right, top, far voxel of the matrix.

Coordinate Differences

A **coordinate difference** d specifies the relative position of one coordinate to another and is written $\langle dx, dy, dz \rangle$, where dx , dy , and dz are (positive or negative) integers. Adding distance $d = \langle dx, dy, dz \rangle$ to coordinate $c = (x, y, z)$, written $c + d$, yields the coordinate $(x + dx, y + dy, z + dz)$.

The **Manhattan length** (or L_1 norm) of a coordinate difference $d = \langle dx, dy, dz \rangle$ is written $m\text{len}(d)$ and defined as $|dx| + |dy| + |dz|$ (the sum of the absolute values of dx , dy , and dz). The Manhattan length of a coordinate difference is always a non-negative integer.

Coordinates c and c' are **adjacent** if there exists a coordinate difference d such that $c' = c + d$ and $m\text{len}(d) = 1$. More intuitively, coordinates are adjacent if they differ in exactly one component by exactly 1.

The **Chessboard length** (or Chebyshev distance or L_∞ norm) of a coordinate difference $d = \langle dx, dy, dz \rangle$ is written $c\text{len}(d)$ and defined as $\max(|dx|, |dy|, |dz|)$ (the maximum of the absolute values of dx , dy , and dz). The Chessboard length of a coordinate difference is always a non-negative integer.

Linear Coordinate Differences

A coordinate difference $d = \langle dx, dy, dz \rangle$ is a **linear coordinate difference** (notated ld) if $dx \neq 0 \wedge dy = 0 \wedge dz = 0$ or $dx = 0 \wedge dy \neq 0 \wedge dz = 0$ or $dx = 0 \wedge dy = 0 \wedge dz \neq 0$. That is, a coordinate difference is a linear coordinate difference if exactly one component is non-zero. (For a linear coordinate difference, the Manhattan length is always equal to the Chessboard length and is always greater than zero.)

A linear coordinate difference ld is a **short linear coordinate difference** (notated sld) if $m\text{len}(ld) \leq 5$. There are exactly 30 short linear coordinate differences.

A linear coordinate difference ld is a **long linear coordinate difference** (notated lld) if $m\text{len}(ld) \leq 15$. There are exactly 90 long linear coordinate differences.

Near Coordinate Differences

A coordinate difference d is a **near coordinate difference** (notated nd) if $0 < m\text{len}(d) \leq 2$ and $c\text{len}(d) = 1$. That is, a coordinate difference is a near coordinate difference if at least one and at most two components have the value -1 or 1 and the other components have the value 0 . There are exactly 18 near coordinate differences.

Far Coordinate Differences

A coordinate difference d is a **far coordinate difference** (notated fd) if $0 < c\text{len}(d) \leq 30$. That is, a coordinate difference is a far coordinate difference if all components have values between -30 and 30 and at least one component is non-zero. There are exactly 226980 far coordinate differences.

Regions

A **region** r specifies opposing corners of a rectangular cuboid and is written $[c_1, c_2]$. A coordinate $c = (x, y, z)$ is a member of a region $r = [c_1, c_2]$, where $c_1 = (x_1, y_1, z_1)$ and $c_2 = (x_2, y_2, z_2)$, if $\min(x_1, x_2) \leq x \leq \max(x_1, x_2)$, $\min(y_1, y_2) \leq y \leq \max(y_1, y_2)$, and $\min(z_1, z_2) \leq z \leq \max(z_1, z_2)$.

Two regions are considered equal if they have the same set of coordinates as members; equivalently, two regions are considered equal if they describe the same rectangular cuboid.

The **dimension** of a region $r = [(x_1, y_1, z_1), (x_2, y_2, z_2)]$ is written $\text{dim}(r)$ and is defined as $(x_1 = x_2 ? 0 : 1) + (y_1 = y_2 ? 0 : 1) + (z_1 = z_2 ? 0 : 1)$. That is, the dimension of a region counts the number of components that differ. A region with dimension 0 is a “point”; a region with dimension 1 is a “line”; a region with dimension 2 is a “plane”; and a region with dimension 3 is a “box”.

Matrix

A **matrix** M has an implicit resolution R and specifies the state of each voxel as either **Full** (containing matter) or **Void** (containing no matter). A matrix M can be considered a function from coordinates valid with respect to the resolution R to either **Full** or **Void**.

Grounded

A **Full** coordinate $c = (x, y, z)$ of a matrix M is **grounded** if either $y = 0$ or there exists an adjacent **Full** coordinate $c' = c + d$ (where $m\text{len}(d) = 1$) that is itself grounded. (Alternatively, a **Full** coordinate c is grounded if there is a (possibly empty) sequence of adjacent **Full** coordinates that starts with the coordinate c and ends with a **Full** coordinate $c' = (x', 0, z')$.)

System State and Execution

State

The state S of an executing Nanobot Matter Manipulation System is comprised of:

- *energy*: the amount of energy expended (an integer)
- *harmonics*: the (global) field harmonics (either *Low* or *High*)
- *matrix*: the matrix of voxels (each voxel either *Full* or *Empty*)
- *bots*: the set of active nanobots
- *trace*: the sequence of commands to be performed by nanobots

The state of an active nanobot *bot* is comprised of:

- *bid*: the (unique) identifier (a positive integer)
- *pos*: the position (a coordinate)
- *seeds*: the finite set of identifiers available for fission

Furthermore, a system state is **well-formed** if it satisfies the following properties:

- If the harmonics is *Low*, then all *Full* voxels of the matrix are grounded.
- Each active nanobot has a different identifier.
- The position of each active nanobot is distinct and is *Void* in the matrix.
- The seeds of each active nanobot are disjoint.
- The seeds of each active nanobot does not include the identifier of any active nanobot.

Execution

Each time step that there are active nanobots, commands are taken from the trace and assigned to nanobots and the system state is updated in response to the commands performed by each nanobot.

In general, it is an error if the commands of different nanobots **interfere**. Examples of interference include: two nanobots moving through the same coordinate; one nanobot creating matter at a coordinate and another nanobot destroying matter at the same coordinate; one nanobot fissioning a nanobot at a coordinate and another nanobot waiting in the same coordinate. More specifically, the commands of one nanobot group *bots₁* interferes with the commands of another nanobot group *bots₂* if the volatile coordinates of the commands of *bots₁* include any of the volatile coordinates of the commands of *bots₂*. The **volatile coordinates** of a nanobot group are those coordinates occupied by nanobots of the group and being “used” by the commands of the group during the time step.

At the beginning of a time step, it is an error if the system state is not well-formed.

The commands to be performed by the active nanobots are taken from the trace. Let $S.bots = \{bot_1, bot_2, \dots, bot_n\}$, where $bot_1.bid < bot_2.bid < \dots < bot_n.bid$. (In other words, the n active nanobots are sorted by identifier.) Let $S.trace = cmd_1 cmd_2 \dots cmd_n \dots$. (It is an error if $S.trace$ contains less than n commands.) Each nanobot bot_i is assigned the command cmd_i and nanobot command groups are formed. Command pre-conditions that would lead to an error are checked with respect to the starting state matrix (before any updates to the state matrix). Interference between the volatile coordinates of nanobot command groups that would lead to an error are checked.

Assuming no errors, then the system state is be updated:

- There is an energy cost each time step to maintain the (global) resonant subspace field:

```

if (S.harmonics == High)
    S.energy := S.energy + 30 * R * R * R
else // (S.harmonics == Low)
    S.energy := S.energy + 3 * R * R * R
endif

```

- There is an energy cost each time step for each active nanobot to maintain its (local) resonant subspace field:

$$S.energy := S.energy + 20 * n$$

- The effects of each nanobot command group on the state energy, matrix, and active bots are applied to the system state. Because none of the nanobot command groups interfere, the order in which the effects of each nanobot command group are applied does not matter.
- The performed commands are removed from the trace:

$$S.trace := drop(S.trace, n)$$

Nanobot Commands

Singleton Nanobot Commands

Most commands are performed by a single nanobot in isolation. In the following descriptions, assume that the command is being performed by nanobot *bot* and let $c = bot.pos$. Note that c (the current position of the nanobot) is always a volatile coordinate, because there would be interference if the command of any other nanobot were to “use” the current position of the nanobot.

- ***Halt:***

It is an error if $c \neq (0, 0, 0)$ or if $S.bots \neq \{ bot \}$ or if $S.harmonics \neq Low$.

The volatile coordinate of this command is the coordinate c .

The effect of this command is:

$$S.bots := \{ \}$$

(The nanobot *bot* is removed from the set of active bots and the system halts. Note that the pre-condition $S.bots == \{ bot \}$ ensures that this was the only nanobot remaining in the system.)

- ***Wait:***

The volatile coordinate of this command is the coordinate c .

This command has no effect on the system state.

- ***Flip:***

The volatile coordinate of this command is the coordinate c .

The effect of this command is:

```
if (S.harmonics == High)
  S.harmonics := Low
else // (S.harmonics == Low)
  S.harmonics := High
endif
```

- ***SMove lld*** (Straight Move):

(*lld* is a long linear coordinate difference.)

Let $c' = c + lld$.

It is an error if c' is not a valid coordinate with respect to the resolution of the matrix. It is an error if any coordinate in the region $[c, c']$ is *Full* in the matrix.

The volatile coordinates of this command are all coordinates in the region $[c, c']$.

The effect of this command is:

$$\begin{aligned} bot.pos &:= c' \\ S.energy &:= S.energy + 2 * mlen(lld) \end{aligned}$$

(The nanobot's position is updated and there is an energy cost proportional the Manhattan length of the move.)

- ***LMove sld1 sld2*** (L Move):

(*sld1* and *sld2* are short linear coordinate differences.)

Let $c' = c + sld1$ and $c'' = c' + sld2$.

It is an error if c' or c'' is not a valid coordinate with respect to the resolution of the matrix. It is an error if any coordinate in the region $[c, c']$ or in the region $[c', c'']$ is *Full* in the matrix.

The volatile coordinates of this command are all coordinates in the regions $[c, c']$ and $[c', c'']$.

The effect of this command is:

$$\begin{aligned} bot.pos &:= c'' \\ S.energy &:= S.energy + 2 * (mlen(sld_1) + 2 + mlen(sld_2)) \end{aligned}$$

(The nanobot's position is updated and there is an energy cost proportional the Manhattan length of the move and a small “turning” cost.)

- ***Fission nd m***:

(*nd* is a near coordinate difference and *m* is a non-negative integer.)

It is an error if $bid.seeds = \{\}$.

Let $\{bid_1, bid_2, \dots, bid_n\} = bid.seeds$ (where $bid_1 < bid_2 < \dots < bid_n$).

Let $c' = c + nd$.

It is an error if c' is not a valid coordinate with respect to the resolution of the matrix. It is an error if coordinate c' is *Full* in the matrix. It is an error if $n < m + 1$.

The volatile coordinates of this command are the coordinates c and c' .

The effect of this command is:

$$\begin{aligned} bot.seeds &:= \{bid_{m+2}, \dots, bid_n\} \\ bot'.bid &:= bid_1 \\ bot'.pos &:= c' \end{aligned}$$

```

bot'.seeds := {bid2, ..., bidm+1}
S.bots := union(S.bots, { bot' })
S.energy := S.energy + 24

```

(The lowest $m + 1$ identifiers are removed from the parent bot's seeds. A new child bot *bot'* is added to the set of active bots. The lowest of the removed identifiers becomes the identifier of the child bot and the remaining m of the removed identifiers become the seeds of the child bot. Energy is expended during the creation of the child bot.)

- **Fill *nd*:**

(*nd* is a near coordinate difference.)

Let $c' = c + nd$.

It is an error if c' is not a valid coordinate with respect to the resolution of the matrix.

The volatile coordinates of this command are the coordinates c and c' .

The effect of this command is:

```

if (S.matrix(c') == Void)
  S.matrix(c') := Full
  S.energy := S.energy + 12
else // (S.matrix(c') == Full)
  S.energy := S.energy + 6
endif

```

(If the voxel had no matter, then energy is converted to matter (a positive energy cost). If the voxel had matter, then energy is lost (a positive energy cost).)

- **Void *nd*:**

(*nd* is a near coordinate difference.)

Let $c' = c + nd$.

It is an error if c' is not a valid coordinate with respect to the resolution of the matrix.

The volatile coordinates of this command are the coordinates c and c' .

The effect of this command is:

```

if (S.matrix(c') == Full)
  S.matrix(c') := Void
  S.energy := S.energy - 12
else // (S.matrix(c') == Void)
  S.energy := S.energy + 3
endif

```

(If the voxel had matter, then the matter is converted to energy (a negative energy cost). If the voxel had no matter, then energy is lost (a positive energy cost).)

Group Nanobot Commands

Some nanobot commands are performed through the coordinated action of a group of two or more nanobots. It is an error if a group is missing one or more partners.

- ***FusionP nd*** (Fusion Primary), ***FusionS nd*** (Fusion Secondary):

(*nd* is a near coordinate difference.)

There are two nanobots bot_p and bot_s such that bot_p is performing ***FusionP nd_p*** and bot_s is performing ***FusionS nd_s***, where $bot_p.pos + nd_p = bot_s.pos$ and $bot_s.pos + nd_s = bot_p.pos$. (The primary nanobot identifies the secondary nanobot's position and the secondary nanobot identifies the primary nanobot's position.)

It is an error if either coordinate $bot_p.pos + nd_p$ or coordinate $bot_s.pos + nd_s$ is not a valid coordinate with respect to the resolution of the matrix.

The volatile coordinates of this command group are the coordinates $bot_p.pos$ and $bot_s.pos$.

The effect of this command group is:

```
S.bots := diff(S.bots, { bots })
botp.seeds := union(botp.seeds, { bots.bid }, bots.seeds)
S.energy := S.energy - 24
```

(The secondary nanobot is removed from the set of active nanobots. The secondary nanobot's identifier and the secondary nanobot's seeds are added to the primary nanobot's seeds. Energy is regained during the destruction of the secondary bot.)

- ***GFill nd fd*** (Group Fill):

(*nd* is a near coordinate difference and *fd* is a far coordinate difference.)

Let r be a region and let $n = 2^{dim(r)}$.

There are n nanobots bot_1, \dots, bot_n such that each bot_i is performing ***GFill nd_i fd_i***, where $r = [bot_i.pos + nd_i, bot_i.pos + nd_i + fd_i]$. (Recall that two regions are considered equal if they have the same set of coordinates as members; equivalently, if they describe the same rectangular cuboid.)

It is an error if any coordinate $bot_i.pos + nd_i$ or coordinate $bot_i.pos + nd_i + fd_i$ is not a valid coordinate with respect to the resolution of the matrix. It is also an error if $bot_i.pos + nd_i = bot_j.pos + nd_j$ (for $i \neq j$). It is also an error if any coordinate $bot_i.pos$ is a member of region r .

Intuitively, the group of nanobots identify a region, with a distinct nanobot at each corner. Two nanobots can fill a "line"; four nanobots can fill a "plane"; and eight nanobots can fill a "box".

The volatile coordinates of this command are the coordinates $bot_1.pos, \dots, bot_n.pos$ and all coordinates of the region r .

The effect of this command group is:

```
for (c' in r)
  if (S.matrix(c') == Void)
    S.matrix(c') := Full
    S.energy := S.energy + 12
```

```

    else // ( $S.matrix(c') == Full$ )
       $S.energy := S.energy + 6$ 
    endif
  endfor

```

(If a voxel in the region had no matter, then energy is converted to matter (a positive energy cost). If a voxel in the region had matter, then energy is lost (a positive energy cost).)

- **GVoid** $nd\ fd$ (Group Void):

(nd is a near coordinate difference and fd is a far coordinate difference.)

Let r be a region and let $n = 2^{dim(r)}$.

There are n nanobots bot_1, \dots, bot_n such that each bot_i is performing **GVoid** $nd_i fd_i$, where $r = [bot_i.pos + nd_i, bot_i.pos + nd_i + fd_i]$. (Recall that two regions are considered equal if they have the same set of coordinates as members; equivalently, if they describe the same rectangular cuboid.)

It is an error if any coordinate $bot_i.pos + nd_i$ or coordinate $bot_i.pos + nd_i + fd_i$ is not a valid coordinate with respect to the resolution of the matrix. It is also an error if $bot_i.pos + nd_i = bot_j.pos + nd_j$ (for $i \neq j$). It is also an error if any coordinate $bot_i.pos$ is a member of region r .

Intuitively, the group of nanobots identify a region, with a distinct nanobot at each corner. Two nanobots can void a “line”; four nanobots can void a “plane”; and eight nanobots can void a “box”.

The volatile coordinates of this command are the coordinates $bot_1.pos, \dots, bot_n.pos$ and all coordinates of the region r .

```

  for ( $c'$  in  $r$ )
    if ( $S.matrix(c') == Full$ )
       $S.matrix(c') := Void$ 
       $S.energy := S.energy - 12$ 
    else // ( $S.matrix(c') == Void$ )
       $S.energy := S.energy + 3$ 
    endif
  endfor

```

(If the voxel in the region had matter, then the matter is converted to energy (a negative energy cost). If the voxel in the region had no matter, then energy is lost (a positive energy cost).)

Traces

A **trace** T specifies the commands performed by each nanobot during an execution. A trace is simply a sequence of commands, implicitly ordered first by time step and then by nanobot identifier.

When executing a time step with n active nanobots, the n commands are taken from the trace and assigned to the active nanobots in identifier order (the first command is assigned to the nanobot with smallest identifier, the second command is assigned to the nanobot with the second smallest identifier, ..., the last command is assigned to the nanobot with the largest identifier).

Trace Files

A trace file is a binary encoding of a trace.

By convention, a trace file has the extension `.nbt`.

A trace file is simply a sequence of encoded commands, where each command is encoded as one, two, or four bytes.

In the following $[b_n \dots b_2 b_1]^n$ represents an n -bit value, where b_1 is the least-significant bit and b_n is the most-significant bit and $[\dots \langle x \rangle^m \dots]^n$ represents the embedding of an m -bit value within a larger n -bit value.

Encoding Coordinate Differences

The different types of coordinate differences that appear in commands have distinct encodings.

Encoding Linear Coordinate Differences

A short linear coordinate difference $sld = \langle dx, dy, dz \rangle$ is encoded as a 2-bit axis a and a 4-bit (unsigned) integer i as follows:

- if $dx \neq 0$, then $a = [01]^2$ and $i = dx + 5$
- if $dy \neq 0$, then $a = [10]^2$ and $i = dy + 5$
- if $dz \neq 0$, then $a = [11]^2$ and $i = dz + 5$

Recall that exactly one component of a short linear coordinate difference is non-zero and a short linear coordinate difference has Manhattan length greater than zero and less than or equal to 5.

A long linear coordinate difference $lld = \langle dx, dy, dz \rangle$ is encoded as a 2-bit axis a and a 5-bit (unsigned) integer i as follows:

- if $dx \neq 0$, then $a = [01]^2$ and $i = dx + 15$
- if $dy \neq 0$, then $a = [10]^2$ and $i = dy + 15$
- if $dz \neq 0$, then $a = [11]^2$ and $i = dz + 15$

Recall that exactly one component of a long linear coordinate difference is non-zero and a long linear coordinate difference has Manhattan length greater than zero and less than or equal to 15.

Encoding Near Coordinate Differences

A near coordinate difference $nd = \langle dx, dy, dz \rangle$ is encoded as a 5-bit (unsigned) integer with the value $(dx + 1) * 9 + (dy + 1) * 3 + (dz + 1)$. Recall that each component of a near coordinate difference must have the value -1 , 0 , or 1 , but not all combinations are legal. In particular, $\langle 1, 1, 1 \rangle$ is not a near coordinate difference; hence the 5-bit value $[11111]^5 = 31$ is not the encoding of any near coordinate difference.

Encoding Far Coordinate Differences

A far coordinate difference $fd = \langle dx, dy, dz \rangle$ is encoded as a sequence of three 8-bit (unsigned) integers with the values $dx + 30$, $dy + 30$, and $dz + 30$. Recall that at least one component of a far coordinate difference is non-zero and each component of a far coordinate difference has a value between -30 and 30 .

Encoding Commands

Each command is encoded by one, two, or four bytes as follows:

- **Halt:**

$$[11111111]^8$$

- **Wait:**

$$[11111110]^8$$

- **Flip:**

$$[11111101]^8$$

- **SMove lld:**

$$[00\langle lld.a \rangle^2 0100]^8 [000\langle lld.i \rangle^5]^8$$

For example, **SMove** $\langle 12, 0, 0 \rangle$ is encoded as $[00010100] [00011011]$ and **SMove** $\langle 0, 0, -4 \rangle$ is encoded as $[00110100] [00001011]$.

- **LMove sld1 sld2:**

$$[\langle sld2.a \rangle^2 \langle sld1.a \rangle^2 1100]^8 [\langle sld2.i \rangle^4 \langle sld1.i \rangle^4]^8$$

For example, **LMove** $\langle 3, 0, 0 \rangle \langle 0, -5, 0 \rangle$ is encoded as $[10011100] [00001000]$ and **LMove** $\langle 0, -2, 0 \rangle \langle 0, 0, 2 \rangle$ is encoded as $[11101100] [01110011]$.

- **FusionP nd:**

$$[\langle nd \rangle^5 111]^8$$

For example, **FusionP** $\langle -1, 1, 0 \rangle$ is encoded as $[00111111]$.

- **FusionS nd:**

$$[\langle nd \rangle^5 110]^8$$

For example, **FusionS** $\langle 1, -1, 0 \rangle$ is encoded as $[10011110]$.

- **Fission nd m:**

$$[\langle nd \rangle^5 101]^8 [\langle m \rangle^8]^8$$

The non-negative integer m is encoded as an 8-bit (unsigned) integer with the value m .

For example, **Fission** $\langle 0, 0, 1 \rangle 5$ is encoded as $[01110101] [00000101]$.

- **Fill nd:**

$$[\langle nd \rangle^5 011]^8$$

For example, **Fill** $\langle 0, -1, 0 \rangle$ is encoded as $[01010011]$.

- **Void nd:**

$$[\langle nd \rangle^5 010]^8$$

For example, **Void** $\langle 1, 0, 1 \rangle$ is encoded as $[10111010]$.

- **GFill** $nd\ fd$:

$$[\llbracket nd \rrbracket^5 001]^8 [\llbracket fd.dx \rrbracket^8]^8 [\llbracket fd.dy \rrbracket^8]^8 [\llbracket fd.dz \rrbracket^8]^8$$

For example, **GFill** $\langle 0, -1, 0 \rangle \langle 10, -15, 20 \rangle$ is encoded as $[01010001] [00101000] [00001111] [00110010]$.

- **GVoid** $nd\ fd$:

$$[\llbracket nd \rrbracket^5 000]^8 [\llbracket fd.dx \rrbracket^8]^8 [\llbracket fd.dy \rrbracket^8]^8 [\llbracket fd.dz \rrbracket^8]^8$$

For example, **GVoid** $\langle 1, 0, 0 \rangle \langle 5, 5, -5 \rangle$ is encoded as $[10110000] [00100011] [00100011] [00011001]$.

Models

A **model** Mdl specifies a 3D object. A model is comprised of the resolution R of a matrix (which is large enough to contain the object) and the set of *Full* coordinates of the matrix that make up the object.

A model is **well-formed** if

- All coordinates of the set of *Full* coordinates must not belong to the reserved left-, right-, top-, near-, or far-face regions of the space. That is, all *Full* coordinates (x, y, z) satisfy $1 \leq x \leq R - 2$ and $0 \leq y \leq R - 2$ and $1 \leq z \leq R - 2$.
- All coordinates of the set of *Full* coordinates must be **grounded**. That is, all *Full* coordinates $c = (x, y, z)$ satisfy either $y = 0$ or there exists an adjacent *Full* coordinate $c' = c + d$ (where $mle(d) = 1$) that is grounded.

Model Files

A model file is binary encoding of a model. (Note that this binary encoding handles both ill-formed and well-formed models.)

By convention, a model file has the extension `.mdl`.

The first byte of the model file encodes the resolution R , interpreting the byte as an 8-bit (unsigned) integer.

The remaining $\lceil (R \times R \times R) / 8 \rceil$ bytes of the model file encode the set of *Full* coordinates. The sequence of bytes are interpreted as a sequence of bits corresponding to the coordinates of the matrix by traversing the x-dimension from 0 to $R - 1$, traversing the y-dimension from 0 to $R - 1$, and traversing the z-dimension from 0 to $R - 1$. More explicitly, coordinate (x, y, z) is *Full* in the model's matrix if and only if bit $x \times R \times R + y \times R + z$ is set. Note that some high-bits of the last byte of the model file may be unused.

Extended Model Files

An extended model file is a binary encoding of a model and a set of nanobot identifiers and positions.

By convention, a model file has the extension `.xmdl`.

As with a model file, the first byte of the extended model file encodes the resolution R , interpreting the byte as an 8-bit (unsigned) integer, and the subsequent $\lceil (R \times R \times R) / 8 \rceil$ bytes of the extended model file encode the set of *Full* coordinates.

Subsequent 4-byte sequences encode the identifier *bid* and position (x, y, z) of nanobots. The first byte encodes *bid*, the second byte encodes x , the third byte encodes y , and the fourth byte encodes z , in each case interpreting the byte as an 8-bit (unsigned) integer.

Model Viewer

A JavaScript and WebGL-based [model viewer](#) is available.

Full Contest

[Saturday 21 July 2018 16:00 UTC](#) to [Monday 23 July 2018 16:00 UTC](#)

Generate and submit nanobot traces to assemble, disassemble, and reassemble target 3D models while minimizing energy used. The initial nanobot (the Build-a-Tron 4000) has 39 seeds.

Problems

Download [problemsF.zip](#), which is a collection of (well-formed) target model files named *FANNN_tgt.mdl*, (well-formed) source model files named *FDNNN_src.mdl*, and (well-formed) source model files and target model files named *FRNNN_src.mdl* and *FRNNN_tgt.mdl*. For each target model file *FANNN_tgt.mdl*, generate a trace file named *FANNN.nbt* that assembles the target model; for each source model file *FDNNN_src.mdl*, generate a trace file named *FDNNN.nbt* that disassembles the source model; for each source model file *FRNNN_src.mdl* and target model file *FRNNN_tgt.mdl* (guaranteed to have equal resolutions), generate a trace file named *FRNNN.nbt* that reassembles from the source model to the target model. A *problemsF.txt* file acknowledges the sources for the problem models.

Assembly Problems

For each *FANNN_tgt.mdl* and corresponding *FANNN.nbt*, let Mdl_{tgt} be the target model encoded by *FANNN_tgt.mdl*, let R be the resolution of Mdl_{tgt} , and let *trace* be the trace encoded by *FANNN.nbt*. The trace is correct for this problem if, when executed from the initial system state S_{init} where

- $S_{init}.energy := 0$
- $S_{init}.harmonics := Low$
- $S_{init}.matrix(c) := Void$ for all coordinates c valid with respect to the resolution R
- $S_{init}.bots := \{ bot_{init} \}$
 - $bot_{init}.bid := 1$
 - $bot_{init}.pos := (0, 0, 0)$
 - $bot_{init}.seeds := \{ 2, \dots, 40 \}$
- $S_{init}.trace := trace$

there are no decoding or execution errors and the final state S_{fini} satisfies

- $S_{fini}.harmonics == Low$
- $S_{fini}.matrix(c) == Mdl_{tgt}(c)$ for all coordinates c valid with respect to the resolution R
- $S_{fini}.bots == \{ \}$
- $S_{fini}.trace == \varepsilon$

The final energy of the trace is $S_{fini}.energy$.

Disassembly Problems

For each $FDNNN_src.md1$ and corresponding $FDNNN.nbt$, let Mdl_{src} be the source model encoded by $FDNNN_src.md1$, let R be the resolution of Mdl_{src} , and let $trace$ be the trace encoded by $FDNNN.nbt$. The trace is correct for this problem if, when executed from the initial system state S_{init} where

- $S_{init}.energy := 0$
- $S_{init}.harmonics := Low$
- $S_{init}.matrix(c) := Mdl_{src}(c)$ for all coordinates c valid with respect to the resolution R
- $S_{init}.bots := \{ bot_{init} \}$
 - $bot_{init}.bid := 1$
 - $bot_{init}.pos := (0, 0, 0)$
 - $bot_{init}.seeds := \{ 2, \dots, 40 \}$
- $S_{init}.trace := trace$

there are no decoding or execution errors and the final state S_{fini} satisfies

- $S_{fini}.harmonics == Low$
- $S_{fini}.matrix(c) == Void$ for all coordinates c valid with respect to the resolution R
- $S_{fini}.bots == \{ \}$
- $S_{fini}.trace == \varepsilon$

The final energy of the trace is $S_{fini}.energy$.

Reassembly Problems

For each $FRNNN_src.md1$ and $FRNNN_tgt.md1$ and corresponding $FRNNN.nbt$, let Mdl_{src} be the source model encoded by $FDNNN_src.md1$, Mdl_{tgt} be the target model encoded by $FDNNN_tgt.md1$, let R be the resolution of Mdl_{src} and Mdl_{tgt} (guaranteed to be equal), and let $trace$ be the trace encoded by $FRNNN.nbt$. The trace is correct for this problem if, when executed from the initial system state S_{init} where

- $S_{init}.energy := 0$
- $S_{init}.harmonics := Low$
- $S_{init}.matrix(c) := Mdl_{src}(c)$ for all coordinates c valid with respect to the resolution R
- $S_{init}.bots := \{ bot_{init} \}$
 - $bot_{init}.bid := 1$
 - $bot_{init}.pos := (0, 0, 0)$
 - $bot_{init}.seeds := \{ 2, \dots, 40 \}$
- $S_{init}.trace := trace$

there are no decoding or execution errors and the final state S_{fini} satisfies

- $S_{fini}.harmonics == Low$
- $S_{fini}.matrix(c) == Mdl_{tgt}(c)$ for all coordinates c valid with respect to the resolution R
- $S_{fini}.bots == \{ \}$

- $S_{\text{fini}}.\text{trace} == \varepsilon$

The final energy of the trace is $S_{\text{fini}}.\text{energy}$.

Default Traces

A provided [dfltTracesF.zip](#) is a collection of default traces. These default traces establish an upper-bound energy for each problem, used for scoring.

Each default trace for an assembly problem applies the same uniform strategy (a “classic” 3D printing): compute a bounding box for the target model, set harmonics to *High*, use a single “head” nanobot to sweep each xz-plane of the bounding box from bottom to top and filling the voxel below the nanobot as dictated by the target model, return to the origin, set harmonics to *Low*, and halt.

Each default trace for a disassembly problem applies the same uniform strategy (the inverse of the “classic” 3D printing): compute a bounding box for the source model, set harmonics to *High*, use a single “head” nanobot to sweep each xz-plane of the bounding box from top to bottom and voiding the voxel below the nanobot as dictated by the source model, return to the origin, set harmonics to *Low*, and halt.

Each default trace for a reassembly problem applies the same uniform strategy: compute a bounding box for the union of the source and target models, set harmonics to *High*, use a single “head” nanobot to sweep each xz-plane of the bounding box from top to bottom and void *Full* voxels of the source model when moving into a voxel and fill *Full* voxels of the target model when moving out of a voxel, return to the origin, set harmonics to *Low*, and halt.

Scoring

A team’s score for each problem depends upon the final energy of their submitted trace, the final energy of the corresponding default trace, and the minimum energy among all teams’ corresponding submitted traces, and the resolution of the problem.

Let $\text{energy}_{\text{team}}$ be the final energy of the team’s submitted trace, $\text{energy}_{\text{dflt}}$ be the final energy of the corresponding default trace, $\text{energy}_{\text{best}}$ be the minimum energy among all teams’ corresponding submitted traces and the value $\text{energy}_{\text{dflt}} - 1$, and R be the resolution of the problem. (If a submitted trace has decoding or execution errors or final energy that exceeds that of the corresponding default trace, then treat it as having final energy equal to that of the corresponding default trace. This ensures that it is always the case that $\text{energy}_{\text{best}} \leq \text{energy}_{\text{team}} \leq \text{energy}_{\text{dflt}}$ and $\text{energy}_{\text{best}} < \text{energy}_{\text{dflt}}$.) The team’s score for the problem is

$$\lfloor (\lfloor \log_2 R \rfloor \times 1000 \times (\text{energy}_{\text{dflt}} - \text{energy}_{\text{team}})) / (\text{energy}_{\text{dflt}} - \text{energy}_{\text{best}}) \rfloor$$

(Intuitively, a team’s score is linearly interpolated from 0 (if the submitted trace is no better than the default) to $\lfloor \log_2 R \rfloor \times 1000$ (if the submitted trace is the best). The $\lfloor \log_2 R \rfloor$ term gives more weight to larger problems and the flooring allows scores to be calculated with (arbitrary-precision) integers.)

A team’s contest score is the sum of their scores for all problems.

The contest winner is the team with the highest score.

Trace Checker

A JavaScript [trace checker](#) is available, which can be used to verify that a trace file successfully decodes to a sequence of commands and to display a prefix and suffix of the full trace.

Trace Executor

A JavaScript and WebGL-based [trace executor](#) is available for testing submissions. A (marginally) faster JavaScript-based [trace executor without visualization](#) is also available for testing submissions.

Registration and Submission

[Register](#) a contest team to obtain a team-specific private identifier (a 32-digit hexadecimal string).

After generating correct traces, prepare a single .zip file containing exactly (no more than and no less than) the files `FANNN.nbt`, `FDNNN.nbt`, and `FRNNN.nbt`; the provided [dfltTracesF.zip](#) demonstrates the submission format. The .zip file may optionally be encrypted (`zip --encrypt`) with the team-specific private identifier (if a team is concerned about posting submissions to a publicly accessible location during the contest). Make the .zip file available at a publicly accessible URL (a personal or institutional web server, Dropbox, Google Drive, etc.). [Submit](#) the URL and SHA256 checksum of the .zip file before the [end of the full contest](#) and watch for a [submission acknowledgement](#). Note that submissions for the full contest open at [2018-07-21T18:00:00Z](#) (two hours into the full contest).

Teams may submit multiple times during the contest (using either a new or the same URL, but different SHA256 checksum), but teams are limited to one submission every 15 minutes; early submissions may be evaluated during the contest for live standings, but only the last submissions for the full contest will be considered for prizes. The last submissions for the full contest should remain available for up to two weeks after the end of the contest.

To be considered for prizes, [within two hours of end of the contest](#), teams must update their [profile](#) with complete team information and submit the URL and SHA256 checksum of a single .zip archive with their source code, a `README.txt` file (brief directions for judges to build/run the solution; description of the solution approach; feedback about the contest; self-nomination for judges' prize; etc.), and any other supporting materials.