# Evolvable Shape Seeds: Progress at York

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# Summary

For more details on authoring R presentations please visit
https://support.rstudio.com/hc/en-us/articles/200486468.

- ▶ Algorithm for 'growing' a set of seed genes
- ▶ Strengths and weaknesses
- ▶ Comparision with L-Systems and CPPNs
- ▶ Novelty search

# Target Shape

```
##      speed           dist
##  Min.   : 4.0  Min.   :  2.00
##  1st Qu.:12.0  1st Qu.: 26.00
##  Median :15.0  Median : 36.00
##  Mean   :15.4  Mean   : 42.98
##  3rd Qu.:19.0  3rd Qu.: 56.00
##  Max.   :25.0  Max.   :120.00
```

## Algorithm pseudocode

```
genetostlfile4 <- function(fn="shape.stl",genes,pos=spos(0,

  while (TRUE)
    posnext <- NULL
    for(pp in 1:nrow(pos)){

      shape <- getshape(pos[pp,],genes)
      domval <- domInZone(pos[pp,],genes)
      if(domval){

        dirs <- genes[genes$dom == domval & dirs$valtyp!=0,
        for(dd in 1:nrow(dirs)){
          direction <- get_direction(dirs)
          posnext <- addposition(dirs[dd],shape,direction,
          drawCStoSTL(pos[pp,],shape,direction)

    if(is.null(posnext) | iterations++ > runlim)
      break
```

# Seed genes

novelty search as a means of measuring the "expressive power" of an encoding

# Strengths & Weaknesses

- ▶ Very flexible *and readable*
- ▶ Compatible with engineering platforms
- ▶ Arbitrary start/stop points
- ▶ Not particularly compact
- ▶ X,Y,Z zones are only loosely joined