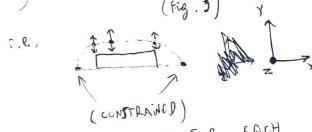
- THE MATLAB SERIPT BRGINS BY SETTING THE VALUES OF THOSE ARRAY VARIABLES CINITIAL SHELL CASE)
- 2) CREATE 1ST GENERATION BY RANDOMLY MUTATING THE GENES OF THIS SHELL

ANNING STAN

a) NOTE FOR THE FIRST GA VERSION, SUGGEST WORKING ONLY ON THE PIS.

- NETHUS SIMPLIFY WORK TO GNLY 3 PTS. PER CURVE (AS THE 15T & LAST PTS. SHOULD REMAIN CONSTRAINED)

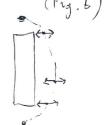


LACTUALLY, THIS WILL BE A DIPPERENT DIMENSION FOR EACH OF THE CVAVES

THUS ONLY ,, Y" VARIED (F3,5)

THUS ONLY "Z" VARIED .





(TOP VIEW)

in) MIDPLE CURVE IS ON THE PLANE DEFINED BY THE DIAGONALL EXTEMA OF THE CHASSIS



(SO Y & Z WILL BE VARIED SIMULTANEOUSLY TO MAKE SURE THE PTS. LIFE ON THIS LINE:

(Fg.8) (Fg.8)

CHRUMOSOMES = CURVES GENE = POINT ON ONE OF THE CURVES (consists of (x, Y, Z) continute vector) INITIAL CASE: ALL GENES KHOWP (SPECIFIED BASED ON EXTREMUM PTS. OF INTERIOR CURVE CHASSIS)

e.g. (Fig.1) ONE SHELL CURVE

(S.DE VIEW) SUGGEST STARTING WITH JUST (Fig. 2) (FRONT VIEW) THESE 5 CURVES (THIS SHOULD ENSURE THAT THE SHELL DOES NOT INTERSECT THE REGILLINEAR CHASSIS) · FURTHER MORE, WE CAN EXPLOIT SYMMETRY TO CNLY WORK ON 3 CURVES · I SUGGEST WE START WITH 5 PTS. AS ON FIG. 1 (ON EACH CURVE) CLATER WE CAN NOD MORE, IN PARTICULAR INTHE TOP SEGMENT) e.g. (Fig. 4) . SD EA CH CHROMOSOME IS A 5+3 MATRIX $\begin{bmatrix} x_{1} & y_{1} & z_{1} \\ x_{2} & y_{2} & z_{2} \\ \vdots & \vdots & \vdots \\ x_{5} & y_{5} & z_{5} \end{bmatrix} (Point 2)$

"AND EACH SHELL" HAS 3 OF THESE MATRICES IN TOTAL

(SHOULD CONCATENATE THEM OR STORE AS

SEPARATE VARIABLES?)

C) SO NOW BOUNDS SPECIFIED & MUTATION HAPPENS WITHIN THEM CURVA_XBOUND = [1, ...] (WHERE CUPY 2- Y BOUND = [Yo, ...] CURV3-2BOUND=[20,...] (AND CURV 2 ZBOUND IS NOT NEEDED AS IT IS SPECIFIED TO MATCH THE EQN. OF (ON CURVE Z) THE LIVE ON FIG. 8) (= Z COORD. OF EACH PT CALCULATED BASED ON THE SPECIFIED Y COORD.) Yo "G" IT THE SIZE OF EACH GENERATION for=1 to 6 CUEV1 - NEW = CURV 1 % MANBE WILL NEED TO APPEND TO Joseph Marie CURVI- MEN [j,2] = PANDOM (CURVI- 1 BOUND, DECIMAL) FOR j= 2 to 4 CURV 2_ NEW [5,2] = RANGEM (CUFUZ_ YBOUND, DECIMAL) CURV 2 _ NEW [[] 3] = a · CURU 2 _ NEW [] 2] + b CURV3_NEW [],3] = RAHDOM (CURV3-ZBOUND PECIMAL) 3/ EVALUATE FITNESS a) SAVE CCCPOS TO TXT/CSV FILE (& SET PARTY BIT FCF X = 1 70 G RUN SOLIDWORKS MACRO (WHICH TAKES THE COORDS. & UPDATES THE MODEL & THEN JETS THE PARTY BIT (TO SIGNIFY IT IS c) RUN COMSOL CFP USING LIVERNIK (WHICH JAVES PESULTS TO ANOTHER CSV/ TXT FILE) -> (& SET ITS PARITY BIT TO 1!) d) READ CEVITYT FIRE & APPEND TO APPRY WITH RESULTS IN MATLAS = (& SET ITS PARITY BIT TO 0?)

4) RANK THE RESULTS (SORT), TAKE "P" BEST TO BETHE PAREMS (EVEN NO.) a) NEXT GENERATION WILL CONSIST OF: (PASSED ON WITHOUT CHANGING) in), P" CHILDREN CREATED VIA CROSSOVER + MUTATION ACTUALLY NOT THIS (WILL BE in) WE CRUSS OVER ALONE STERED IN MEMORY WITH A DOUBLE MUTATION (WITH A DOUBLE MUTATION FREQUENCY) NSTEAD) be) NCTE: TMO in) is redundrant when we already have in) BUT WE CAN TRY & SEE WAAT WE GET C) ALSO , FCR IV) COULD USE SOME OF THE NON-BEST RESULTS, BUT THIS MIGHT LEAD TO SLOWER CONVERGENCE 5) CROSSOVER PONE WA: a) c-PATE = ... 0/c cross over frequency, SET TO BE A FRACTION WITH AN INVERSE THAT IS AN INTEGER (e.g. 2, 4, 16...) for i = 2 70 4 RAND = FANDOM (C-RATE) INTEGER TEMP= FIRST_CURVE [i] IF RAND == 1 FIRST-CURVE [] = SECOND-CURVE [] SECOND-CURVE (I) = FIRST-CURVE (I) W LATER CAN TO MORE ELABORATE CROSSOVER SCHEMES & TEST WHICH LEADS TO FASTER CONVER GENCE OF THE GA

6) MUTATION DONE VIA:

M_RATE = ... 1/0 MUTATION FREQUENCY

(SET SCITHAT INVERSE IS AN INTEGER, AS FOR

THE C_FATE)

PAND = RANDOM (1/meate) INTEGER

TF RAND == 1 CURVE [1,2] = RANDOM (CURVE_BOUND, DECIMAL) (CR 3, TF, Z" & VARIED)

- T) ONCE NEW GENERATION IS READY, PEPEAT STEPS 3 & 4)

 (& THEN ALSO 5) & 6) TO GET

 NEW GENERATION)
 - a TERMINATE WHEN CONVERGENCE CRITERIA HAS BEEN REACHED
 - (NUMBER OF FIRM GENERATIONS)
 - TIME

 TO SEE HOW IT CONVERGES OVER

 TIME
 - in) & thus WE CAP TEST DIFFERENT SETTINGS OF THE GA UNTIL WE ARE HAPPY WITH IT
 - LATER WE LAN ALSO SET A CONDITION BASED ON THE RATE OF CHANGE BETWEEN SUBSECUENT GENERATIONS PRAG VALUES