Figure 1 Genetic Sequencing Statistics. (Mb = megabase, Kb = kilobase; 1 "base" = 1 DNA building block).

Size of an entire genome	Yeast: 12.5 Mb Human: 3000 Mb
Current rate of production sequencing	5 kb/week
Number of samples needed to produce sequencing	50 samples/kb
Number of steps handling each sample	30

Figure 2. Comparison of Genesis, Biotest, and SYGI. All three routines carry out the same protocol, transferring the contents of 2 48 well sample plates to a single 96 well plate. A) Genesis procedure, as printed from Genesis; this does not reflect Genesis' programming style. B) SYGI procedure. C) Biotest procedure; commands are numbers 1-90. Indented lines following commands are parameters for that command. Note that several files are used.

A) GENESIS Example

```
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METHOD: TMPM

SUBROUTINE: TMP

FUNCTION: CONFIG CAHNGE
TIPS:   P250 TIPS
TRAY 1: 48 WELL
TRAY 2: 48 WELL
TRAY 3: 96 WELL V-BOTTOM
TOOL A: P200
TOOL B: EMPTY
TOOL C: EMPTY
TOOL D: EMPTY
PARAMETER SET: [UNSPECIFIED]

FUNCTION: WEL2WELL
VOLUME: 100 microliters                         TOOL: P200
SRC: TRAY 1 BY ROW      A1-F8       STOP
DEST:TRAY 3 BY ROW      A1-D12      STOP
SOURCE HGT: BOTTOM                  DEST. HGT: TOP
RATE: 3 TO CONTAIN: BLOWOUT         NO TIP TOUCH
TIP CHANGE ALWAYS       NO PREWET
NO LOG

FUNCTION: WEL2WELL
VOLUME: 100 microliters                         TOOL: P200
SRC: TRAY 2 BY ROW      A1-F8       STOP
DEST:TRAY 3 BY ROW      E1-H12      STOP
SOURCE HGT: BOTTOM                  DEST. HGT: TOP
RATE: 3 TO CONTAIN: BLOWOUT         NO TIP TOUCH
TIP CHANGE ALWAYS       NO PREWET
NO LOG
```

B) SYGI Example

```
# A simple "pipette from here to there" routine.
proc move_fluid {dir vol plate_type area well} {
   global tablet_height     ;# Must be defined prior to entering this routine.
   global z                 ;# This too must be externally defined.
   source $plate_type.sgi   ;# Read files which define physical plate parameters
   source tablet.sgi
   set save_z $z            ;# Save the current height
   set j [expr 1*($well-1)/$cols+1]
                            ;# set variables to find the correct well
   set i [expr 1*$well-($j-1)*$cols]
                            ;# Now move in 2 steps: first over to the new well
   move biomek $tablet_x($area)+$tx($i) $tablet_y($area)+$ty($j) ' '
                            ;# where tablet_x,_y are defined in tablet.sgi
                            ;# and tx() and ty() are defined in $plate_type.sgi
   move biomek ' ' {$tablet_height-$height+$well_depth-50} '
                            ;# move down into well and pipette
   pipette $dir $vol
   move biomek ' ' $save_z ';# Move back to the original Z location and quit
}
# This routine takes two 48 well plates and transfers them into one
# 96 well Costar V-bottom plate.
# Note that it refers to the user defined procedure "move_fluid", defined
# above.
proc show_loop {} {
    for {set ol 1} {$ol <= 2} {incr ol} {
        for {set il 1} {$il <= 48} {incr il} {
            set counter96 $il+48*($ol-1)
            get tip $counter96                        ;# Get a tip
            home biomek z                             ;# Home the biomek Z
            move biomek ' ' 1800 '                    ;# Move to a safe Z height
            move_fluid in 100 costar48 1+$ol $il      ;# Pick up the sample
            move_fluid out 100 costarv 4 $counter96   ;# Deliver the sample
            unget tip                                 ;# Drop the tip
        }
    }
}
```

C) BIOTEST Example

```
*** Contents of the primary file ***
16                    # configuration set-up
   3                     # a P200 tool in position 0
   1                     # other positions empty
   1
   1
   1                     # a P250 tip rack is in place
7                     # get a tool...
   0                     # from position 0
19                    # read in a file to defines plate and well locations into
                      # variables [100]-[200]
   wells.txt
19                    # Now jump into another file to do looping
   combine.txt
8                     # Remove the tool
90                    # Quit
*** Contents of the file combine.txt ***
[10] = 1              # and another counter variable for the inner loop
[0] = 1               # set a counter variable for the outer loop.
19                    # Read a file
   tablet1.txt           # This sets an offset for tablet position 1 to be used
                      # by the routine    xfer.txt (sets variables [200] &
[201])
19                    # Now start pipetting in the routine xfer.txt
   xfer.txt
[0] = 1               # reset the counter variable for the outer loop.
19                    # Read a file
   tablet2.txt           # This sets an offset for tablet position 2 to be used
                      # by the routine xfer.txt (sets variables [200] & [201])
19                    # Now start pipetting in the routine xfer.txt
   xfer.txt
*** Contents of the file xfer.txt ***
9                     # Get a tip..
   [10]
[1] = 1+([0]-1)/6     # Set indexes to allow access to coded source locations
[2] = [0]-([1]-1)*6
4                     # Move the biomek over the correct well
   [200]+[100+[1]]       # This uses the variables set in the file tabletX.txt
   [201]+[107+[2]]
   1800
4                     # Move down into the well
   [200]+[100+[1]]
   [201]+[107+[2]]
   [120]
11                    # Pipette in...
   100                   # 100 microliters
4                     # Move the biomek over the correct well
   [200]+[100+[1]]       # Move back up to clear the plate
   [201]+[107+[2]]
   1800
[3] = 1+([10]-1)/12   # Set indexes to allow access to coded target locations
[4] = [10]-([1]-1)*12
4                     # Move the biomek over the correct well
   [150+[3]]             # This uses the variables set in the file wells.txt
   [157+[4]]
   1800
4                     # Move down into the well
   [150+[3]]
   [157+[4]]
   [120]
13                    # Pipette out...
   100                   # 100 microliters
4                     # Move the biomek over the correct well
   [150+[3]]             # Move back up to clear the plate
   [157+[4]]
   1800
10                    # Get rid of the tip
[0] = [0] + 1         # now increment the counters and continue.
[10] = [10]+1
< 48
*** Contents of the file wells.txt
[100]-[105] x-positions of wells in the labware relative to position set in
tabletX.txt
[107]-[110] y-positions of wells in the labware relative to position set in
tabletX.txt
[120] is depth of pipetting
[150]-[155] x-positions of destination plate
[157]-[160] y-positions of destination plate
*** Contents of the file tabletX.txt ***
[200] the x-position of tablet position X
[201] the y-position of tablet position Y
```