NATIONAL AERONAUTICS AND SPACE ADMINISTRATION

Technical Memorandum 33-661

Planetary Quarantine Computer Applications

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(NASA-CR-136220) PLANETARY QUARANTINE COMPUTER APPLICATIONS (Jet Propulsion Lab.) 65 p HC $5 25 CSCL 06M
N74-12773
Unclas
G3/04 24567

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PASADENA, CALIFORNIA

December 15, 1973

Preface

The work described in this report was performed by the Project Engineering Division of the Jet Propulsion Laboratory.

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ABSTRACT

This document identifies the computer programs pertaining to planetary quarantine activities within the Project Engineering Division, both at the Air Force Eastern Test Range and on site at the Jet Propulsion Laboratory. A brief description of each program and program inputs are given and typical program outputs are shown.

INTRODUCTION

All the computer programs in the Planetary Quarantine area of the Project Engineering Division can be categorized into one of the following types:

1. Data storage and retrieval - this includes reorganizing input data into a more meaningful form.
2. Data analysis - these programs interpret experimental data in order to establish whether certain characteristics are present.
3. Simulation - here situations are simulated on the computer which are not studied in experiments or obtained from actual life data for some reason.

All the JPL programs run on a Univac 1108 while AFETR's programs run on a CDC 3600. An outline of the computer programs and the present outlook on planetary quarantine follows. Also a summary matrix and program descriptions for both JPL and AFETR are included.

Figure 1 identifies specific programs within each of these categories.

Fig. 1. PLANETARY QUANRANTINE COMPUTER PROGRAMS (PROJECT ENGINEERING DIVISION)

Data Storage and Retrieval Group I	Data Analysis Group II	Simulation Group III
• S/C Bioassay Program	• Five Factor, Analysis of Variance	• Microbial Burden Prediction Model (MBPM)
• Vacuum Temperature, Data Manipulation	• D Value Regression Analysis	• Recontamination
* File Preparation Program (FILE)	• 3-D Computer Plotting	• Entry Heating
* Data Storage Program (DAST)	• Yang's VT Curve Fitting Model	• Sterilization Process Analysis Network (SPAN)
	* Lunar Inventory Program	
	* Qualitative Storage Program (QUAL)	
	* Qualitative Summary Program (QUALSUM)	
	* MARCEL	
	* Statistical Comparison of Undying Means (SCUM)	

• Jet Propulsion Laboratory

* Planetary Quarantine Lab, AFETR

CURRENT OUTLOOK

Jet Propulsion Laboratory:

JPL programs in the PQ field not given in the report include the SADL and the Mariner '69 program which are predecessors to the Spacecraft Bioassay Program.

It has been indicated that there is a need for the development of an experimental data storage and retrieval program to facilitate the preparation of inputs for the statistical programs (i.e. five factor analysis of variance). The 3-D computer plotting, entry heating, and recontamination programs are in various stages of development. All the other programs are operational on the JPL Univac 1108. Furthermore, the Yang program could be updated to analyze irradiation data as well as the vacuum temperature data (Table 1) if a need arises.

Planetary Quarantine Lab, AFETR

Many of the planetary quarantine programs of AFETR were written by Sandia Laboratories for the Apollo flights. These programs include: FILE, DAST, Lunar Inventory Program, QUAL, QUALSUM, and MARCEL. FILE, DAST, and the Lunar Inventory Program were applicable to the moon shots only and it would not be reasonable to try to adapt them to other flight projects. QUAL and QUALSUM are presently being rewritten to be used on all flight projects and experimental data. The testing of the MARCEL program has not been completed yet.

Soon the Planetary Quarantine Lab will have a gas chromatograph which will be used for supplemental identification of microorganisms along with standard laboratory testing procedure. Since the output from the machine represents integrated areas under individual curves, a new microbial identification program must be written (i.e., QUAL is the only identification program presently).

Pertinent information for each of the AFETR programs is given in Table 8.

PLANETARY QUARANTINE COMPUTER PROGRAMS
AT JPL

Table 1. JPL planetary quarantine computer programs

PROGRAM TITLE	STATUS			APPLICATION		DATA SOURCE	
	Discontinued Use (Operational)	Operational	In Progress	General	Flight Project	Experimental Data	Spacecraft
Bioassay Data Storage and Retrieval		X			X		X
Vacuum Temperature, Data Manipulation		X		X		X	
Five Factor Analysis of Variance		X		X		X	
D-Value Regression Analysis		X		X		X	
3-D Computer Plotting			X	X		X	
Yang's VT Curve Fitting Model		X		X		X	
Microbial Burden Prediction Model		X			X		X
Recontamination			X		X	X	X
Entry Heating			X		X	X	X
Sterilization Process Analysis Network	X				X		

DATA STORAGE AND RETRIEVAL

JPL GROUP I (SEE FIG. 1)

PROGRAM TITLE: BIO-ASSAY DATA STORAGE AND RETRIEVAL

Additional References: No Published Material

Application: Any Flight Project

Data Source: Spacecraft During Assembly and Test

Status: Operational

Program Description:

This program establishes and manipulates data from three master files. The first file is the area file which contains areas and parts of the spacecraft of interest. It is used as information for the spacecraft file. The spacecraft file is concerned with bacteria counts obtained from coupons affixed to parts of the ship. The third file contains information on bacteria counts present in the immediate environments surrounding the spacecraft and is referred to as the environmental file. There is a further description of these in the input section which follows.

The user can choose between the following capabilities of the program:

1. Initial sort/creation of master file.
2. Sort/merge (assuming a master file and new data, sort/merge refers to the creation of a new master file).
3. Update (adding, deleting, and/or changing a master file and creating a new one).
4. Data retrieval (retrieving subsets of a master file)
5. Arithmetic and statistical calculations which include burdens, histograms, Kolmogorov-Smirnov test (K-S test), T-test, and F-test to establish whether two samples differ statistically.

Program Input:

The program input is the information that makes up the three master files. The following is a further breakdown of these three files.

Spacecraft File:
- Spacecraft Number
- Event
- Sample Method
- Zone
- Subzone
- Part
- Part Site
- Environmental Site
- Time Sampled

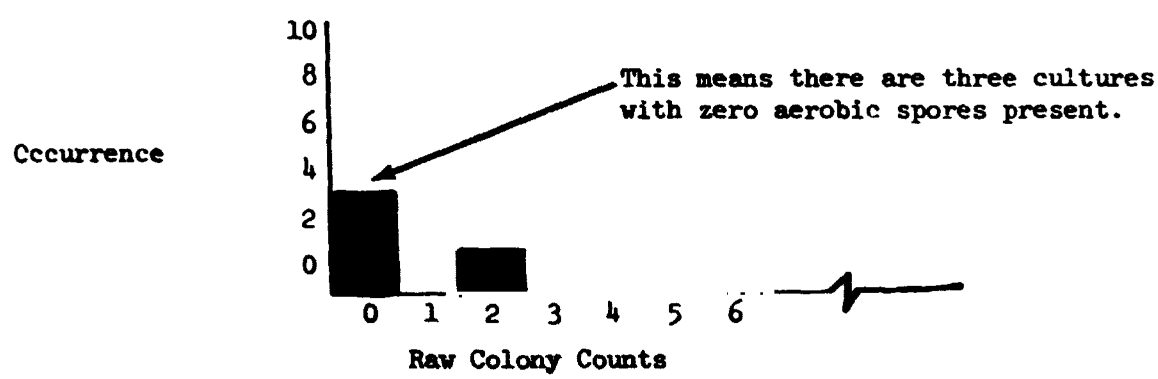
Environmental File:
Environmental Site
Year
Day
Sample Method
Spacecraft Number
Event

Area file (used with the spacecraft file) contains areas in square meters of the spacecraft parts.

Program Output:

The results of this program can be illustrated best by an example drawn from Table 2. Basically, the program is comparing the two subsets of data.

The first part of the output contains the numbers necessary to construct a histogram of the frequency of occurrence of aerobic spores (AS) and aerobic vegetative organisms (AV). Note that anaerbobic spores (NS) and anaerobic vegetative organisms (NV) have no meaning in this run (i.e. equal zero). The beginnings of a histogram for the aerobic organisms from this run would look like this:



The extrapolated counts are the raw counts with the appropriate areas (from the area file) applied plus factors for swab efficiency and bioassay dilution.

The second half of the first page of the example is a cumulative distribution of the above material.

The last page of the illustration shows the results of three tests used to test the hypothesis:

$H_0 : \mu_1 = \mu_2$

That is , if the hypothesis H_0 is accepted the two subsets come from populations with the same mean or they come from the same population. A significant difference between these tests is the fact that the Kolmogorov-Smirnov test is nonparametric; that is, no assumptions are made on the underlying distributions while the T and F tests are parametric. Also, note that the T and F values are only printed out; the user must then compare these with the critical values in a table to accept or reject the hypothesis.

Table 2. Typical output; Bioassay Data Storage and Retrieval Program

SUBSETS 1 AND 2
HISTOGRAM AT SUBSET LEVEL

histogram values

INTERVAL FOR RAW COUNTS		RAW COUNTS FIRST SUBSET AS	AV	NS	NV	SECOND SUBSET AS	AV	NS	NV	INTERVAL FOR EXTRA-POLATED COUNTS		EXTRAPOLATED COUNTS FIRST SUBSET AS	AV	NS	NV	SECOND SUBSET AS	AV	NS	NV
0-	0	3	1	9	8	2	1	8	8	.00	.10+01	4	2	9	9	5	4	8	8
1-	1	0	1	0	0	1	1	0	0	.10+01	.10+02	0	0	0	0	0	0	0	0
2-	2	1	0	0	0	1	1	0	0	.10+02	.10+03	0	0	0	0	0	1	0	0
3-	3	0	0	0	1	0	0	0	0	.10+03	.10+04	0	1	0	0	1	0	0	0
4-	4	0	0	0	0	0	0	0	0	.10+04	.10+05	5	2	0	0	2	1	0	0
5-	5	0	0	0	0	0	0	0	0	.10+05	.10+06	0	1	0	0	0	2	0	0
6-	6	1	2	0	0	0	0	0	0	.10+06	.10+07	0	1	0	0	0	0	0	0
7-	7	1	0	0	0	0	0	0	0	.10+07	.10+08	0	0	0	0	0	0	0	0
8-	8	0	0	0	0	1	0	0	0	.10+08	.10+09	0	0	0	0	0	0	0	0
9-	9	1	0	0	0	0	0	0	0	.10+09	.10+10	0	0	0	0	0	0	0	0
10-	10	0	0	0	0	0	0	0	0	.10+10	.10+11	0	0	0	0	0	0	0	0
11-	11	0	0	0	0	0	0	0	0	.10+11	.10+12	0	0	0	0	0	0	0	0
12-	12	0	0	0	0	1	0	0	0	.10+12	.10+13	0	0	0	0	0	0	0	0
13-	13	0	0	0	0	0	0	0	0	.10+13	.10+14	0	0	0	0	0	0	0	0
14-	14	1	0	0	0	0	0	0	0	.10+14	-.10+01	0	0	0	0	0	0	0	0
15-	15	0	0	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
16-	16	0	0	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
17-	17	0	0	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
18-	18	0	0	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
19-	19	1	1	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
20-	100	0	1	0	0	1	2	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
101-	200	0	1	0	0	1	2	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
201	300	0	0	0	0	0	1	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0
301-	1000000.00	0	2	0	0	0	0	0	0	-.10+01	-.10+01	0	0	0	0	0	0	0	0

CUMULATIVE DISTRIBUTIONS

	RAW AS	AV	NS	NV	AS	AV	NS	NV	EXTRAPOLATED							
0	.333+00	.111+00	.100+01	.889+00	.250+00	.125+00	.100+01	.100+01	.444+00	.222+00	.100+01	.100+01	.625+00	.500+00	.100+01	.100+01
1	.333+00	.222+00	.100+01	.889+00	.375+00	.250+00	.100+01	.100+01	.444+00	.222+00	.100+01	.100+01	.625+00	.500+00	.100+01	.100+01
2	.444+00	.222+00	.100+01	.889+00	.500+00	.375+00	.100+01	.100+01	.444+00	.222+00	.100+01	.100+01	.625+00	.625+00	.100+01	.100+01
3	.444+00	.222+00	.100+01	.100+01	.500+00	.375+00	.100+01	.100+01	.444+00	.333+00	.100+01	.100+01	.750+00	.625+00	.100+01	.100+01
4	.444+00	.222+00	.100+01	.100+01	.500+00	.375+00	.100+01	.100+01	.100+01	.556+00	.100+01	.100+01	.100+01	.750+00	.100+01	.100+01
5	.444+00	.222+00	.100+01	.100+01	.500+00	.375+00	.100+01	.100+01	.100+01	[illegible]	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
6	.556+00	.444+00	.100+01	.100+01	.500+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
7	.667+00	.444+00	.100+01	.100+01	.500+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
8	.667+00	.444+00	.100+01	.100+01	.625+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
9	.778+00	.444+00	.100+01	.100+01	.625+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
10	.778+00	.444+00	.100+01	.100+01	.625+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
11	.778+00	.444+00	.100+01	.100+01	.625+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
12	.778+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
13	.778+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01
14	.889+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
15	.889+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
16	.889+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
17	.889+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
18	.889+00	.444+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
19	.100+01	.556+00	.100+01	.100+01	.750+00	.375+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
20	.100+01	.667+00	.100+01	.100+01	.875+00	.625+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
101-200	.100+01	.778+00	.100+01	.100+01	.100+01	.875+00	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
201-300	.100+01	.778+00	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000
301-	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.100+01	.000	.000	.000	.000	.000	.000	.000	.000

Table 2. (contd)

KOLMOGOROV-SMIRNOV TEST

MAXIMUM DIFFERENCES:		.250000+00	.222222+00	.000000	.111111+00	.305556+00	.402778+00	.000000	.000000
CRITICAL VALUES AT LEVEL	.100	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED	.592813+00 ACCEPTED
	.050	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED	.660841+00 ACCEPTED
	.025	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED	.719151+00 ACCEPTED
	.010	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED	.792038+00 ACCEPTED
	.005	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED	.840629+00 ACCEPTED
	.001	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED	.947530+00 ACCEPTED

SUBSET1 SUBSET2 SPACECRAFT ZONE SUBZONE	T-TEST AS	AV	NS	NV	F-TEST AS	AV	NS	NV
DIVIDE OVERFLOW AT LOCATION 017550								
DIVIDE OVERFLOW AT LOCATION 017550 - DIVIDE BY ZERO								
DIVIDE OVERFLOW AT LOCATION 017550			Indeterminate				Indet.	
DIVIDE OVERFLOW AT LOCATION 017550 - DIVIDE BY ZERO	-1.[illegible]308	.3242	~~.0000~~	~~.0000~~	.0092	2.8628	~~.0000~~	~~.0000~~

NUMBER OF INDICES OF SUBSETS TO BE COMPARED: 2

INDICES OF SUBSETS TO BE COMPARED: 3 4

STATISTICAL OPTIONS CONTROL CARD: V33V33V V33 1 1 1 1 1.33000 2.50000

Because of O's in NS, NV cols

PROGRAM TITLE: VACUUM TEMPERATURE, DATA MANIPULATION

Additional References: "JPL Planetary Quarantine," NASA Spacecraft Sterilization Technology Seminar; July 11, 12, 1973; Denver, Colorado.

Application: General

Data Source: Experimental Data

Status: Operational

Program Description:

This is a plotting program which analyzes the results from a ground test which simulates flight conditions to study the effect of a vacuum temperature environment on microbial survival. The result is a graph of survival ratio versus test duration for various temperatures.

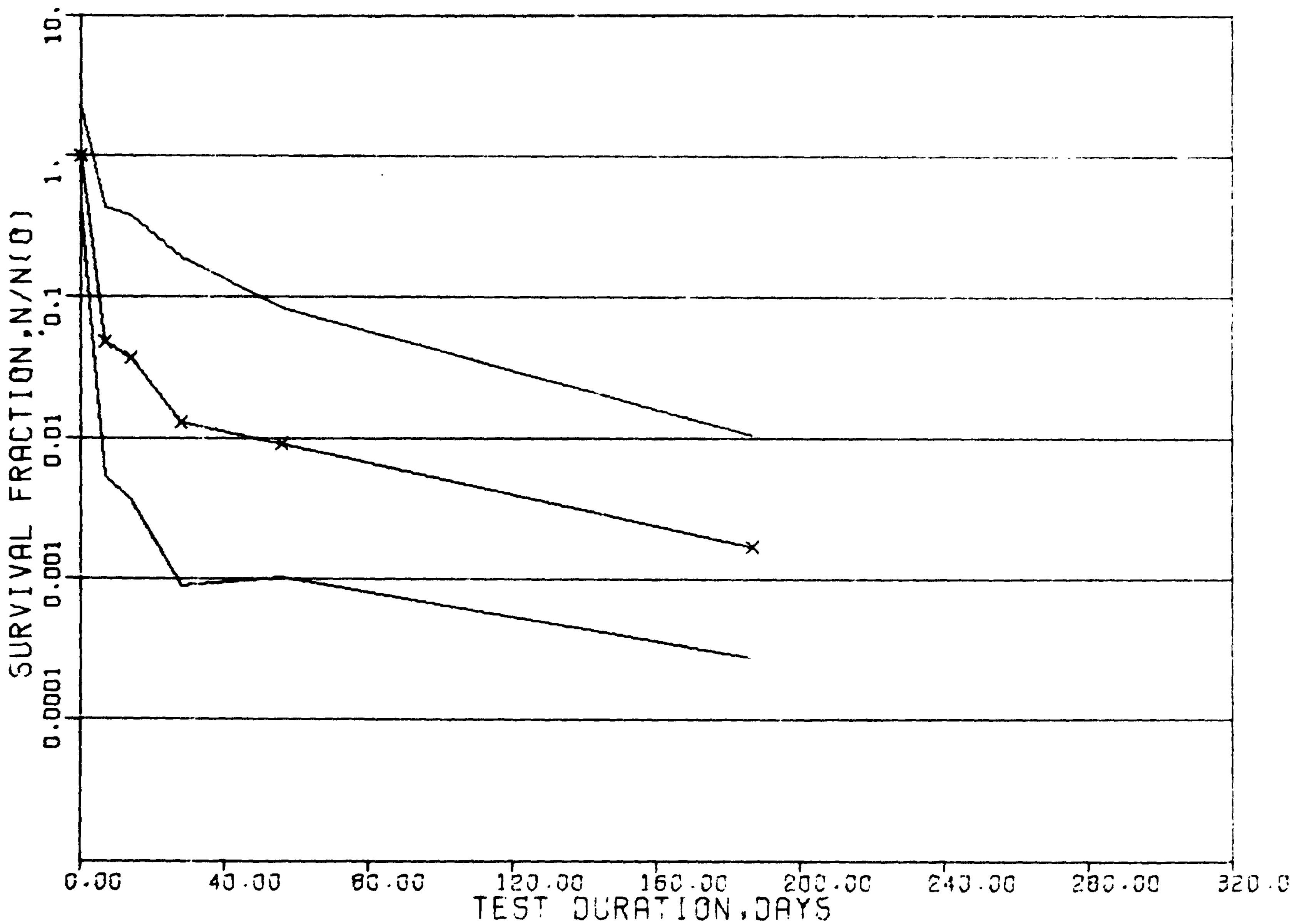
Program Input:

The parameters necessary for the calculations and construction of the graph include experiment type, microorganism isolate, duration of exposure, survival fraction, and temperature.

Program Output:

The end result is a series of graphs of the survival fraction versus the test duration at different temperatures. Figure 2 shows a typical output for a specific temperature.

Fig. 2. Typical output: Vacuum Temperature Data Manipulation Program



DATA ANALYSIS

JPL GROUP II (SEE FIG. 1)

PROGRAM TITLE: FIVE FACTOR ANALYSIS OF VARIANCE

Additional References: No Documentation

Application: General

Data Source: Experimental Data

Status: Operational

Program Description:

This program (obtained from Texas A&M) is applied to radiation experiments to determine the survivability of microorganisms when irradiated by electrons and protons. It takes any five factors (or less), such as temperature, isolate, or duration of exposure and determines if there is any interaction between them. The program accomplishes this by performing an analysis of variance and the Duncan multiple range test on the mean survival fractions obtained from the data of the irradiation experiments. An analysis of variance is essentially testing the following hypotheses:

$$H_o : \mu_{I_1T_1D_1}(x, y) = \mu_{I_1T_2D_1}(x, y) = \mu_{I_2T_2D_1}(x, y) = \cdots$$

where μ : average survival fraction
I : isolate
T : temperature
D : duration
x, y : any other 2 parameters (program handles a maximum of five)

The subscripts indicate different levels. For example, T_1 may equal 20° C and T_2 means -20° C.

Program Input:

The necessary data for the program consists of the survival ratio obtained from the irradiation experiments and the various temperatures, exposure durations, and other parameters relevant to the experiment.

Program Output:

The major part of the output shows the interactions between the five (or less) factors and gives some values helpful in performing further statistical calculations not handled by the program. This can be seen from the sample output shown in Table 3 and Table 4.

Table 3. Typical output: Five-Factor Program (Duncan Multiple-Range Test)

```
DUNCAN MULTIPLE RANGE TEST FOR 5 PERCENT LEVEL BASED ON RESIDUAL

ORGAN        MEAN
  9        2.89939  *
  8        2.87370  **
  5        2.83300   **
  7        2.82018   **
  6        2.79837    *
  4        2.52775     *
  3        2.51703     **
  2        2.50168     ***
  1        2.46014       *
 10        2.39574        *
```

The absence of an asterisk in the same column indicates the means are statistically different. Ex:
Organ 8,5 - correlation present
Organ 9,5 - statistically different

```
DUNCAN MULTIPLE RANGE TEST FOR 5 PERCENT LEVEL BASED ON RESIDUAL

FLUX         MEAN
  1        2.72668  *
  3        2.63155   *
  2        2.62387   *
```

```
DUNCAN MULTIPLE RANGE TEST FOR 5 PERCENT LEVEL BASED ON RESIDUAL

ENERG        MEAN
  3        2.98599  *
  2        2.83908   *
  1        2.16303    *
```

```
DUNCAN MULTIPLE RANGE TEST FOR 5 PERCENT LEVEL BASED ON RESIDUAL

DOSE         MEAN
  1        3.35842  *
  2        2.66609   *
  3        1.96359    *
```

```
DUNCAN MULTIPLE RANGE TEST FOR 5 PERCENT LEVEL BASED ON RESIDUAL

TEMP         MEAN
  1        2.74775  *
  2        2.57765   *
```

Table 4. Typical output: Five-Factor Program (Analysis of Variance)

OPC DATA CONTROL NUMBER ODIP - 1 - 0 - 2   DATA CARD FIELD NUMBER 7

FACTORIAL ANALYSIS OF VARIANCE   These values are necessary for statistical calculations.

-5 factors

Comparisons

SOURCE	D. F.	SUM OF SQUARES	MEAN SQUARE	SEMD	STD ERROR	F
TOTAL	539	.32890920+03				
ORGAN	9	.18922089+02	.21024544+01	.26849292-01	.18905317-01	108.02
TEMP	1	.39059330+01	.39059330+01	.12007369-01	.84904917-02	200.68
DOSE	2	.17510432+03	.87552160+02	.14705953-01	.13398686-01	4498.19
FLUX	2	.11221536+01	.56107679+00	.14705963-01	.10398686-01	28.83
ENERG	2	.69352563+02	.34676290+02	.14705963-01	.13399686-01	1791.57
ORGAN TEMP	9	.13209987+01	.14677763+00	.37970533-01	.26849292-01	7.54
ORGAN DOSE	18	.51210823+01	.28450457+00	.46504338-01	.32893533-01	14.62
ORGAN FLUX	18	.84180753+00	.46767085-01	.46504338-01	.32883533-01	2.40
ORGAN ENERG	18	.19515773+01	.10842397+00	.46504334-01	.32883533-01	5.57
TEMP DOSE	2	.20348466+01	.10174273+01	.20797372-01	.14705563-01	52.27
TEMP FLUX	2	.54365936+00	.27182999+00	.20797372-01	.14705363-01	13.97
TEMP ENERG	2	.33077172-01	.16539586-01	.20797372-01	.14705963-01	.85
DOSE FLUX	4	.36502229+00	.91255573-01	.25471475-01	.18311053-01	4.68
DOSE ENERG	4	.16437834+02	.41094586+01	.25471475-01	.18011053-01	211.13
FLUX ENERG	4	.64076514+01	.16019123+01	.25471475-01	.18311053-01	82.30
ORGAN TEMP DOSE	18	.43201457+00	.24000810-01	.65767066-01	.46504338-01	1.23
ORGAN TEMP FLUX	18	.48620136+00	.27311187-01	.65767056-01	.46504338-01	1.39
ORGAN TEMP ENERG	18	.49303505+00	.27390636-01	.65757066-01	.46504338-01	1.41
ORGAN DOSE FLUX	36	.28877211+01	.93214476-01	.93547877-01	.56955950-01	4.12
ORGAN DOSE ENERE	36	.25339265+01	.70388646-01	.80547677-01	.56955950-01	3.62
ORGAN FLUX ENERG	36	.17923875+01	.49510754-01	.80547877-01	.56955950-01	2.54
TEMP DCSE FLUX	4	.32554357-01	.81385893-02	.36022106-01	.25471475-01	.42
TEMP DOSE ENERG	4	.10866735+01	.27166938+00	.36022106-01	.25471475-01	13.36
TEMP FLUX ENERG	4	.10189409+01	.25473521+00	.36022106-01	.25471475-01	13.09
DOSE FLUX ENERG	8	.62674075+01	.78342533+00	.44117589-01	.31196058-01	40.25
ORGAN TEMP DOSE FLUX	36	.12155361+01	.33764892-01	.11391190+00	.80547877-01	1.73
ORGAN TEMP DOSE ENERG	36	.64319556+00	.17866541-01	.11391191+00	.80547877-01	.92
ORGAN TEMP FLUX ENERG	36	.11669775+01	.32416043-01	.11391191+00	.80547877-01	1.67
ORGAN DOSE FLUX ENERG	72	.32988902+01	.45817919-01	.13951301+00	.98650599-01	2.35
TEMP DOSE FLUX ENERG	8	.69772193+00	.87215241-01	.62392117-01	.44117689-01	4.48
RESIDUAL	72	.14013395+01	.19463881-01	.00000000		

** F VALUES ARE BASED ON RESIDUAL WHICH IS NOT NECESSARILY THE APPROPIATE ERROR TERM

MEANS

ORGAN
2.4601 2.5017 2.5170 2.5278 2.8330 2.7994 2.8202 2.8737 2.9994 2.3357

TEMP
2.7477 2.5776

DOSE
3.3584 2.6361 1.9636

FLUX
2.7267 2.6239 2.6375

ENERG
2.1630 2.8391 2.9960

PROGRAM TITLE: D VALUE REGRESSION ANALYSIS

Additional References: "Visual Material from Planetary Quarantine and Sterilization Program"; OSSA Quarterly Status Review (not published at present time)

Application: General

Data Source: Experimental Data

Status: Operational

Program Description:

The program is used to study dry heat inactivation of microorganisms on spacecraft surfaces. The program performs linear regression analysis to calculate:

1. the regression equation, $y = b_o + b_1X$ (here X = time)
2. the "D" value equals 1/lb.1 (i.e. the time it takes to reduce the population by 90%)
3. the 95% confidence limit about the "D" value
4. the R^2 term (tests correlations between number of survivors and time - see sample output)

The program is adaptable to any experimental data where the die-off is logarithmic with time or exposure.

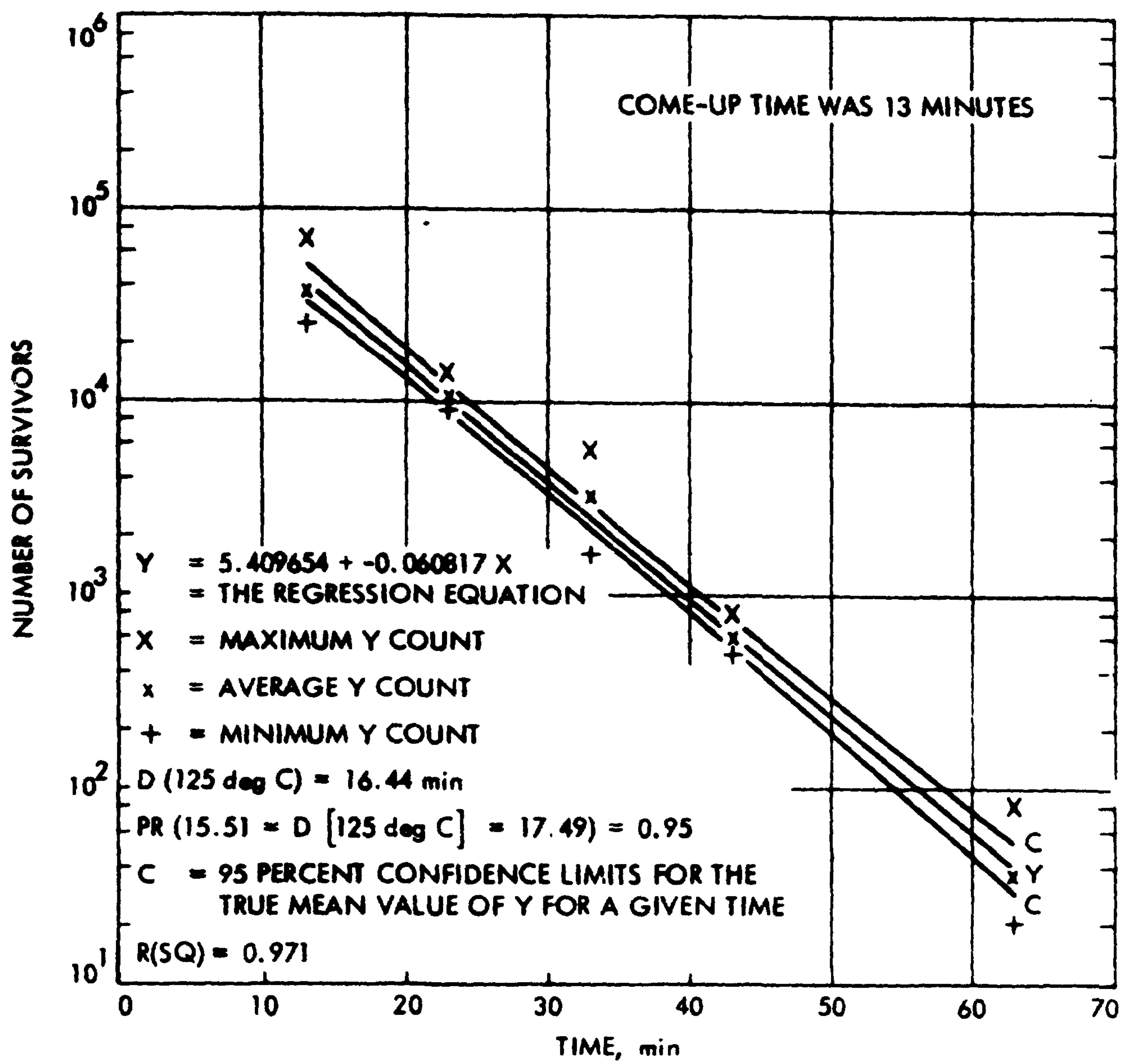
Program Input:

The program input is the number of survivors and time taken from the microbial heat resistent test.

Program Output:

The program prints out the above four items in the program description in graph form. An example is shown in Fig. 3.

Fig. 3. Typical output: D-Value Regression Analysis Program



SRAD PROGRESS REPORTS & 1122s
DVAC

PROGRAM TITLE: 3-D COMPUTER PLOTTING

Additional References: None Currently

Application: General

Data Source: Experimental Data

Status: In Progress

Program Description:

The program will make a three dimensi lot of either the vacuum temperature data or irradiation data. The m will be unique because it will allow the user to specify uneve rements on the three axes.

Program Input:

The values of the function and the information needed to construct a graph are read in.

Program Output:

The program when finished will give a three dimensional plot of the variables specified by the program user. A typical output of this program is not included herein.

PROGRAM TITLE: YANG'S VT CURVE FIT G MODEL

Additional References: "Planetary Quarantine Semi-annual Review Space Research and Technology," Appendix A, 1 July - 31 December 1972, 900-608

Application: General

Data Source: Experimental Data

Status: Operational

Program Description:

Presently the program takes vacuum temperature data and fits a first, second, and third order equation to it. This provides an empirical equation that could be used for interpolation and extrapolation of the data.

If necessary, the program could be updated to handle irradiation data.

Program Input:

The data necessary is the survival fraction and test duration for each isolate studied.

Program Output:

The program prints out functional values and the resulting graphs of survival fraction versus test duration for two to four term curves for each isolate. Examples of the graphs are shown in Figures 4a, b and c.

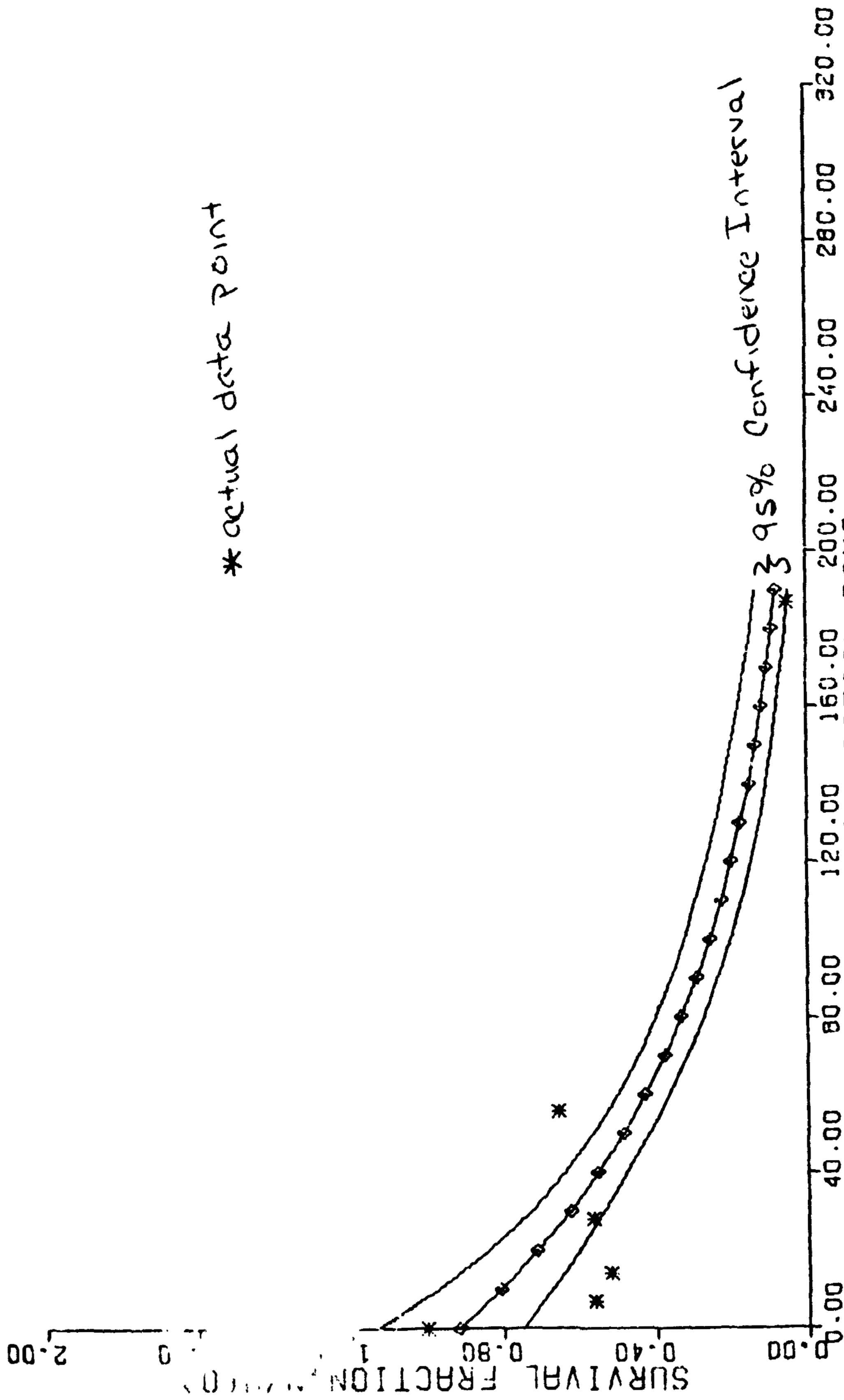


Fig. 4. Typical output: Yang's VT Curve-Fitting Model Program
(a) 2-Term Functional Approximation to Data Isolate 2, +40C

Fig. 4. (contd)
(b) 3-Term Functional Approximation to Data Isolate 2, +40C

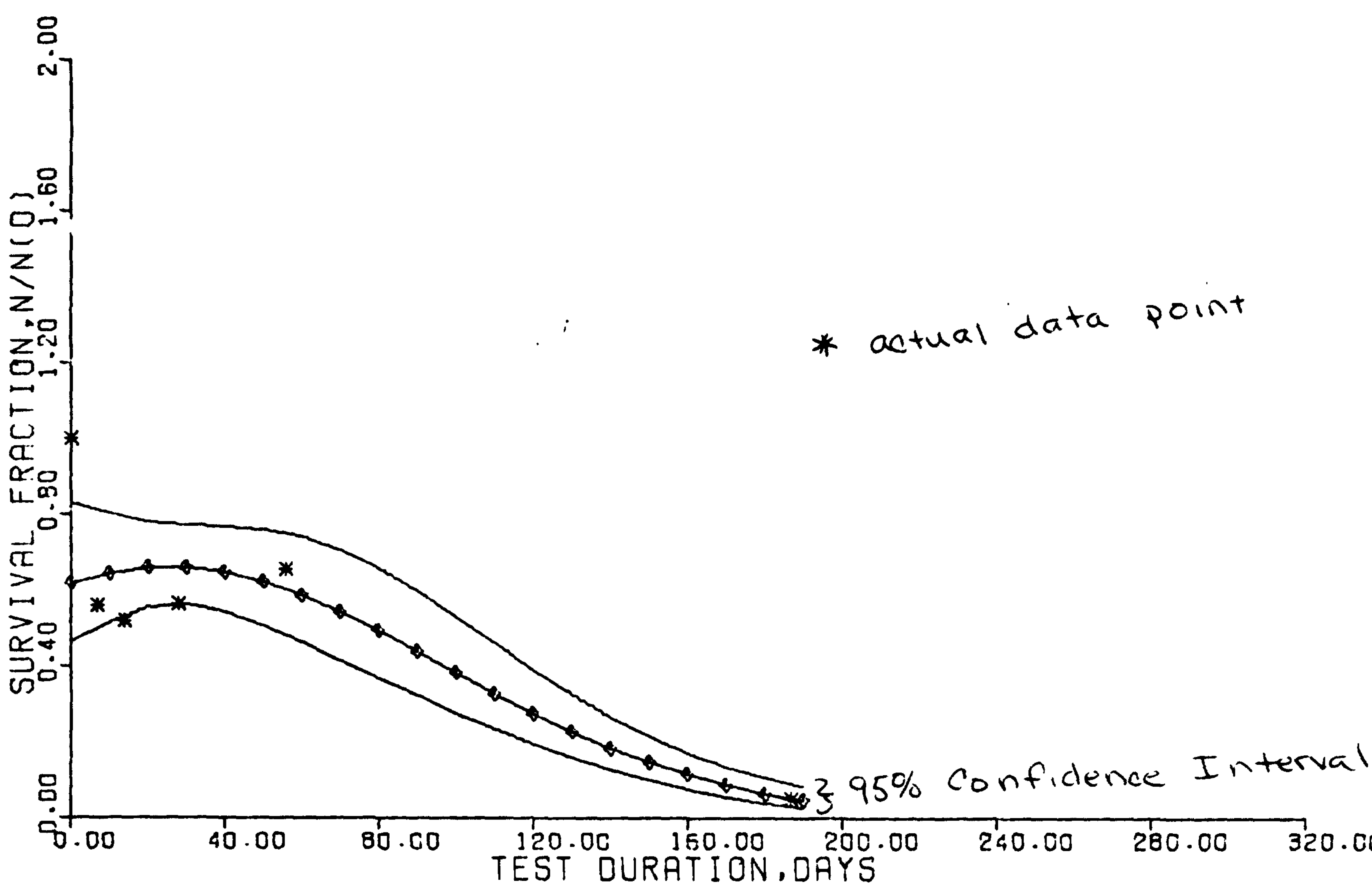
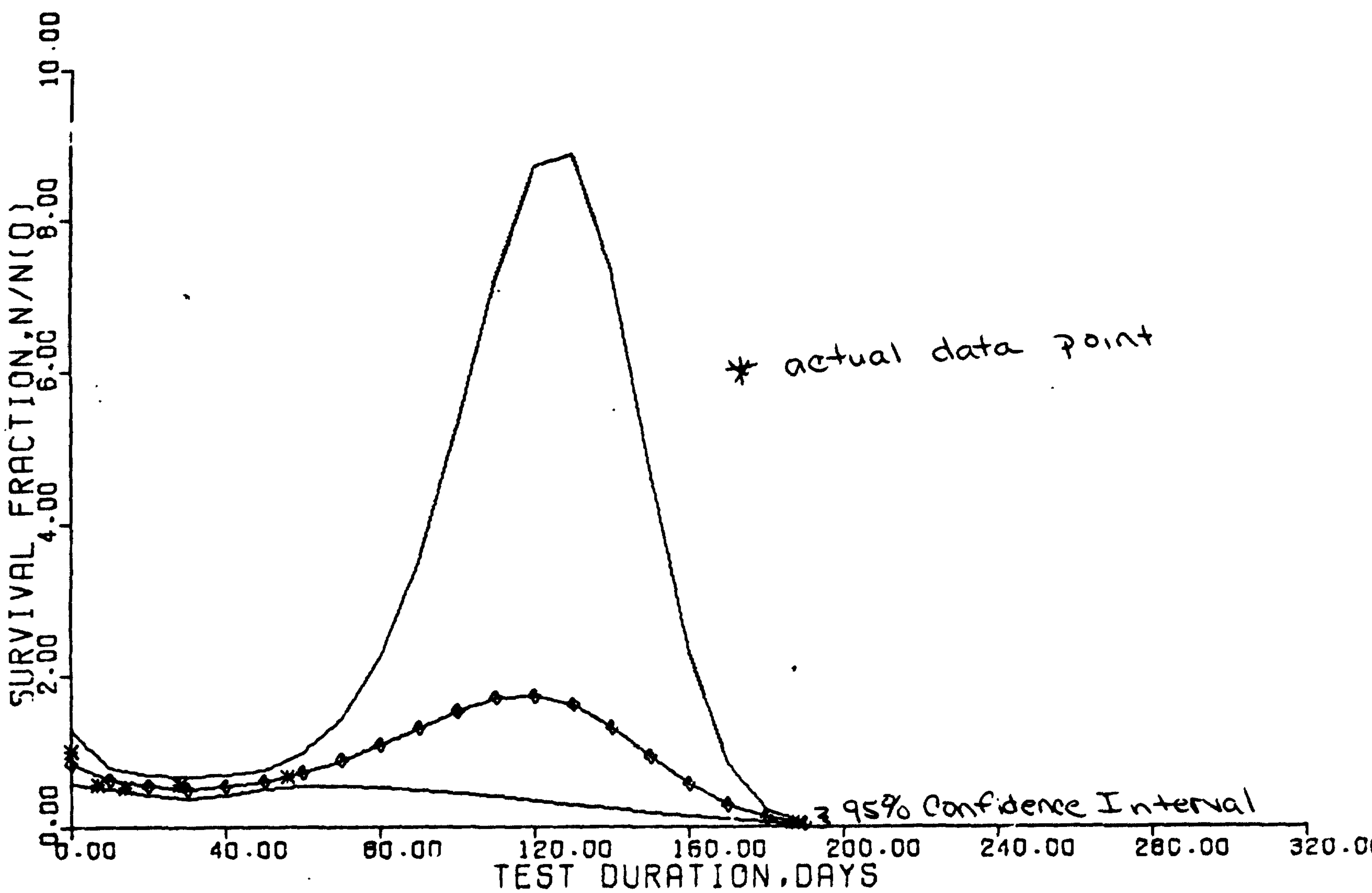


Fig. 4. (contd)
(c) 4-Term Functional Approximation to Data Isolate 2, +40C



SIMULATION

JPL GROUP III (SEE FIG. 1)

PROGRAM TITLE: MICROBIAL BURDEN PREDICTION MODEL (MBPM)

Additional References: "Microbial Burden Prediction Model for Unmanned Planetary Spacecraft;" June 30, 1972; 900-566.

Application: Any Flight Project

Data Source: Spacecraft During Assembly and Test

Status: Operational

Program Description:

The program tracks the microbial burden buildup during the spacecraft assembly and test operations on a daily basis. The program is used to predict the burden when biological assays are not taken. MBPM has the following features:

1. Flexibility - it can be used to simulate the assembly and test of any type of spacecraft, manned or unmanned, or any part thereof.

2. Analysis of Operations - the MBPM provides the capability to analyze assembly and test operations in terms of discrete, repetitive procedural steps for the purpose of identifying significant microbial accumulation events.

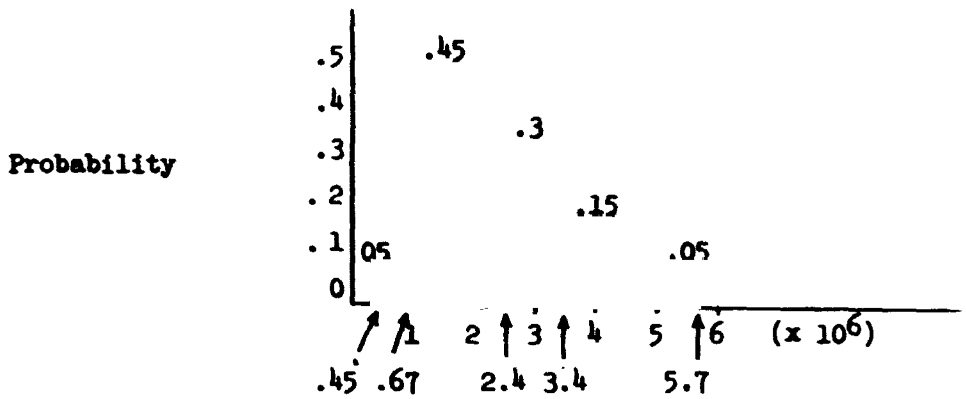
3. Versatility - the MBPM can be used before, during, or after the actual assembly is performed. As such it can serve as a planning tool, control tool, or post launch analysis tool, respectively.

Program Input:

There are many different parameters which this program needs but the main ones are time, men, environment, tools, operations, parts necessary for one step in the spacecraft assembly and test sequence, and the spacecraft part or parts affected during a task.

Program Output:

The program prints out a daily summary of burden buildup by spacecraft surface on a daily basis. The assembly and test operations of a spacecraft can be divided into a maximum of twenty stages. Each stage, in turn, is separated into 24-hour task intervals. The example on Table 5 is of the last task (here thirteen) of the last stage. The output is the information necessary to construct histograms of microbial burden versus probability for the three types of surfaces (exposed, mated, and occluded) and the total surface area. A histogram constructed from this output for the total surface area would be:



Microbial burden of total surface of S/C
at the end of stage 12, task 13

Table 6 is an example of the summary for an entire stage of the spacecraft assembly and test sequence (here stage 12).

Table 5. Typical output: Microbial Burden Prediction Model

```
TASK SUMMARY
RUN 1, STAGE 12, TASK  13   DAY 412  07/01/75
                            TASK START TIME   =   .96880+04
                            TASK FINISH TIME  =   .99120+04

BURDEN TOTALS BY SURFACE  - - - - - - - - - - - -          Histogram Values

SURFACE 1, TOTAL AREA= 2669.097, TOTAL BURDEN MEAN VALUE =   .25076+07
 PROBABILITY =          .05000     .45000     .30000     .15000     .05000 (x axis)      TOTAL } histogram values
 RANGE =      .45+06    .67+06     .24+07     .34+07     .50+07     .57+07 (y axis)              in example

SURFACE 2, TOTAL AREA= 1127.378, TOTAL BURDEN MEAN VALUF =   .27664+06
 PROBABILITY =          .05000     .45000     .30000     .15000     .05000               EXPOSED
 RANGE =      .16+05    .79+05     .28+06     .41+06     .47+06     .49+06

SURFACE 3, TOTAL AREA=   56.889, TOTAL BURDEN MEAN VALUE =   .54096+05
 PROBABILITY =          .05000     .45000     .30000     .15000     .05000               MATED
 RANGE =      .32+04    .95+04     .53+05     .77+05     .11+06     .13+06

SURFACE 4, TOTAL AREA= 1485.171, TOTAL BURDEN MEAN VALUE =   .50753+06
 PROBABILITY =          .05000     .45000     .30000     .15000     .05000               OCCLUDED
 RANGE =      .21+06    .23+06     .45+06     .71+06     .87+06     .94+06

- - - - - - - - - - - - - - - - - - - - - - - - -

  no meaning for this run - total of all four above
TOTAL, ALL SURFACES,  AREA= 5338.535,  BURDEN MEAN VALUE =   .33453+07
 PROBABILITY =          .05000     .45000     .30000     .15000     .05000
 RANGE =      .89+06    .12+07     .33+07     .45+07     .60+07     .67+07
```

Table 6. Typical output: Microbial Burden Prediction Model Summary

```
MICROBIAL BURDEN PREDICTION MODEL
RUN    1, VIKING PLANNED '75
STAGE 12, LAUNCH COMPLEX
STAGE SUMMARY-

  TASK       MEAN      FINISH
            BURDEN      TIME

     1     .335+07  9623.989
     2     .335+07  9647.989
     3     .335+07  9671.989
     4     .335+07  9695.989
     5     .335+07  9719.989
     6     .335+07  9743.989
     7     .335+07  9767.989
     8     .335+07  9791.989
     9     .335+07  9815.989
    10     .335+07  9839.989
    11     .335+07  9863.989
    12     .335+07  9887.989
    13     .335+07  9911.989
DATA IGNORED - IN CONTROL MODE
```

Summary of stage 12

no meaning for this run

note: no burden buildup for this stage

```
@PMD,ELP

PMD 23-B 07/12-21:10
SYS$*RLIB$. LEVEL 47  02
```

PROGRAM TITLE: RECONTAMINATION

Additional References: "JPL Planetary Quarantine;" NASA Spacecraft Sterilization Technology Seminar; July 11 and 12, 1973; Denver, Colorado

Application: Any Flight Project

Data Source: Experimental Data, Spacecraft Data

Status: In Progress

Program Description:

This program is intended to study the transfer of microorganisms from nonsterile to sterile parts of the spacecraft during space flight. Here the important environments for particle release are pyro events and meteoroid impacts. The computer codes for the approximate analytical solutions for meteoroid impact have been completed and some numerical results obtained. Codes for more exact analytical solutions are in development. Analyses and computer codes for the electric field at and near an illuminated plate in the solar wind plasma and for the charging rates and equilibrium potential of particles have been completed. The preliminary trajectory code has been exercised with the electric field and the particle charging subroutines in several simple physical configurations. The results indicate that the initial velocity of a released particle is a critical parameter. A paradigm of what the program will ultimately include in order to study recontamination is shown in Fig. 5.

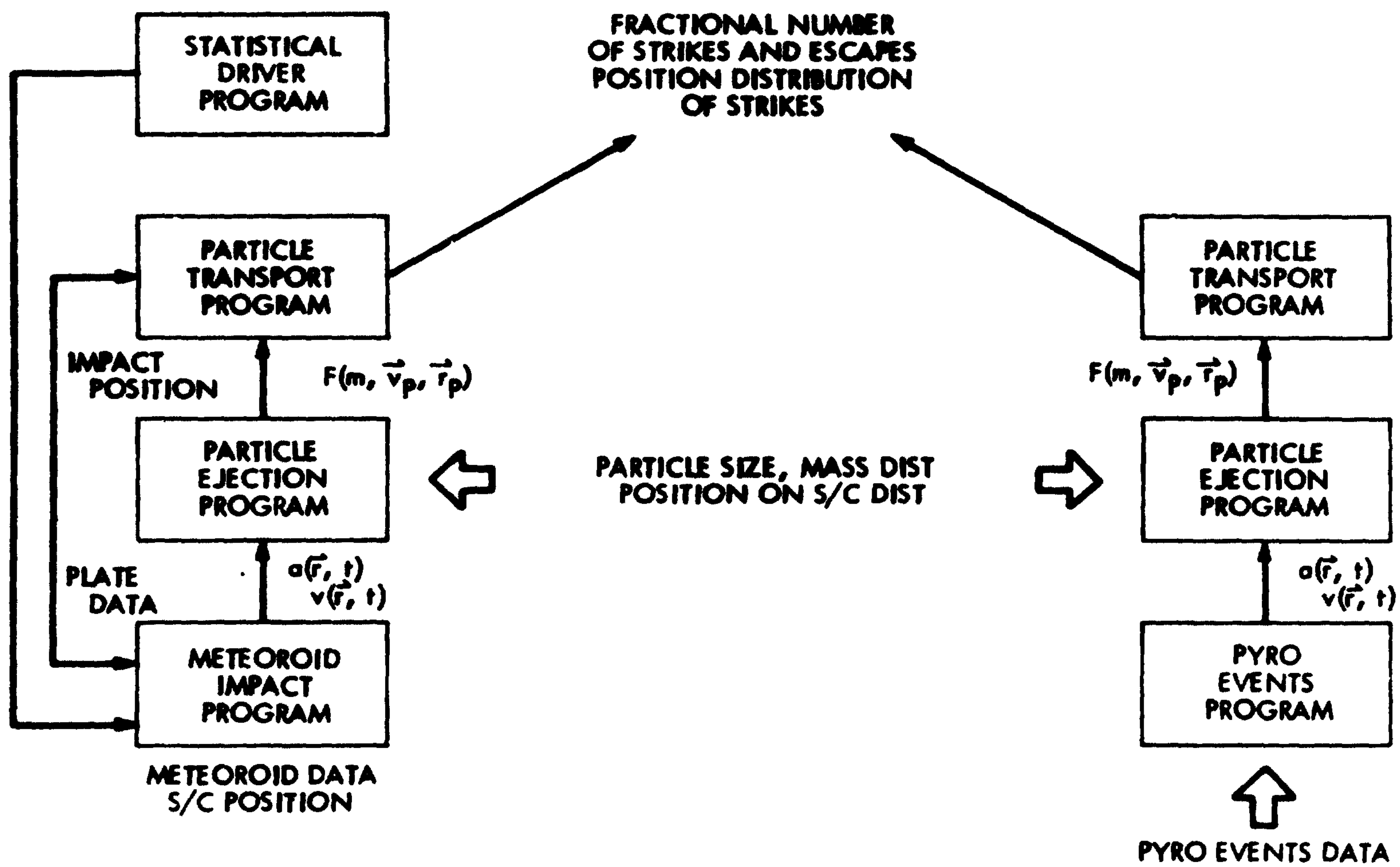
Program Input:

Inputs include velocity and density of meteroid impacts, spacecraft orientation and geometry, and information relative to spacecraft onboard dynamic events.

Program Output:

Eventually the program will indicate the number of hits of a sterilized surface by a contaminated particle and the number of particles that will leave the region of the spacecraft.

Fig. 5. Partial Model for Development of Recontamination Computer Program



PROGRAM TITLE: ENTRY HEATING

Additional References: "Spacecraft Microbial Burden Reduction Due to Atmospheric Entry Heating - Jupiter"

Application: Outer Planet Missions

Data Source: Experimental Data, Spacecraft Data

Status: In Progress (Division 35)

Program Description:

Planetary quarantine analyses performed for recent unmanned Mars and Venus missions assumed that the probability of contamination by a spacecraft (given accidental impact) was equivalent to one. However, in the case of the gaseous outer planets, the heat generated during the inadvertent entry of a spacecraft into the planetary atmosphere might be sufficient to cause significant microbial burden reduction. This could affect navigation strategy by reducing the necessity for biasing the aim point away from the planets. An effort has been under way at JPL to develop the tools necessary to predict temperature histories for a typical spacecraft during inadvertent entry. The thermal response of the spacecraft component and debris resulting from disintegration is determined. Guidelines are given to indicate the types of components and debris most likely to contain viable organisms, which could contaminate the lower layers of the Jovian atmosphere.

Program Input:

The significant particle parameters relating to the debris analyses are size, density, drag coefficient, accommodation coefficient, and surface emittance.

Program Output:

The program will give a tabulated result of temperature profile as a function of time at different entry angles. This tabulated information can then be used to plot a graph as shown in Fig. 6.

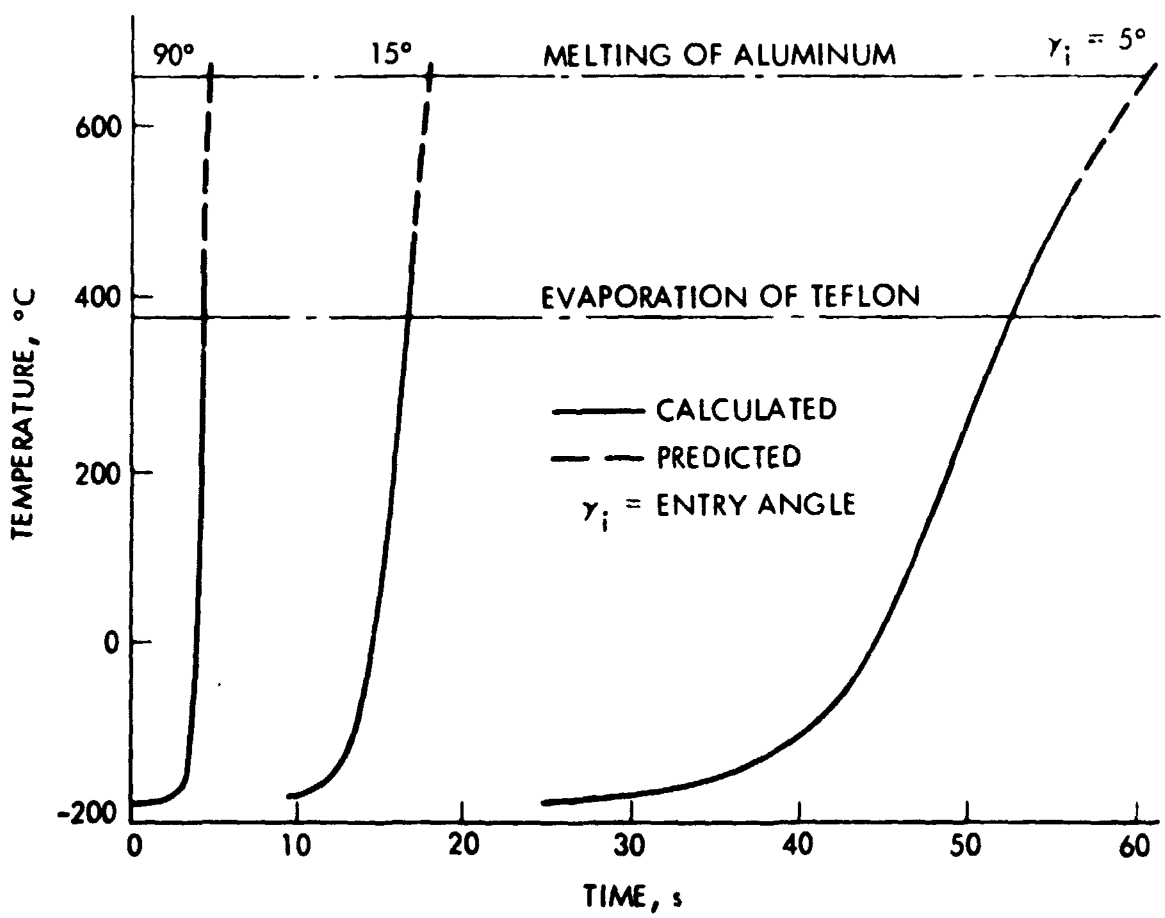


Fig. 6. Typical graph plotted from output of entry heating program

PROGRAM TITLE: STERILIZATION PROCESS ANALYSIS NETWORK (SPAN)

Additional References: "Microbial Burden Prediction Model Program: Production Version;" NASA Tech Brief, October, 1971.

Application: Any Flight Project

Data Source: Spacecraft During Assembly and Test Prior to Sterilization

Status: Discontinued Use

Program Description:

SPAN is primarily used in conjunction with a thermal analysis program for performing sterilization process calculations and sensitivity studies prior to the sterilization of the capsule. To achieve the appropriate probability of sterility required by the planetary quarantine constraints, a dry heat thermal sterilization process may be applied to a planetary capsule prior to launch. To minimize the severity of the sterilization cycle and also assure that the desired level of sterility is attained, it is necessary to account for the reductions in microbial population that occur during the transient phases of heating and cooling as well as the restrictions that occur during the steady state phase. This program computes a measure of the sterilizing process that, when equal to unity, is indicative that sterility has been achieved and then calculates the time necessary for heat application, the additional time required at steady state conditions, and the time necessary for cooling.

Program Input:

The basic inputs that are required are: (1) a thermal analysis of the capsule, (2) the probability of survival that must be achieved at the end of the cycle, (3) the microbial heat resistance characteristics, and (4) the number of microorganisms present at the time of capsule sterilization.

Program Output:

SPAN gives the total time needed to perform a sterilization process in hours or minutes as a function of various sterilizing temperatures and microbial heat resistance. This can be seen in the sample output in Table 7. The section enclosed in brackets is of major interest to the program user.

Table 7. Typical output: Sterilization Process Analysis Network Program

```
HEATING AREA=     0.632175370E 01     COOLING AREA=     0.161710111E 01 FOR NODE NO.=  135     TOTAL AREA=     0.793885480E 01
          0.100000E 02      0.290000E 02
          0.719326E-01      0.114003E 00
          0.163110E 00      0.200157E 00
          0.258512E 00      0.301403E 00
          0.333882E 00      0.333882E 00
          0.369860E 00      0.369860E 00
          0.389277E 00      0.409714E 00
          0.431225E 00      0.431225E 00
          0.453864E 00      0.453864E 00
          0.453864E 00
          0.453864E 00      0.369860E 00
          0.180687E 00      0.796834E-01
          0.527674E 01      0.817320E 00
          0.260000E 02      0.260000E 02
HEATING AREA=     0.527673170E 01     COOLING AREA=     0.817319930E 00 FOR NODE NO.=  142     TOTAL AREA=     0.609405069E 01
          0.700000E 01      0.280000E 02
          0.409658E-01      0.882582E-01
          0.245584E 00      0.317184E 00
          0.333836E 00      0.409658E 00
          0.409658E 00      0.431166E 00
          0.369809E 00      0.333836E 00
          0.389224E 00      0.333836E 00
          0.389224E 00      0.369809E 00
          0.409658E 00      0.389224E 00
          0.389224E 00      0.369809E 00
          0.369809E 00      0.351362E 00
          0.351162E 00      0.190147E 00
          0.796729E-01
          0.656497E 01      0.405666E 00
          0.260000E 02      0.260000E 02
HEATING AREA=     0.654492070E 01     COOLING AREA=     0.405664270E 00 FOR NODE NO.=  221     TOTAL AREA=     0.695063350E 01
```

NODE	B C	DTR	TH(K)	TS(K)	TC(K)	TTOL(K)
103	2.	0.670000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
104	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
107	2.	0.670000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
111	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
114	3.	0.350000E 01	0.260000E 02	0.176130E 02	0.140000E 02	0.576130E 02
118	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
122	2.	0.670000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
123	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
126	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
130	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
131	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
135	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
142	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02
221	1.	0.330000E 00	0.260000E 02	0.000000E-38	0.140000E 02	0.400000E 02

```
ENODEMAX= 104          INODEMAX= 114          MNODEMAX= 103
TMAXE=    0.400000E 02 TMAXI=     0.576130E 02 TMAXM=     0.400000E 02
```

BC: BURDEN CLASSIFICATION — DTR: D VALUE AT REFERENCE TEMPERATURE (@ 125°C)

1 exposed surface — TH(K): TIME FOR HEATING AT K^{th} NODE

2. mated surface — TS(K): " IN STEADY STATE AT K^{th} NODE

3 encapsulated — TC(K): FOR COOLING AT K^{th} NODE

TTOL: ROW TOTALS

ENODEMAX: exposed node maximum → TMAXE ACTUAL VALUE

INODEMAX: encapsulated node " → TMAXI "

MNODEMAX: mated node " → TMAXM = "

PLANETARY QUARANTINE COMPUTER PROGRAMS AT AFETR

Table 8. AFETR Planetary Quarantine Computer Programs

PROGRAM TITLE	STATUS				APPLICATION			DATA SOURCE	
	Discontinued Use (Operational)	Operational	Operational (Undergoing Changes)	In Progress	Apollo Mission	Any Flight Project	General	Experimental Data	Spacecraft
File Preparation Program	X				X				X
Data Storage Program	X				X				X
Lunar Inventory Program	X				X				X
Qualitative Storage Program			X			X	X	X	X
Qualitative Summary Program			X			X	X	X	X
MARCEL				X		X		X	
Statistical Comparison of Undying Means		X				X		X	

DATA STORAGE AND RETRIEVAL

AFETR GROUP I (SEE FIG. 1)

PROGRAM TITLE: FILE PREPARATION PROGRAM (FILE)

Additional References: Roark, A. L. and W. R. Gavin; User's Manual for the Planetary Quarantine Lunar Information System; Sandia Laboratories; SC-M-70-604; November, 1970.

Application: Apollo Missions

Data Source: Spacecraft during Assembly and Test

Status: Discontinued Use

Program Description:

This program maintains a file on the Apollo launches. The capabilities of FILE are the following:

1. Establishes environmental sampling locations of the spacecraft (i.e. location, length of time at location, and module identification).
2. Establishes Apollo flight configurations (i.e. astronaut, module identification, astronaut's suit identification, launch date, landing coefficients).
3. Modifies or deletes either of these.

Program Input:

The user must provide the information needed to construct the file.

Program Output:

The output format varies with the type of computer run which is being made. It consists in most cases of several pages. The first is the same for each run. See Fig. 7 for an outline of the output.

Fig. 7. Output outline: File Preparation Program

"VERSION NUMBER X"

This version number will always be the same for a given program deck.

The other pages of output are self-explanatory and we shall only outline them.

A. Establishment of Apollo Flight Configurations and Plans

Page 2:

1st line FLIGHT

2nd line LAUNCH DATE = ___________ LANDING COORDINATES, _______ ,
___________ MOD ID's ___ ___ ___ ___ ___ ___ ___

3rd line: ASTRO ID's _____ _____ _____ _____ _____ _____
SUIT ID's _____ _____ _____ _____ _____ _____

4th line: LAUNCH PAD ______________

B. Estalishment of Environmental Sampling Location

None.

C. Module Transfer

Page 2: MODULE ___________ FLIGHT CHANGED FROM _______, FLIGHT
CHANGE TO ___ __________

Page 3: Same as page 2 in Establishment of Apollo Flight.

D. Landing Coordinate Update

Page 2 LANDING COORDINATES __________ __________

Page 3: Same as page 2 in Establishment of Apollo Flight.

E. Launch Date Update

Page 2: LAUNCH DATE __________

Page 3 STANDARD QUANTITATIVE OUTPUT I (see Chapter 3)

Page 4: STANDARD QUANTITATIVE OUTPUT II (see Chapter 3)

Page 5: STANDARD QUALITATIVE OUTPUT (see Chapter 3)

Page 6: Same as page 2 in A above.

F. Suit Transfer

Page 2: SUIT CHANGED _____________ FOR ASTRO _______ _______
ASTRO. J.
where J = number of the astronaut, in order of placement
into computer

Page 3. Same as page 2 in Establishment of Apollo Flight.

PROGRAM TITLE: DATA STORAGE PROGRAM (DAST)

Additional References: Roark, A. L. and W. R. Gavin; User's Manual for the Planetary Quarantine Lunar Information System; Sandia Laboratories; SC-M-70-604; November, 1970.

Application: Apollo Missions

Data Source: Spacecraft during Assembly and Test

Status: Discontinued Use

Program Description:

DAST stores data from strip sampling of the environment and swab sampling from the surfaces of Apollo modules. The program was also intended to perform estimations and predictions of both qualitative and quantitative loads at the time of sampling, at launch, and at the lunar surface but the necessary deck for this part of the program was never supplied by Sandia Laboratories.

Program Input:

For each sample taken the following information must be supplied: sampling date; sample site; number of times sampled; sample type (swab or strip); number of aerobic vegetative, anerobic vegetative, aerobic spore-formers, and anaerobic spore-formers; and finally colony identification.

Program Output:

An example of the output format is shown in Fig. 8 and is self-explanatory.

Fig. 8. Output format: Data Storage Program

A. Surface Data

Page 2: INPUT DATA

Module = ____________

Sampling Date = ____________

Location = ____________

Sampling Method = ____________

Sample ID = ____________

NUM AER VEG = ____________

NUM ANER VEG = ____________

NUM AER S F = ____________

NUM ANER S F = ____________

Colonies IDENT

____________	____________
____________	____________
____________	____________
____________	____________

Page 3: Quantitative Output I

MODULE = ____________

SAMPLING DATE = ____________

Mean No.	SAMPLE DATE	LAUNCH DATE	IMPACT DATE
AER. VEG.	______	______	______
ANAER. VEG.	______	______	______
AER. S. F.	______	______	______
ANER. S. F.	______	______	______
90% Conf. Limit			
AER. VEG.	______	______	______
ANAER. VEG.	______	______	______
AER. S. F.	______	______	______
ANAER. S. F.	______	______	______

Fig. 8. (contd)

Page 4: Quantitative Output II

Same as Quantitative Output I, except numbers are given per square foot rather than loads for the entire module.

Page 5: Qualitative Output

MODULE = ____________________

SAMPLING DATE = ____________

SAMPLE DATE	LAUNCH DATE	IMPACT DATE
________	________	________

(list of organisms; room for 100)

PROBABILITY ALL HAVE BEEN IDENTIFIED = .XX

B. Environmental Strip Data

Page 2: INPUT DATA

LOCATION = ____________________

SAMPLING DATE = ____________

LENGTH OF EXPOSURE = ____________

NUM AER VEG = ____________

NUM ANER VEG = ____________

NUM AER S F = ____________

NUM ANER S F = ____________

COLONIES IDENT.

____________________ ____________________

Page 3: Environmental Output

LOCATION = ____________________

SAMPLING DATE = ____________

		FALLOUT RATE	REMOVAL RATE
AERO VEG =	________	________	________
ANERO VEG =	________	________	________
AERO S F =	________	________	________
ANERO S F =	________	________	________

DATA ANALYSIS

AFETR GROUP II (SEE FIG. 1)

PROGRAM TITLE: LUNAR INVENTORY PROGRAM

Additional References: Roark, A. L. and W. R. Gavin; User's Manual for the Planetary Quarantine Lunar Information System; Sandia Laboratories; SC-M-70-604; November, 1970.

Application: Apollo Missions

Data Source: Spacecraft during Assembly, Test, and Flight

Status: Discontinued Use

Program Description:

The Lunar Inventory Program computes and displays microbial densities and probability of sample contamination by earthborne microbes delivered by lunar probes. Total lunar bio burden is also calculated. The microbial densities and probabilities of sample contamination are functions of time and lunar coordinates. The total lunar bio burden is a function of time only. All calculations are done for spore-forming and vegetative microbes.

Program Input:

The input consists of a lunar inventory file, which contains one record for each lunar impactor and a record which contains the date and coordinate of the current inquiry. The lunar inventory file holds the following information: impactor identification, launch date, landing date of impactor, longitude and latitude of lunar impact, total bio burden of craft at launch, fraction of bio burden exposed to ultra violet light, fraction of spore-formers in bio burden, type of impact (i.e. hard or soft), and mass of probe.

Program Output:

The program gives the predicted bio burden on the moon for a specified date and location (or the total moon surface). A sample is in Table 9.

Table 9. Typical output: Lunar Inventory Program

```
AT COORDINATES       180.000       -0.000     DATE   200.00
DENSITY OF VIABLE VEGETATIVE  MICROBES IS LESS THAN  4.49159E-05 PER SQUARE METER
DENSITY OF VIABLE SPOREFORMER MICROBES IS LESS THAN  5.97102E-05 PER SQUARE METER
PROBABILITY OF CONTAMINATION OF A ONE SQUARE METER SAMPLE
       BY VEGETATIVE MICROBES         4.49149E-05
       BY SPOREFORMER MICROBES        5.97084E-05
       BY ANY VIABLE MICROBE          1.04621E-04
TOTAL BURDEN ON LUNAR SURFACE AS OF DATE
  VEGETATIVE    1.213E+08
 SPOREFORMER    1.457E+08
```

PROGRAM TITLE: QUALITATIVE STORAGE PROGRAM (QUAL)

Additional References: Roark, A. L. and W. R. Gavin; User's Manual for the Planetary Quarantine Lunar Information System; Sandia Laboratories; SC-M-70-604; November, 1970.

Application: Originally written for Apollo flights but adaptation is being completed which will allow the program to be used for any flight project or laboratory testing (i.e. heat studies)

Data Source: Spacecraft or Experimental Data

Status: Operational, Undergoing Change

Program Description:

QUAL is a program used to identify microorganisms given the results of tests made on a sample. After a microbiologist supplies the test results QUAL makes the microbial identification and then stores it on tape. The tape can then be used by the Qualitative Summary Program to prepare a final report on the qualitative information gathered by the Planetary Quarantine Lab.

Program Input:

The user must supply the experimental results mentioned above. A sample of the form supplied the microbiologist is shown in Fig. 9.

Program Output:

The first output from QUAL consists of the identification number, sample date, sample number, the portion of the spacecraft sampled, the name of the microorganism. The succeeding lines consist of lists of the test numbers and the result of those tests which is the summary of the input. Note that in the example shown in Fig. 10 the test numbers are offset by twelve from the input data sheet.

Note: A program (BUG ID) was the original QUAL and was later used to test the accuracy of QUAL.

Fig. 9. Typical input data sheet: Qualitative Storage Program

MICROBIAL IDENTIFICATION

(Circle Code Number that Applies) | AREA:

(1 5) Identification Number

(6 11) Date

(12) Sample Number

(13) Sample Treatment
Aerobic 1
Anaerobic 2
Heat Sh Aerobic 3
Heat Sh Anaerobic 4
Blood Agar Aerobic 5
Blood Agar Anaerobic 6
MacConkey 7
Mycophil 8

(14) Pigment
Black 1 Pink 6
Brown 2 Red 7
Green 3 White 8
Grey 4 Yellow 9
Orange 5

(15) Translucent 1
Opaque 2
Soluble pigment 3

(16) Growth characteristics
Aerobic 1
Anaerobic 2

(17) Cellular morphology
Rods 1 Spores 3 Yeasts 5 Actinom 7
Cocci 2 Pleo 4 Molds 6 Streptom. 8

(18) Gram Stain
− 1 + 2

(19) P R Aesculin
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(20) P R Arabinose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(21) P.R. Glucose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(22) P R Glycerol
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(23) Malonate Broth
ND 0 + 3
NC 1
NG 2

(24) P R Lactose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(25) P R Maltose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(26) P R Mannitol
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(27) Tyrosine
ND 0
− 1
+ 2

(28) Phenylalanine
ND 0
− 1
+ 2

(29) Casein
ND 0
− 1
+ 2

(30) P R. Sucrose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(31) P.R Xylose
ND 0 A 3
NC 1 AG 4
NG 2 ALK 5

(32) O F. Glucose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(33) Gas − 1 + 2

(34) O F. Maltose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(35) Gas − 1 + 2

(36) B.P Arabinose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(37) B.P. Glucose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(38) B.P. Lactose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(39) B P Maltose
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(40) B P Mannitol
ND 0 AO 3
NC 1 AF 4
NG 2 ALK 5

(41) Catalase
ND 0 − 1 + 2

(42) Coagulase
ND 0 − 1 + 2

(43) Phosphatase
ND 0 − 1 + 2

(44) Hemolysis
ND 0 Beta 2
Alpha 1 Gamma 3

(45) Litmus Milk
ND 0 Acid 2
NC 1 ALK 3

(46) Stormy − 1 + 2

(47) Soft 1 Hard 2 No curd 3

(48) Red. Litmus − 1 + 2

(49) Peptonization − 1 + 2

(50) Gelatin ND 0 − 1 + 2

(51) Starch ND 0 − 1 + 2

(52) Oxidase ND 0 − 1 + 2

(53) V. P. ND 0 − 1 + 2

(54) M. R. ND 0 − 1 + 2

(55) Indol ND 0 − 1 + 2

(56) Citrate ND 0 − 1 + 2

(57) Nitrate ND 0 − 1 + 2

(58) TSI
ND 0 S+ 2
S− 1 ALK 3

(59) B− 1 B+ 2 ALK 3

(60) H2S− 1 H2S+ 2

(61) No gas 1 Gas 2

(62) Optochin ND 0 − 1 + 2

(63) Urease ND 0 − 1 + 2

(64) Motility (SIM)
ND 0 − 1 + 2

(65) AK#2 ND 0 NG 1 G 2

(66) Heat Shock S− 1 S+ 2

(67) H− 1 H+ 2

(68) Peptone Broth
ND 0 Gas 2
NG 1 No Gas 3

(69) 10°C ND 0 NG 1 G 2

(70) 45°C ND 0 NG 1 G 2

(71) 6.5% NaCl
ND 0 NG 1 G 2

(72) Anaerobic Growth
ND 0 NG 1 G 2

(73) 0.1% M.B. Milk
ND 0 NG 1 G 2

(74) MacConkey
ND 0 P 2
NG 1 G 3

(75) Flagella
ND 0 − 1 + 2

(76) Capsule
ND 0 − 1 + 2

(77 79)

(80) Portion of Spacecraft Sampled
CMI 1 IU 5
LAI 2 S4B 6
LAE 3 SLA 7
LDE 4

REMARKS

HSM 8.27 (CDC)
REV. 11 72

Fig. 10. Typical output· Qualitative Storage Program

```
                                                   Identification       Test Results
 H0117      060173                1      B,LENTUS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41     -
44     -          45     -          60       NG
 H0112      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    +           39     +              41     -
44     -          45     +          60       NG
 H0120      060173                1     B,BREVIS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     +          16     -          17    +           39     +              41     -
44     +          45     +          60       NG
 H0129      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     -              41     -
44     -          45     -          60       NG
 H0213      060173                1      B,LENTUS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41     -
44     -          45     -          60       NG
 H0331      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     -              41     -
44     -          45     -          60       NG
 H0519      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     -              41     -
44     -          45     -          60       NG
 H0406      060173                1     B,BREVIS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     -              41     -
44     -          45     +          60       NG
 H0611      060173                1     B,BREVIS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    +           39     -              41     -
44     -          45     +          60       NG
 H0612      060173                1      B,LENTUS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41     -
44     -          45     -          60       NG
 H0620      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     -              41     -
44     -          45     -          60       NG
 H0625      060173                1     ATYP,BAC,SPP,
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    +           39     +              41     -
44     -          45     -          60       NG
 H0628      060173                1      B,LENTUS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41     -
44     -          45     -          60       NG
 H0632      060173                1      B,LENTUS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41     -
44     -          45     -          60       NG
 H0711      060173                1     B,COAGULANS
 1  AEROBIC        4  AEROBIC        5  SPORE          6     +              14     NC
15     -          16     -          17    -           39     +              41      +
44     -          45     +          60       G
```

PROGRAM TITLE: QUALITATIVE SUMMARY PROGRAM (QUALSUM)

Additional References: **Roark, A. L. and W. R. Gavin; User's Manual for the Planetary Quarantine Lunar Information System; Sandia Laboratories; SC-M-70-604; November, 1970**

Application: **Originally written for Apollo flights but adaptation is being completed which will allow the program to be used for any flight projects or laboratory testing (i.e. heat studies)**

Data Source: **Spacecraft or Experimental Data**

Status: **Operational, Undergoing Change.**

Program Description:

The program reformulates and summarizes data giving percentages of total colony count, number of total identifications, and number of different test sequences.

Program Input:

This program's input is the tape output from QUAL.

Program Output:

The typical program output together with pertinent annotations is given in Table 10.

Table 10. Typical output: Qualitative Summary Program

PERCENTAGES ON CRAFT H FROM 43 COLONIES IDENTIFIED ON THIS CRAFT BY SAMPLE TREATMENT AEROBIC,

KEY	ORGANISM	NUMBER	PERCENT	KEY	ORGANISM	NUMBER	PERCENT	KEY	ORGANISM	NUMBER	PERCENT
21	B,BREVIS	4	9,302	24	B,COAGULANS	1	2,320	27	B,LENTUS	22	51,163
88	ACTINOMYCETES	1	2,320	94	ATYP,BAC,SPP,	15	34,884				

microorganism identification — number of colonies — % of total

Translation: For microorganism 27 B. Lentus 22 of the 43 colonies were of this type (ie 51.163 %)

COLONY IDENTIFICATION CATALOGUE FOR H MODULE

KEY	ORGANISM	OBSERVED	SEQUENCE (coding for test results)
21	B,BREVIS	1	1 1,32 , , 121,2 , , , , , , 2 ,1 2,2 , , , 1,
		1	1 1,32 , , 111,1 , , , , , , 1 ,1 1,2 , , , 1,
		1	1 1,32 , , 111,2 , , , , , , 1 ,1 1,2 , , , 1,
		1	1 1,32 , , 121,2 , , , , , , 1 ,1 1,1 , , , 1,
24	B,COAGULANS	1	1 1,32 , , 111,1 , , , , , , 2 ,2 1,2 , , , 2,
27	B,LENTUS	18	1 1,32 , , 111,1 , , , , , , 2 ,1 1,1 , , , 1,
	22 in total	2	1 1,32 , , 311,2 , , , , , , 2 ,1 1,1 , , , 1,
		1	1 1,32 , , 311,1 , , , , , , 2 ,1 1,1 , , , 1,
		1	1 1,32 , , 311,1 , , , , , , 2 ,1 1,2 , , , 1,
88	ACTINOMYCETES	1	1 1,7 , , , , , , , , , , , , , ,
94	ATYP,BAC,SPP,	5	1 1,32 , , 111,2 , , , , , , 2 ,1 1,2 , , , 1,
		5	1 1,32 , , 111,1 , , , , , , 1 ,1 1,1 , , , 1,
		2	1 1,32 , , 111,2 , , , , , , 2 ,1 1,1 , , , 1,
		1	1 1,32 , , 111,1 , , , , , , 2 ,1 1,2 , , , 1,
		2	1 1,32 , , 112,1 , , , , , , 2 ,1 1,2 , , , 1,

4 different sequences identify B. Lentus

MICROBE KEY	DISTINCT TEST SEQUENCES	TOTAL TESTS
21	4	4
24	1	1
27	4	22
88	1	1
94	5	15

END OF PROGRAM

Summary of Above

total of 22 identifications of type 27 microorganism
4 different test sequences were accepted for identification

PROGRAM TITLE: MARCEL

ADDITIONAL REFERENCES: Roark, A. L. and M. C. Reynolds; A Computerized Program for Statistical Treatment of Biological Data; Sandia Laboratories

APPLICATION: Any Flight Project

DATA SOURCE: Experimental Data

STATUS: In Progress

Program Description:

This program will be used to compare subtle changes in the destruction pattern of microorganisms when exposed to sterilization. The use of standard pour plate techniques for microbial assay during experimentation in some cases yields hundreds of data bits (plate counts). These must be reduced in a way that these successive samples taken during process application represent the destruction rate of microorganisms as a consequence of the process. This program handles the statistical aspects of the data reduction. With plate counts of each successive sampling period as an input, the program computes the mean value of the replicate plate counts, the variance, standard deviation, upper and lower .95 confidence intervals and the coefficient of variation for each sampling interval. Based on the coefficient of variation values for a sampling period, the dilution or data set exhibiting the best values are selected for each period. These best sets are then used in computing the survivor curve based on a least square fit of the logarithmic model.

Note that the program is running but a sufficient data set to test the program completely has not yet been acquired.

Program Input:

The user supplies plate counts of each successive sampling period.

Program Output:

As given in the Program Description above, the output can best be shown by an example depicted in Figs. 11, 12, and 13. An output format precedes the example. Note that the transition from the data sets to the plotted means are offset by a factor of 10^1. By using the variable names from the sample that follows, the following formula is applied:

$$\text{SAMP} = \text{MEAN} \times 10^{\text{ORDER OF DIL.} + 1} \longleftarrow \text{correction factor of } 10^1$$

Example (from data set 1):

$$2.72875 \times 10^6 = 272.875 \times 10^{3+1}$$

Fig. 11. Typical output format: MARCEL Program

```
                                  TITLE OF EXPERIMENT

Repeat for each        Data Set = ___
sampling time period   Time = ___
                       Number of Dilutions = ___ (For this time period)
      Repeat for         Number of Data Points = ___ (Number of plate counts for this time period and dilution)
      each dilution      Order of Dilution = ___
                         Date (Plate Counts):
                         Mean = ___  Variance = ___  S.D. = ___             Upper .95 C.I. = ___                          Lower .95 C.I. = ___  C.V. = ___
                                                     (Standard Deviation) (Upper limit of 95% Confidence Interval)(C.I.)                         (Coefficient of Variation)
                           Dilution Chosen = ___ (Dilution chosen for this time period on the basis of the coefficient of variation)
Slope = ___ (Slope of line of best fit to log of selected means)  D-Value = ___  Intercept = ___ (Theoretical value of initial population*)
Corr. Coef. = ___  Stand. Err. in Est. Slope = ___  Stand. Err. of Est. = ___  Stand. Err. of Est. Inter. = ___

                                        .95 Conf. Interval (95% Confidence Interval about Model)
T (Time)   SAMP (Data)   MODEL (Log Model Value)   Upper (Upper Limit of 95% Confidence Band)   Lower (Lower Limit of 95% Confidence Band)
  ___         ___              ___                           ___                                          ___
  ___         ___              ___                           ___                                          ___
  ___         ___              ___                           ___                                          ___
  ___         ___              ___                           ___                                          ___
  ___         ___              ___                           ___                                          ___
```

*In computer output, E + 05 means 10^5 e.g., 2.31E + 06 represents 2.31×10^6

Fig. 12. Typical program printout: MARCEL Program

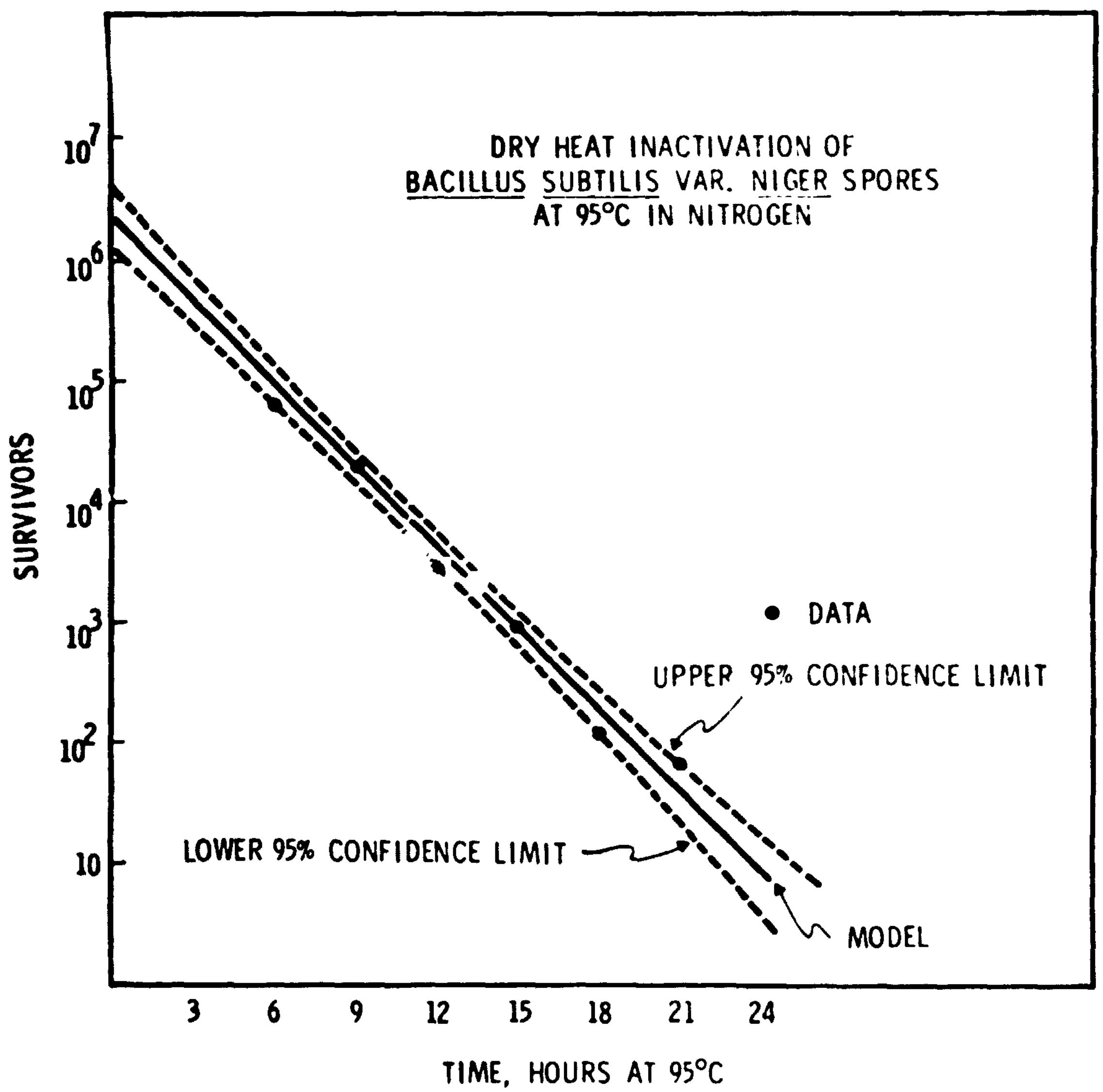
```
                              24 NOVEMBER 1970

 DATA SET =     1
TIME=   0.000
 NO. DIL.=     1
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     3
DATA
  265.00   282.00   292.00   267.00   250.00   277.00   265.00   285.00
MEAN= 272.875  VARIANCE=   155.8  S.D.=     13.6  UPPER .95 C.I.=   284.2  LOWER .95 C.I.=   261.5  CV =   .0498
 CIL. CHOSEN =     3

 DATA SET =     2
TIME=   3.000
 NO. DIL.=     1
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     3
DATA
   67.00    54.00    62.00    57.00    51.00    79.00    88.00    72.00
MEAN=  69.250  VARIANCE=    99.4  S.D.=     10.0  UPPER .95 C.I.=    73.6  LOWER .95 C.I.=    56.7  CV =   .1520
 CIL. CHOSEN =     3

 DATA SET =     3
TIME=   6.000
 NO. DIL.=     1
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     2
DATA
   58.00    63.00    80.00    83.00    62.00    66.02    75.00    63.00
MEAN=  68.750  VARIANCE=    86.2  S.D.=      9.3  UPPER .95 C.I.=    76.5  LOWER .95 C.I.=    61.0  CV =   .1351
 CIL. CHOSEN =     2

 DATA SET =     4
TIME=   9.000
 NO. CIL.=     1
NUMBER DATA POINTS=     9
 ORDER OF DIL. =     1
DATA
  270.00   212.00   197.00   201.00   214.00   255.00   236.00   231.00
MEAN= 225.000  VARIANCE=   777.7  S.D.=     27.9  UPPER .95 C.I.=   251.2  LOWER .95 C.I.=   204.5  CV =   .1223
 CIL. CHOSEN =     1

 DATA SET =     5
TIME=  12.000
 NO. DIL.=     1
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     1
DATA
   40.00    37.00    37.00    25.00    25.00    21.00    42.00    29.00
MEAN=  33.000  VARIANCE=    99.4  S.D.=      9.5  UPPER .95 C.I.=    40.9  LOWER .95 C.I.=    25.1  CV =   .2866
 CIL. CHOSEN =     1

 DATA SET =     6
TIME=  15.000
 NO. DIL.=     1
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     0
DATA
  116.00   125.00    87.00    62.00    95.00    82.30    85.00    84.06
MEAN=  93.250  VARIANCE=   508.5  S.D.=     22.5  UPPER .95 C.I.=   112.3  LOWER .95 C.I.=    74.5  CV =   .2410
 CIL. CHOSEN =     0

 DATA SET =     7
TIME=  18.000
 NO. DIL.=     2
NUMBER DATA POINTS=     8
 ORDER OF DIL. =     0
DATA
   20.00    16.00    12.00    14.00    11.00    10.00    10.03     9.00
MEAN=  14.500  VARIANCE=    18.9  S.D.=      9.6  UPPER .95 C.I.=    19.1  LOWER .95 C.I.=     9.9  CV =   .3031
NUMBER DATA POINTS=     4
 ORDER OF DIL. =    -1
DATA
  157.00   117.00    92.00   162.00
MEAN= 132.000  VARIANCE=  1110.7  S.D.=     33.4  UPPER .95 C.I.=   183.2  LOWER .95 C.I.=    80.8  CV    .2542
 CIL. CHOSEN =    -1

 DATA SET =     8
TIME=  21.000
 NO. DIL.=     1
NUMBER DATA POINTS=     4
 ORDER OF DIL. =    -1
DATA
   51.00    90.00    93.30    85.00
MEAN=  78.750  VARIANCE=   549.6  S.D.=     23.4  UPPER .95 C.I.=   106.7  LOWER .95 C.I.=    54.0  CV =   .3314
 CIL. CHOSEN =    -1


SLOPE=   -.521       B VALUE=    4.421       INTERCEPT=     2.31043806396E+06
CORR. COEF.=    .50010 STAND. ERR. IN EST. SLOPE=    .01896 STAND. ERR. CF EST.=    .13595 STAND. ERR. IN EST. INTER.=    .19913
                                        .95 CONF. INTERVAL
      T                    SAMP              MODEL              UPPER               LOWER
   0.                 2.72875000000E+06  2.31043806396E+06  4.12367845590E+06  1.29456263330E+06
   3.00000000000E+00  6.92500000000E+05  4.04095780760E+05  7.76226633090E+05  3.82609756050E+05
   6.00000000000E+00  6.87500000000E+04  1.81638719530E+05  1.46828424044E+05  6.94109951780E+04
   9.00000000000E+00  2.25000000000E+04  2.12523803646E+04  2.96863303310E+04  1.53596143170E+04
   1.20000000000E+01  3.30000000000E+03  4.45293134617E+03  6.16139549046E+03  3.21919911390E+03
   1.50000000000E+01  9.32500000000E+02  9.33805600310E+02  1.36324972720E+03  6.38567313900E+02
   1.80000000000E+01  1.32000000000E+02  1.99609003110E+02  3.12040261030E+02  1.22233149290E+02
   2.10000000000E+01  7.87500000000E+01  4.09600770020E+01  7.31022303980E+01  2.29504314700E+01
```

offset by a factor of 10' from mean values below

Points to make up graph (see next page)

from means above

Fig. 13. Typical graph of MARCEL Program output



PROGRAM TITLE: STATISTICAL COMPARISON OF UNDYING MEANS (SCUM)

Additional References: No Published Material

Application: Any Flight Project

Data Source: Experimental Data

Status: Operational

Program Description:

The program performs statistical calculations to determine whether all the samples come from the same population. It provides the reliability of the initial population count for sterilization studies.

Program Input:

This consists of the estimated total count on the teflon strips.

Program Output:

The program prints out the ranked total count data to the nearest tenth and the percentage of data samples which this count represents. Standard statistics on the samples are also given (i.e. mean, standard deviation, etc.). A sample together with explanatory annotations is given in Table 11.

Table 11. Typical output: Statistical Comparison of Undying Means Program

(no. of organisms)

X VALUES	TOTAL	PERCENT
20	[illegible]	2,3[illegible]
30	7	1,8[illegible]
40	1[illegible]	2,6[illegible]
50	1[illegible]	3,91
60	1[illegible]	4,43
70	1[illegible]	3,39
80	1[illegible]	4,0[illegible]
90	1[illegible]	3,3[illegible]
100	1[illegible]	3,13
110	[illegible]	1,82
120	[illegible]	2,0[illegible]
130	[illegible]	1,3[illegible]
140	21	5,47
150	1[illegible]	3,13
160	1[illegible]	4,17
170	[illegible]	1,30
180	1	4,17
190	11	2,8[illegible]
200	[illegible]	0,78
210	7	1,82
220	22	5,73
230	[illegible]	1,56
240	1[illegible]	3,3[illegible]
250	7	1,82
260	11	2,8[illegible]
270	[illegible]	1,30
280	[illegible]	1,30
290	5	1,30
300	[illegible]	1,30
310	4	1,04
320	4	1,04
330	4	1,04
340	[illegible]	1,56
35[illegible]	[illegible]	[illegible]

← 9 samples were found with 20 organisms present. The 9 samples = 2.34% of the total # of samples

Continues to 2400 ↓

MIN = 20 MAX = 2400 MEAN = 229.01 N = 384 (total samples)

MEDIAN = 180.00 VARI = 58542.10 STAN DEV = 241.9547

STAN ERR = 12.3472 CLL(95) = 204.81 CLU(95) = 253.21

CLL(99) = 197.15 CLU(99) = 260.87 COEFF VARI = 1.06

CLL & CLU = lower and upper confidence intervals

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