

PROGRAM FOR ESTIMATION OF GLUCOSE UTILIZATION BASED ON
COMPARTMENTAL MODELS

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Assumes value of α of 0 fine at blood com
 α, β \rightarrow individuals
5, 100

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PROGRAM FOR ESTIMATION OF GLUCOSE UTILIZATION BASED ON COMPARTMENTAL MODELS

This program is a modified version of the optimization program originally written by Mark Mintun to estimate the utilization of glucose on the basis of compartment models. Modifications were added by Joanne Markham and Ken Larson. Ken Larson wrote the subroutine which computes the compartmental model solutions and Joanne Markham incorporated this subroutine and additional modifications. A description of the model and the commands and input files required to estimate parameters for glucose utilization are included in this document along with listings of a input data case and the output from the processing of the data case.

This program performs only the optimization step for computing parameter estimates from regional tissue time-activity curves and an arterial blood curve and does not require the original PET scan data files. The generation of the tissue time-activity curves must be performed in another program and the curves saved in a disc file.

The optimization is performed by a weighted Marquardt algorithm for nonlinear optimization with the weights computed as the inverse of the variance of each data value. An estimate of the standard deviation of each data value is computed from the data by using a function derived from empirical data.

The compartment model implemented is described in section IV. Any version of the model can be used by setting the appropriate transport rates to zero, although some models may be of little use. See the text following the model description for additional information. The program can also be used in a simulation mode in which no estimation is performed, but the solution corresponding to the input parameters is computed. See the description of the input file PBLK-.RPO for the correct input for simulation.

There are four restrictions on data determined by array sizes (set in dimension statements) in the program. The maximum number of regions and maximum number of points per region that can be processed is 100, and the time coordinates for both the blood curve and the tissue data cannot be greater than 8000 seconds (2.3 hours). In addition, the blood curve is assumed to consist of less than 500 data values. The appropriate dimension statements must be changed and the task program regenerated to permit processing of data which violates these limits.

I. PROGRAM EXECUTION

A command file, GLUCRUN.CSS, has been created to perform the file assignments and generate the necessary commands for execution of the program. The following statement is an example of the command that the user will type to execute the program. This statement corresponds to the sample data case processed for this report.

GLUCRUN TESTFDG,TESTP.TSC,TESTP.DTA,PBLKFDG.RPO

TESTFDG	identification used as prefix for output files
TESTP.TSC	tissue time-activity data for all regions
TESTP.DTA	blood curve data values
PBLKFDG.RPO	file containing parameter information for estimation process

Four output files, TESTFDGA.LOG, TESTFDGB.LOG, TESTFDGC.LOG, and TESTFDGD.LOG, are created by the program. A brief description of their content is given below and listings for the data case processed by the above statement are on pages 10 – 17.

II. DESCRIPTION OF INPUT FILES

Input Files:	XXXXXXX.DTA	blood curve file
	XXXXXXX.TSC	tissue time-activity data file
	PBLK XXXX.RPO	parameter estimation information

- A. XXXXXXXX.DTA, the blood curve file must contain:
 - a. title or identification
 - b. number of data points
 - c. data consisting of time and blood activity
 - d. time shift value to be subtracted from time data (program assumes 0 if no value is entered)

- B. XXXXXXXX.TSC file

This file contains the computed time-activity curves for all regions-of-interest in the following format:

- a. title or identification
- b. number of time points and number of columns (number of ROI +2)
- c. for each time value, the activity values for all regions: scan start time, scan length, activity for ROI 1, activity for ROI 2, ... (maximum of 100 regions)
- d. the identification for each of the regions

C. PBLK XXXX.RPO

This file must contain

- a. 20 values for the parameters (0 if parameter is not used)
- b. n – number of parameters to be estimated (enter 0 for simulation mode)
- c. i j k ... – indices for variable parameters, n values (1–20)
- d. m – number of parameters with values varying by region
- e. i j k ... – indices for parameters varying by region
- f. values for m parameters for region 1, followed by values for the remaining regions

For glucose utilization, the parameters and units are

- 9 parameter →
1. blood flow (ml/min/100g)
 2. blood volume (ml/100g)
 3. blood glucose $\mu\text{mol}/\text{ml}$ (arterial concentration)
 4. 0 (not input for glucose model)
 5. k_{21} (1/min)
 6. k_{12} (1/min)
 7. k_{32} (1/min)
 8. k_{43} (1/min)
 9. To (sec) – shift for blood curve
 10. $t(1/2)$ – half-life of tracer in seconds; if blood and tissue curves have been decay corrected, enter 0. Otherwise the value entered will be used to include the effects of tracer decay in the model.

Parameters 11–20 are not used and zero should be entered for their values.

Input for a typical case is listed below. Since the values for blood flow and blood volume usually vary by region, values for these parameters are entered at the end. For this example, there are three regions to be processed; values for 4 kinetic parameters (k_{21} , k_{12} , k_{32} , and k_{43}) are to be estimated with initial estimates as shown. In addition, the input blood curve is to be corrected for delay by a variable shift which is initially equal to 2. For region 1, the value of flow is 105 ml/min/100g and the value of blood volume is 6.42 ml/100g; blood glucose concentration is 65 for all 3 regions.

0. 0. 65. 0. 2.0 1.0 .5 0.0055 2.0 11*0.
5 -# parameter to estimate
5. 6 7 8 9 -# of the parameters to estimate
2 -# parameter with regional values which will be specified below
1 2 -# of the parameter with region values to be specified below
105. 6.42
65.7 4.72
55.1 5.26

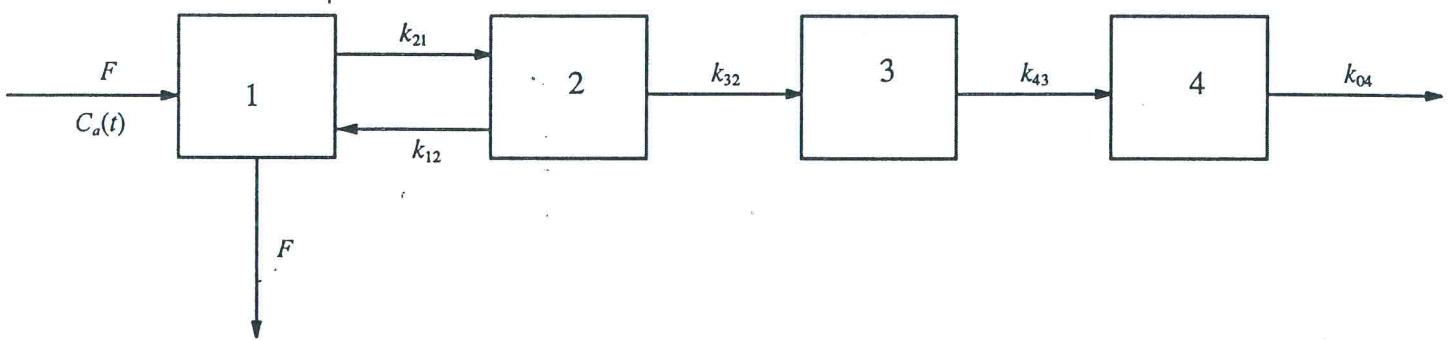
For simulation mode with the above parameters, the second line would consist of 0 and the third line would be omitted. All other input data would be identical to that listed above.

III. DESCRIPTION OF OUTPUT FILES

Four output files are generated with names composed of the identification entered as the first argument in the program executuion command and the letters A-D with the extension .LOG as illustrated below.

RUNIDA.LOG	formal report
RUNIDB.LOG	curves of data vs. estimated/fitted function
RUNIDC.LOG	error log
RUNIDD.LOG	parameter values only

IV. DESCRIPTION OF THE COMPARTMENTAL MODEL



Compartment 1 – free glucose in vascular space

Compartment 2 – free glucose in extravascular space

Compartment 3 – metabolites in extravascular space

Compartment 4 – metabolites in vascular space

$q_i(t)$	– amount of tracer in compartment i at time t	μmol
$C_a(t)$	– arterial blood concentration	($\mu\text{mol}/\text{ml}$) ($\mu\text{mol}/\text{m}^3$)
F	– blood flow	(ml/min)
V_1	– vascular volume	(ml)
k_{21}	– rate constant for transport from compartment 1 to 2	($1/\text{min}$)
k_{12}	– rate constant for transport from compartment 2 to 1	($1/\text{min}$)
k_{32}	– rate constant for transport from compartment 2 to 3	($1/\text{min}$)
k_{43}	– rate constant for transport of labeled metabolites	($1/\text{min}$)
k_{04}	– rate constant for washout of labeled metabolites	($1/\text{min}$)

For PET data, all quantities are per ml or g of brain

Parameters which are estimated are k_{21} , k_{12} , k_{32} , and k_{43} . Note that k_{04} is set equal to F/V_1 in the program if k_{43} is not zero.

The kinetic behaviour of tracer is described by the following system of differential equations:

$$\frac{dq_1(t)}{dt} = F C_a(t) - \frac{F}{V_1} q_1(t) - k_{21} q_1(t) + k_{12} q_2(t) \quad [1]$$

$$\frac{dq_2(t)}{dt} = k_{21} q_1(t) - (k_{12} + k_{32}) q_2(t) \quad [2]$$

$$\frac{dq_3(t)}{dt} = k_{32} q_2(t) - k_{43} q_3(t) \quad [3]$$

$$\frac{dq_4(t)}{dt} = k_{43} q_3(t) - k_{04} q_4(t) \quad [4]$$

The impulse response ($\tilde{q}_1(t)$, $\tilde{q}_2(t)$, $\tilde{q}_3(t)$, $\tilde{q}_4(t)$) of the system is given by the following equations:

$$\tilde{q}_1(t) = \frac{1}{(\beta - \alpha)} \left[(k_{22} - \alpha) e^{-\alpha t} + (\beta - k_{22}) e^{-\beta t} \right] \quad [5]$$

$$\tilde{q}_2(t) = k_{21} \frac{1}{(\beta - \alpha)} \left[e^{-\alpha t} - e^{-\beta t} \right] \quad [6]$$

$$\begin{aligned} \tilde{q}_3(t) &= k_{21} k_{32} \left[\frac{e^{-\alpha t}}{(\beta - \alpha)(k_{43} - \alpha)} + \frac{e^{-\beta t}}{(\beta - \alpha)(\beta - k_{43})} \right. \\ &\quad \left. + \frac{e^{-k_{43}t}}{(k_{43} - \beta)(k_{43} - \alpha)} \right] \end{aligned} \quad [7]$$

$$\begin{aligned}\tilde{q}_4(t) = & k_{43} k_{32} k_{21} \left[\frac{e^{-\alpha t}}{(\beta - \alpha)(k_{43} - \alpha)(k_{04} - \alpha)} \right. \\ & + \frac{e^{-\beta t}}{(\alpha - \beta)(k_{43} - \beta)(k_{04} - \beta)} \\ & + \frac{e^{-k_{43}t}}{(k_{43} - \alpha)(k_{43} - \beta)(k_{04} - k_{43})} \\ & \left. + \frac{e^{-k_{04}t}}{(\alpha - k_{04})(\beta - k_{04})(k_{43} - k_{04})} \right]\end{aligned}\quad [8]$$

where

$$k_{11} = F/V_1 + k_{21} \quad [9]$$

$$k_{22} = k_{12} + k_{32} \quad [10]$$

$$\alpha + \beta = k_{11} + k_{22} \quad [11]$$

$$\alpha\beta = k_{11} k_{22} - k_{21} k_{12} \quad [12]$$

The response to an arbitrary input $C_a(t)$ is then given by

$$q_i(t) = F \tilde{q}_i(t) * C_a(t), \quad i = 1, 2, 3, 4 \quad [13]$$

Tracer activity detected by PET is the sum of activity in all compartments,

$$q_T(t) = q_1(t) + q_2(t) + q_3(t) + q_4(t) \quad [14]$$

The program can be used for several types of models if the correct values are entered for the parameters and the parameter estimation variables. Note that removal of tracer from the first compartment is never zero, but is assumed to occur at the rate given by F/V_1 .

For a simple one-compartment model, k_{21} must be entered as zero. The rate for removal of tracer from the compartment can then be manipulated by entering arbitrary values for V_1 in order to utilize the program for a simple one-compartment model.

If values for k_{32} and k_{12} are entered as zero, the solution consists of the amount of tracer in the two compartments with the concentration of tracer in the second

compartment always increasing. If k_{12} is not equal to zero, but k_{32} is zero, the solution is computed for a two-compartment model with exchange of tracer at the rates k_{12} and k_{21} . If k_{43} is entered as zero, tracer accumulates in compartment 3. However when k_{43} is not zero, the rate k_{04} for clearance of tracer from compartment 4 is assumed to be equal to F/V_1 .

Seven variables are computed from the parameters of the compartmental model. These variables and the equations used for their computation are listed below.

Utilization fraction

GMR	- $\mu \text{ mol/min}/100\text{g}$
CHI	- $1/\text{min}$
KD	- $\text{ml/min}/100\text{g}$
CG	- $\mu \text{ mol/ml}$ (average blood concentration)
Forward Flux	- $\mu \text{ mol/min}/100\text{g}$
Brain free glucose	- $\mu \text{ mol/g}$

The variable CHI, χ , is defined as

$$\chi = (k_{21} k_{32}) / (k_{12} + k_{32}) \quad [15]$$

unless k_{32} is zero; then $\chi = k_{21}$. The net utilization fraction, UF , or the fraction of glucose entering the region per unit time that is utilized per unit time in the steady state is then given by

$$UF = \chi \bar{t}_1 / (1 + 0.835 \chi \bar{t}_1) \quad [16]$$

where the vascular mean transit time is

$$\bar{t}_1 = V_1/F \quad [17]$$

The glucose utilization or metabolic rate, GMR, is

$$GMR = \chi CG V_1 \quad [18]$$

where CG is the average concentration of glucose in the blood and is computed from the input arterial glucose concentration, CG_a , by

$$CG = CG_a / (1 + 0.835 \chi \bar{t}_1) \quad [19]$$

The clearance constant K_d is computed as

$$K_d = k_{21} V_1 \quad [20]$$

and the forward flux is equal to

$$K_d CG = k_{21} V_1 CG$$

Brain free glucose is computed by dividing GMR by k_{32} ,

$$GMR/k_{32} \quad [21]$$

V. LISTINGS OF INPUT FILES

TESTFDG.CSS

```
GLUCRUN TESTFDG, TESTP.TSC, TESTP.DTA, PBLKFDG.RPO
$EXIT
```

GLUCRUN.CSS

```
*****
* GLUCRUN -- TEST GLUCOSE METABOLISM OPT PROGRAM
*****
V BR3

XDEL @1A.LOG
XDEL @1B.LOG
XDEL @1C.LOG
XDEL @1D.LOG
AL @1A.LOG, IN
AL @1B.LOG, IN
AL @1C.LOG, IN
AL @1D.LOG, IN

XDEL @1.CON
AL @1.CON, IN, 132
* @2 = TSC (TISSUE CURVES) FILE
* @3 = BLOOD CURVE
* @4 = PARAM BLOCK FILE
$BUILD @1.CMD
@2
@3
@4
1
@1A.LOG
3
@1B.LOG
$ENDB
LO GLUCOPT
AS 1, @1.CON
AS 0, @1.CMD
AS 12, @1C.LOG
AS 9, @1D.LOG
START
$EXIT
```

TESTP.DTA

@01@ APRIL 9 1987 P1194 FG1, 12-12-89, WJP

31,2

3.	96.	0.12000	0.61000	0.05	3.51	435	10.
9.	85.	0.16000	0.61000	0.11	4.22	355	10.
12.	409.	0.12000	0.60000	0.14	4.37	1815	10.
15.	9088.	0.15000	0.66000	0.17	4.51	42762	10.
19.	22275.	0.15000	0.82000	0.21	5.20	136126	10.
24.	30899.	0.15000	0.61000	0.26	5.36	130857	10.
27.	23988.	0.14000	0.59000	0.29	5.51	99274	10.
29.	15305.	0.17000	0.68000	0.31	6.21	71335	10.
33.	11299.	0.15000	0.63000	0.35	6.36	49567	10.
36.	10284.	0.13000	0.61000	0.38	6.52	45037	10.
55.	7700.	0.15000	0.66000	0.57	7.16	35684	10.
68.	5522.	0.15000	0.64000	1.10	7.32	24568	10.
87.	4171.	0.13000	0.72000	1.29	7.47	22192	10.
104.	5082.	0.18000	0.63000	1.46	8.18	20707	10.
122.	4478.	0.11000	0.60000	2.04	8.32	19801	10.
139.	4536.	0.09000	0.61000	2.21	8.47	21217	10.
156.	4299.	0.13000	0.66000	2.38	9.14	20427	10.
178.	3913.	0.12000	0.62000	3.00	9.39	17522	10.
238.	3517.	0.22000	0.68000	4.00	9.54	14497	10.
298.	3226.	0.22000	0.73000	5.00	10.35	29262	20.
364.	3854.	0.24000	0.59000	6.06	11.02	24124	20.
418.	2823.	0.18000	0.58000	7.00	11.27	20087	20.
478.	2698.	0.23000	0.65000	8.00	11.52	20084	20.
538.	2555.	0.14000	0.68000	9.00	13.39	24033	20.
603.	2474.	0.16000	0.70000	10.05	12.23	23458	20.
755.	2079.	0.13000	0.81000	12.37	14.05	24378	20.
898.	2034.	0.11000	0.68000	15.00	15.07	19972	20.
1198.	1781.	0.17000	0.80000	20.00	20.10	18667	20.
1499.	1538.	0.21000	0.88000	25.01	26.13	24693	30.
2047.	1346.	0.11000	0.72000	34.09	34.18	18749	30.
2398.	1176.	0.24000	0.82000	40.00	40.24	29980	60.

0

TESTP.TSC

PET/DATA FILE: P1194.RPO REGION FILE: P1194.REG

13, 4
2.0, 120.0, 170606.0, 156673.0
123.0, 120.0, 197999.0, 207452.0
244.0, 120.0, 223657.0, 228240.0
365.0, 120.0, 251521.0, 250627.0
486.0, 120.0, 282814.0, 259168.0
607.0, 120.0, 283159.0, 267851.0
728.0, 120.0, 311438.0, 293755.0
849.0, 120.0, 324657.0, 304829.0
970.0, 120.0, 325557.0, 314857.0
1091.0, 120.0, 348436.0, 327726.0
1230.0, 300.0, 965880.0, 900867.0
1531.0, 300.0, 1.01377E+06, 956907.0
1832.0, 300.0, 1.14496E+06, 1.05264E+06
R GM
GM

PBLKFDG.CSS

4*0. 1.3 1. 0.04 13*0.
3
5 6 7
3
1 2 3
48.3 4.45 100.
42.32 3.91 100.

VI. LISTINGS OF OUTPUT FILES

TESTFDGA.LOG

```
*****
      REGIONAL
      PARAMETER
      OPTIMIZATION
*****
```

R.P.O. RUN ON 8/13/91 AT 15:37:21 USING INPUT FROM BR3:TESTFDG.CMD/P

***** ECHO INPUT DATA *****

NUMBER OF REGIONS READ IN 2
 TISSUE ACTIVITY DATA FILE TESTP.TSC
 BLOOD ACTIVITY FILE TESTP.DTA
 NUMBER OF SECONDS BLOOD CURVE OBTAINED: 2399
 PARAMATER BLOCK FILE PBLKFDG.RPO
 NUMBER OF PARAMETERS TO BE ESTIMATED: 3
 PARAMETERS NUMBERS..... 5, 6, 7
 NUMBER OF REGION-DEPENDENT PARAMETERS: 3
 PARAMETER NUMBER
 1
 2
 3

DATA SET = 1

-- REGION NUMBER 1 --	REGION NAME	R	GM
48.300	BLOOD FLOW		ML/MIN/100G
4.4500	BLOOD VOL		ML/100G
100.00	BLD GLUCOSE		uMOL/ML
10.854	K-01 (F/V1)		PER MIN
7.6231	K-21		PER MIN
1.4880	K-12		PER MIN
0.22558	K-32		PER MIN
0.00000	K-43		PER MIN
0.00000	T0		SEC
0.00000	T(1/2)		SECONDS
0.85830E-01	UTILIZATION FRACTION		
414.56	GLUCOSE MET		uMOL/MIN/100G
1.0035	CHI		PER MIN
33.923	KD		ML/MIN/100G
92.833	CG - BLOOD		uMOL/ML
3149.1	FORWARD FLUX		uMOL/MIN/100G
18.377	BRAIN FREE GLUC		uMOL/G

PARAMETER	SD	F D (%)
0.762306E+01	0.198624E+01	26.056
0.148803E+01	0.539409E+00	36.250
0.225582E+00	0.222493E-01	9.863

CORRELATION MATRIX

COLUMN

ROW 1	1.00	0.98	0.58
ROW 2	0.98	1.00	0.72
ROW 3	0.58	0.72	1.00

WEIGHTED SUM-OF-SQUARES & RMSE	2.108	0.459
--------------------------------	-------	-------

UNWEIGHTED SUM-OF-SQUARES & RMSE	2136522000.	14617.
----------------------------------	-------------	--------

DATA SET = 2

-- REGION NUMBER 2 -- REGION NAME GM

42.320	BLOOD FLOW	ML/MIN/100G
3.9100	BLOOD VOL	ML/100G
100.00	BLD GLUCOSE	uMOL/ML
10.824	K-01 (F/V1)	PER MIN
6.3137	K-21	PER MIN
0.81056	K-12	PER MIN
0.15940	K-32	PER MIN
0.00000	K-43	PER MIN
0.00000	T0	SEC
0.00000	T(1/2)	SECONDS
0.88757E-01	UTILIZATION FRACTION	
375.62	GLUCOSE MET	uMOL/MIN/100G
1.0376	CHI	PER MIN
24.686	KD	ML/MIN/100G
92.589	CG - BLOOD	uMOL/ML
2285.7	FORWARD FLUX	uMOL/MIN/100G
23.565	BRAIN FREE GLUC	uMOL/G

PARAMETER	SD	F D (%)
0.631365E+01	0.517661E+00	8.199
0.810563E+00	0.101794E+00	12.558
0.159400E+00	0.723140E-02	4.537

CORRELATION MATRIX

COLUMN

ROW 1	1.00	0.97	0.58
ROW 2	0.97	1.00	0.75
ROW 3	0.58	0.75	1.00

WEIGHTED SUM-OF-SQUARES & RMSE	0.488	0.221
--------------------------------	-------	-------

UNWEIGHTED SUM-OF-SQUARES & RMSE	462652400.	6802.
----------------------------------	------------	-------

***** END OF JOB *****

TESTFDGB.LOG

-- REGION # 1 NAME = R GM
13, 4
62.0 1421.72 1414.34 0.0
183.0 1649.99 1733.56 0.0
304.0 1863.81 1850.77 0.0
425.0 2096.01 2078.77 0.0
546.0 2356.78 2202.07 0.0
667.0 2359.66 2359.16 0.0
788.0 2595.32 2496.39 0.0
909.0 2705.48 2652.59 0.0
1030.0 2712.98 2806.74 0.0
1151.0 2903.63 2949.64 0.0
1380.0 3219.6 3194.95 0.0
1681.0 3379.23 3492.65 0.0
1982.0 3816.53 3778.07 0.0
-- REGION # 2 NAME = GM
13, 4
62.0 1305.61 1291.89 0.0
183.0 1728.77 1774.31 0.0
304.0 1902.0 1884.69 0.0
425.0 2088.56 2065.57 0.0
546.0 2159.73 2153.98 0.0
667.0 2232.09 2272.62 0.0
788.0 2447.96 2380.58 0.0
909.0 2540.24 2509.05 0.0
1030.0 2623.81 2641.81 0.0
1151.0 2731.05 2766.27 0.0
1380.0 3002.89 2979.28 0.0
1681.0 3189.69 3238.16 0.0
1982.0 3508.8 3490.38 0.0

TESTFDGC.LOG (/ S⁺ U E [n,c,v σ_Y, i_Y])

BLOODACT = 929867.0, 482965.0, 418225.0, 365323.0, 309723.0, 279544.0, 2
 492311.0, 443850.0, 411629.0
 TISORIG = 170606.0, 197999.0, 223657.0, 251521.0, 282814.0, 283159.0, 31
 965880.0, 1.01377E+06, 1.14496E+06
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 1.3, 1.0, 4.0E-02, 3*0.0, 4.58898
 576.283, 5.54119
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 1.31313, 1.0, 4.0E-02, 3*0.0, 4.6
 99.613, 582.081, 5.59694
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 1.3, 1.0101, 4.0E-02, 3*0.0, 4.54
 99.6205, 576.304, 5.48809
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 1.3, 1.0, 4.0404E-02, 3*0.0, 4.63
 99.6131, 576.262, 5.53882
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 5.16188, 0.877147, 0.638846, 3*0.0
 85.6647, 1967.75, 12.9799
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 5.2135, 0.877147, 0.638846, 3*0.0,
 85.542, 1984.58, 13.091
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 5.16188, 0.887247, 0.638846, 3*0.0
 85.746, 1969.62, 12.9063
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 5.16188, 0.877147, 0.645234, 3*0.0
 85.594, 1966.13, 12.9148
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.18483, 1.47165, 6.38846E-02, 3*0
 31.9725, 97.7521, 3125.38, 20.3537
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.25668, 1.47165, 6.38846E-02, 3*0
 97.7301, 3155.92, 20.5526
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.18483, 1.48636, 6.38846E-02, 3*0
 31.9725, 97.773, 3126.04, 20.1648
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.18483, 1.47165, 6.45235E-02, 3*0
 31.9725, 97.731, 3124.7, 20.3409
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.14872, 1.34664, 0.206591, 3*0.0,
 93.1838, 2964.35, 19.085
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.22021, 1.34664, 0.206591, 3*0.0,
 93.1203, 2991.95, 19.2627
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.14872, 1.36011, 0.206591, 3*0.0,
 93.2384, 2966.08, 18.9321
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.14872, 1.34664, 0.208657, 3*0.0,
 93.1289, 2962.6, 19.0484
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.55768, 1.46655, 0.224344, 3*0.0,
 92.8384, 3122.31, 18.4655
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.63326, 1.46655, 0.224344, 3*0.0,
 92.7719, 3151.28, 18.6367
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.55768, 1.48122, 0.224344, 3*0.0,
 92.8955, 3124.23, 18.3179
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.55768, 1.46655, 0.226587, 3*0.0,
 92.7808, 3120.37, 18.4295
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.65312, 1.49729, 0.226002, 3*0.0,
 92.8321, 3161.53, 18.3458
 PBLOCK = 48.3, 4.45, 100.0, 10.8539, 7.65297, 1.49725, 0.226001, 3*0.0,
 92.8321, 3161.46, 18.3459

TESTFDGD.LOG

TESTP.TSC	TESTP.DTA
2, 20	
48.3, 4.45, 100.0, 10.8539, 7.62306, 1.48803, 0.225582, 3*0.0, 8.58299E	
3149.15, 18.3773, 3*0.0	
42.32, 3.91, 100.0, 10.8235, 6.31365, 0.810563, 0.1594, 3*0.0, 8.87569E	
2285.68, 23.5646, 3*0.0	