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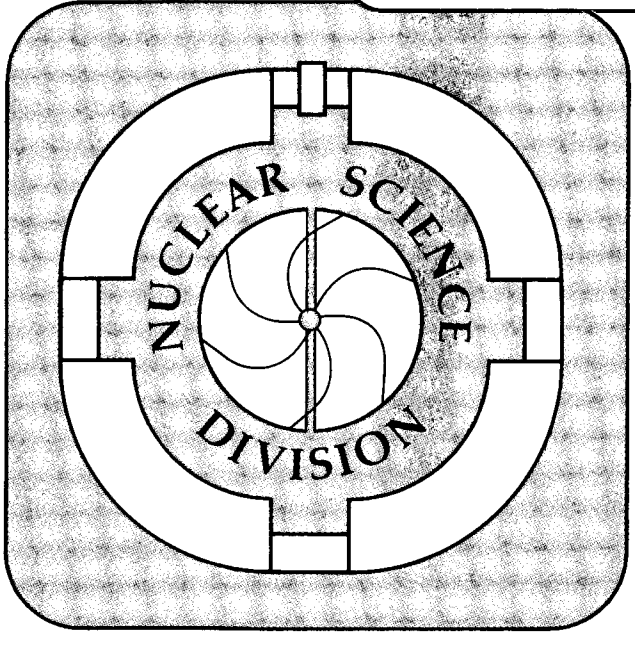

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DISCLAIMER

BRANDEX: A FORTRAN/Pascal Code to Calculate the Multiple Binary Splitting of an Excited Nucleus.

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ABSTRACT

BRANDEX is a statistical calculation based on averages of physical distributions that will predict cross sections for particle coincidence channels resulting from the breakup of an excited nucleus through a sequential binary process. With minor modification, it can make predictions for an arbitrary nucleus, integrating over an arbitrary weighted range of excitation. An example is given for ^{16}O breakup using the experimentally obtained excitation energy distribution.

Introduction

BRANDEX is a calculation designed to simulate the breakup of a nucleus with a given excitation energy distribution through a series of binary decays. It is not a Monte Carlo calculation. A Monte Carlo calculation typically starts with a compound nucleus, picks its excitation energy randomly from a given distribution, and then follows the decay of that nucleus. At each step, it randomly determines the decay from statistical weighting of possible binary splits, again picking physical quantities from distributions. BRANDEX takes a different approach. Rather than following one nucleus at a time, repeating the process many times, and counting the results at the end, it calculates probabilities for all possible final coincidence channels at once. (We use the term "coincidence channel" to mean one possible set of particles resulting from the breakup of an excited nucleus.) At each step, it does not pick values randomly, and (except for the excitation energy in the primary nucleus, where it integrates over a range), BRANDEX assumes average values of physical quantities rather than using distributions.

The program is written in a combination of VAX FORTRAN and VAX Pascal. Because it uses recursion, which is available in Pascal but not in FORTRAN, the core of the program is in Pascal. It produces output in the form of a number of text files. It was originally written to run on a Digital Equipment Corporation VAX 11-780, and has also been run on a DEC VAXstation 2000.

The Calculation

The core of BRANDEX is a recursive subroutine called BUILDLIST that, given a nucleus with a certain amount of excitation energy, will return the final decay channels for this nucleus. BUILDLIST first determines which binary splits are possible for the nucleus, the relative probability associated with each split, and the residual excitation energy after each split. It then calls itself in order to determine the decay channels for the breakup of the two daughter nuclei from each binary split. Figure 1 is a flowchart summary of the algorithm of BUILDLIST.

To determine which binary splits are energetically allowed, BUILDLIST makes use of an existing table of binary splits for all nuclei in the mass table. This table contains the two daughter nuclei of each split, the ground state Q value of each split, and the Coulomb barrier of each split. BUILDLIST uses this table to calculate a value U, which is equal to the excess potential at the saddle point of a split (see Figure 2):

$$U = E^* + Q - V_b \tag{1}$$

For every split where U is non-negative, it then calculates relative probabilities using the state density formula found in the external function RELPROB [1,2]:

$$\text{Prob} = \left(\frac{T}{2\pi}\right)\left(\frac{E^*}{U}\right)^2 \left(\frac{\exp(2\sqrt{aU})}{\exp(2\sqrt{aE^*})}\right) \tag{2}$$

where T is the temperature, calculated from U [1]:

$$U = aT^2 - \frac{3}{2}T \tag{3}$$

and a is the state density parameter (a=A/8.5, A is the mass of the compound nucleus; see *Input*). From the excess potential (U), a value equal to twice the temperature goes into kinetic energy (E_k) of the daughter nuclei if $U \geq 2T$; otherwise, all of the remaining energy goes into kinetic energy. The value 2T was chosen because it is the average value for E_k in the Maxwellian:

$$\text{Prob}(E_k) \propto E_k \exp(-E_k / T) \qquad (4).$$

The excess excitation energy ($U-E_k$) is proportionally divided as excitation energy between the two daughter nuclei according to their masses. Some corrections are applied to the proportional division of excitation energy; for instance, protons and neutrons cannot carry off excitation energy, and light nuclei that have no states below their lowest threshold for particle decay cannot have an amount of excitation energy less than this threshold.

If there are no splits where $U > 0$ but there are splits where $E^*+Q \geq 0$ and $U < 0$, BRANDEX allows the nuclei to tunnel through those channels. In order to pass a positive value of U to the function RELPROB, BRANDEX artificially adds the same constant to U for each of the splits for a given parent nucleus such that all values of U will be positive. In the case of channels where $U < 0$ the daughter nuclei are cold: they have no residual excitation energy.

At this point, BUILDLIST has a list of those binary splits, complete with probabilities and residual excitation energies, that are possible given the current nucleus and its excitation energy. For each split, BUILDLIST calls itself twice, first passing one member of the split, then passing the other. These calls will return a table of final channels from the breakup of each member of the split. It then pairs each final channel from the left member of the split with each final channel from the right member of the split, building a table of final channels for the current nucleus. Once it has done this for all possible binary splits, BUILDLIST returns a complete table of final coincidence channels for the given nucleus and corresponding excitation energy.

In the event of the simplest case, a nucleus that has no potential binary splits where $E^*+Q \geq 0$, BUILDLIST merely returns the nucleus it was given. Thus, BRANDEX has a recursive definition for sequential binary decay.

Output

The primary output from BRANDEX is a number of text files containing the final coincidence channels for the decay of the primary nucleus. These present the results sorted in different ways. Additionally, there is a file containing the relative yields of individual nuclei.

The two files CHR.SQVAL and CHR.SPROB present all of the final channels. For each channel, the Q value, the probability (normalized to 100%), and the resultant nuclei are listed. In CHR.SPROB the channels are sorted from the most probable channel to the least probable channel. In CHR.SQVAL, they are sorted from least negative Q value to most negative Q value.

The file CHR.SAMEZ presents the results in a form that does not have isotope resolution. All channels whose resultant nuclei contain the same elements, regardless of differences in isotopes and ignoring any excess neutrons, are listed as a single channel. The probability reported is the sum of the probabilities for the component channels; the Q value reported is the least negative Q value among the component channels. Mass numbers are not given with the resultant nuclei, and neutrons are not reported among the final nuclei. For example, two channels resulting from the breakup of ^{16}O, $^{12}C+^{4}He$ and $^{12}C+^{3}He+^{1}n$, would be reported together as C+He. This channel would be given the Q value -7.16, the value for the $^{12}C+^{4}He$ channel and the greater of the two Q values. CHR.SAMEZ also reports two other quantities, the "neutron count" and "proton count." The neutron count is the average number of free neutrons associated with each isotope-independent channel, and the proton count is the average number of free protons associated with each channel.

Two additional files, CHR.ZAPBE and CHR.PDRES are also included. These two files were created in order to facilitate the comparison of the output from BRANDEX with the experiment around which BRANDEX was initially designed. CHR.ZAPBE is essentially the same as

CHR.SAMEZ, only here a Beryllium is indistinguishable from two Heliums. Thus, the channels He+He+He+He, Be+He+He, and Be+Be would all be reported together as He+He+He+He. The file CHR.PDRES is also essentially the same as CHR.SAMEZ, only here protons are kept separate from deuterons and tritons. Thus, the channels $^{15}N+^{1}H$ and $^{14}N+^{2}H$ would be reported separately, but $^{14}N+^{2}H$ and $^{13}N+^{3}H$ would be summed together as N+d.

Finally, the file CSR.DAT contains the relative cross sections for all elements produced by BRANDEX. There will be a list of nuclei, each followed by a percentage. This is the percentage among all nuclei produced, weighted by probability, that is each nucleus. Percentages are given for individual isotopes, and for all isotopes of one element summed together.

A secondary output from BRANDEX is relative kinetic energy spectra. At the end of a run the program will ask the user if he wishes any relative kinetic energy spectra, and if so, for which channels. The plot will be a histogram of total relative kinetic energy for all of the members of the selected channel versus probability. The total probability (assuming all of the relative kinetic energy falls within preset limits) will be equal to the probability of the relevant coincidence channel. The plots are text files, formatted to be used with the graphic program TOPDRAWER, but the format is straightforward, and should be easily modified to run with other graphic programs.

Note that these relative kinetic energy spectra should be viewed with the limitations of BRANDEX in mind. BRANDEX does all of its calculations with averages, rather than distributions. For any particular binary split, it assumes an average amount of energy goes into kinetic energy, and assumes an average division of residual excitation between the daughters of the split. Consequently, for any single path to a final channel, there will be only one relative kinetic energy, rather than a distribution as would be the case in reality. However, as most channels can be obtained through a number of different paths, BRANDEX can produce a number of different relative kinetic energies. Because the program also integrates over an excitation curve for the primary nucleus, calling the recursive splitting routine for each bin in

that curve, different initial excitations can produce different kinetic energies. Thus, somewhat of a distribution will result. While it is not possible to directly compare this distribution with a measured distribution, it is reasonable to compare the general range and location of peaks in the two cases.

Input

BRANDEX should be run by executing the command file BRANDEX.COM. When run, BRANDEX will prompt the user for some information about the nucleus it is to split. This includes what the nucleus is, what range of excitation energies the program should integrate over, and a number of adjustable parameters.

The first thing it will ask for is the "radius parameter for coulomb barrier." This value (R_0), given in fermis, is used to calculate the potential at the coulomb barrier of a binary split according to the following formula:

$$V_b = \frac{Z_1 \, Z_2 \, e^2}{R_0 \, (A_1^{1/3} + A_2^{1/3})} \qquad (5).$$

Next, it will ask for the charge and mass of the primary nucleus. After that, it will ask for the minimum and maximum excitation energy, and the number of bins to divide this range into. BRANDEX will calculate the decay channels for each bin, evenly spaced between the minimum and maximum excitation energy, and then weight the output of each bin according to the relative probability of that bin as defined in the external function EXPROB. Note that it is important to modify EXPROB so that it contains the correct primary excitation curve (see *Modification*).

Next BRANDEX will prompt the user for "minimum, maximum expected kinetic energy." This sets the limits of the relative kinetic energy spectra produced at the end of a run (see *Output*). The program then asks the user for the number of bins to divide a kinetic energy spectrum into. If, during the run, the program calculates a relative kinetic energy outside of

the preset limits, it will generate a warning, and the particular value will not be used to increment the spectrum.

Finally, the program will ask the user for a "state density parameter (a=A/?)." This is used in the calculation of the temperature of a nucleus from its excitation energy, and in the state density formula found in RELPROB. The default value for this parameter is 8.5 [1,2].

Additional inputs may be added for parameters that need to be passed to a customized EXPROB (see *Modification*).

Modification

BRANDEX is written in a combination of VAX FORTRAN and VAX Pascal. The core of BRANDEX, the subroutine BUILDLIST and its support routines, are written in Pascal. The reason for this is that Pascal allows recursion (a subroutine may call itself), and Pascal has certain convenient data structures (linked lists); neither feature is available in FORTRAN. The main routine that handles integration over a primary excitation curve, and the routines that produce the various outputs, are, however, written in FORTRAN. Additional modules that sort and output the results may be added. The program is designed so that the most common modifications will be straightforward.

One modification that will often be a prerequisite for other modifications is changing the dimensions of various arrays. To facilitate this, there is a file, SPLITCONST.FOR, which is included in all relevant FORTRAN routines. This contains a number of constants that have some bearing on array sizes:

CHANMAX	The maximum number of final decay channels BRANDEX can produce without crashing.
CHANSIZE	The maximum number of nuclei in one final channel. Does not need to be larger than the mass of the primary nucleus.

SPLITMAX	Must be equal to or larger than the greatest number of binary splits possible for any nucleus in the run time mass table.
NUCARRAY	The dimension of the run time mass table. The total number of nuclei in the table must not exceed this constant.
MAXZ, MAXA	Maximum charge and mass found in the run time mass table.

The best way to determine the maximum number of splits (and thus an appropriate value for SPLITMAX) is to temporarily change SPLITMAX to a large number, and compile and run the program WRITESPLITS. This will produce a text file BINARY.DAT, which contains a list of all binary splits for all nuclei in the mass table.

Within the subroutine that builds the run time mass table, MTABLE, are DATA statements that detail the minimum and maximum atomic mass for each element to be placed in the mass table. This must be modified to include those elements which the user wants in his mass table. MTABLE will read the masses for each nucleus in the mass table from the external data file MASAS.DAT [3].

Also in SPLITCONST.FOR is the character array NAME. This is the two letter name for each element, indexed by atomic number.

The five constants in SPLITCONST.FOR are also found at the beginning of the main Pascal module, SPLITTER.PAS, in a "const" declaration. They must have the same value as their FORTRAN equivalents. There is one additional constant in the Pascal module, M_CUTOFF. Nuclei with a mass lower than this value will not be allowed to carry off any excitation energy when they are the lighter member of a binary split. The advantage of this is that BRANDEX need not calculate any further splits for those nuclei which have no excitation energy, thus improving the speed of the program. This constant is normally zero, but may be increased in order to save memory or running time.

One modification that must be made is to the external function EXPROB found in EXPROB.FOR. This function contains the excitation curve for the primary nucleus. Given an excitation energy and the width of the bin around that energy, EXPROB must return the relative probability of the primary nucleus having this excitation energy. It is not necessary to return an absolute probability; normalization is taken care of within the main FORTRAN routine. The default EXPROB.FOR uses a probability curve defined in a DATA statement found in EXEN.FOR. This probability curve defines a relative probability for all excitation energies between 0 MeV and 150 MeV in 1 MeV steps. If a bin passed to EXPROB does not fall evenly with bins defined in EXEN.FOR, EXPROB will take care of the integration. Any arbitrary curve can be defined in EXEN.FOR; alternatively, EXPROB could be replaced with a function containing a mathematical expression. In the declaration of EXPROB there are two additional parameters, PRAM1 and PRAM2, which are not used in the default EXPROB but may (with some modification of the main FORTRAN routine) be used for anything.

After any modifications have been made, one should use the command files COMP.COM or LINK.COM to compile BRANDEX. COMP.COM will compile all of the component modules of either BRANDEX or WRITESPLITS (see Appendix A) and link them together. If only a few modules have been modified, and object files exist for all of the other modules, one can compile the modified modules independently and use LINK.COM to link them to the remaining modules.

Note that in the three command files COMP.COM, LINK.COM, and BRANDEX.COM, the logical name BRANDEX$ should be defined to be the directory in which BRANDEX is run.

Performance

BRANDEX was designed around an experiment studying the breakup of an excited nucleus following a peripheral collision with a target nucleus. The experiment to which these calculations were compared was performed at the 88 Inch Cyclotron at LBL [4]. On the whole, BRANDEX's predictions, when compared with data, are reasonable but not excellent. Figure 3 shows a comparison of data and BRANDEX predictions for coincidence cross sections for the

breakup of ^{16}O. In general, BRANDEX underpredicts the channels with very negative Q values. Specifically, BRANDEX is particularly low on several channels containing Lithium.

Note that BRANDEX actually produces many more final coincidence channels than Figure 3 would indicate. Figures 5 and 6 are plots of Q value of output channel (relative to the primary nucleus) versus the percentage yield of that channel, for ^{16}O and ^{28}Si respectively. In these figures, different isotopes of an element are kept separate, that is, $^{12}C+^{4}He$ and $^{13}C+^{3}He$ are considered different channels (unlike in Figure 3). Note that even these figures show only a fraction of the channels which Brandex can produce, for there were many channels with a percentage yield lower than 10^{-5}%. These runs whose results are plotted in theses two figures both used the following exponential primary excitation curve:

$$\text{Prob}(E^*) \propto \exp(-E^*/15\ \text{MeV}) \qquad (6).$$

The distribution in both of these figures decreaces roughly exponentially with decreacing Q value. The shape of this distribution is dependent both on the identity of the primary nucleus and the primary excitation curve used.

The primary advantage of BRANDEX over a Monte Carlo calculation is speed of operation for lighter nuclei. BRANDEX does not produce nearly as much information as does a Monte Carlo calculation (for instance, angular momentum or distribution spectra) because it works with averages rather than randomly choosing values from distributions. However, BRANDEX will produce coincidence channels, and is relatively fast to run for lighter nuclei. For example, it can calculate probabilities for the final coincidence channels, including weak channels, for an ^{16}O nucleus over a range of excitation from 7 MeV to 100 MeV divided into 1 MeV bins in about three minutes of CPU time on a VAX 11-780. Thus it is quite easy to determine the sort of effects one could expect from different input to the program. For instance, one can quickly see how changing the primary excitation curve would affect the predicted results, or the effects of splitting ^{17}O rather than ^{16}O on isotope-independent channels.

Although BRANDEX is relatively fast for lighter nuclei, the amount of time and memory required to predict coincidence channels for larger nuclei at higher excitation energies grows

rapidly. Because it calculates probabilities for all possible coincidence channels, including very weak ones, as the number of possible channels increases, so does the amount of information BRANDEX must keep track of. One way to reduce the time and memory required is to adjust the constant M_CUTOFF (see *Modification*). This will most likely cut out some weaker channels, but it will also reduce the amount of information BRANDEX must keep track of. In spite of any practical limitations, BRANDEX's algorithm should work for any arbitrary nucleus, and a solution to the problem of memory limiting the scope of the program would be to run it on a more powerful machine.

It is important to note that BRANDEX is not intended to replace Monte Carlo calculations; rather, it is a means of making relatively fast and hopefully reasonable predictions of coincidence channels from the breakup of an excited nucleus through a sequential binary mechanism.

APPENDIX A: Files associated with BRANDEX.

COMPONENTS OF BRANDEX:

SPLITTER.PAS	Contains the Pascal routines that are the core of BRANDEX. The structure of the program is such that the main program is in SPLITTER.PAS, but all it does is call the main FORTRAN routine, which drives the program and calls the Pascal routines.
RELPROB.PAS	Contains the state density formula used to calculate the relative probability between one binary split and another.
SPLITERANGE.FOR	This is the main FORTRAN routine that handles the input, integrates over the primary excitation distribution, and calls the output subroutines.
EXPROB.FOR	A function containing the excitation energy distribution for the primary nucleus. Given an excitation energy, it returns the relative probability of that energy.
EXEN.FOR	A large FORTRAN DATA statement that defines the primary excitation distribution for the default EXPROB.FOR. Gives a relative probability for all excitations from 0 to 150 MeV in 1 MeV bins (151 element DATA array).
MTABLE.FOR	Builds up the run time mass table.
MASAS.DAT	Data file that contains masses for many nuclei. It is used as input for MTABLE.FOR.
SPLIT2.FOR	Contains the subroutine that calculates all possible binary splits for all nuclei in the run time mass table.
SPLITCONST.FOR	Contains various constants used in BRANDEX.
SORTCH_Q.FOR	Handles one output from BRANDEX. Sorts the list of final decay channels by Q value and outputs them in the file CHR.SQVAL.
SORTCH_P.FOR	Sorts the list of final decay channels by probability and outputs the to CHR.SPROB.
SAMEZ.FOR	Writes the output file that has charge but no isotope resolution.

SAMEZPD.FOR	Writes the output file that has proton vs. deuteron or triton resolution, but no other isotope resolution.
BE_HEHE.FOR	Writes the output file that sums channels containing a Be with equivalent channels containing two He.
ICSEC.FOR	Writes the output file containing the relative cross sections for individual nuclei.
PLOTKE.FOR	Handles requests for and creation of relative kinetic energy spectra.

RELATED FILES:

WRITESPLITS.FOR	Will write all possible binary splits given the run time mass table. Also uses MTABLE.FOR and SPLIT2.FOR.
COMP.COM	Will compile BRANDEX or WRITESPLITS. First it compiles all of the component files, then links them together.
LINK.COM	Assuming that all of the component files have been compiled, this command procedure will link all of them together.
BRANDEX.COM	Runs BRANDEX.

APPENDIX B: Sample output from BRANDEX.

The following is a selection from the file CHR.SPROB produced by running BRANDEX for ^{16}O over a range of excitation from 7 MeV to 100 MeV in 1 MeV bins. The excitation distribution used is shown in Figure 4. The run took approximately two minutes and fifty seconds of CPU time on a VAX 11-780.

Splits for 16O with excitation E from 0.0 to 120.0, sorted by Prob.

#	PERCENT	Q VALUE	RESULTANT NUCLEI.....					
1	3.792E+01	-7.16	12C	4He				
2	2.364E+01	-14.44	4He	4He	4He	4He		
3	1.217E+01	-12.13	15N	1H				
4	5.399E+00	-15.66	15O	1n				
5	4.155E+00	-22.96	14N	1H	1n			
6	2.300E+00	-23.12	11B	4He	1H			
7	2.040E+00	-22.34	14C	1H	1H			
8	1.293E+00	-30.51	13C	1H	1H	1n		
9	1.266E+00	-25.88	11C	4He	1n			
10	1.028E+00	-31.79	7Li	4He	4He	1H		
11	7.551E-01	-34.25	4He	4He	4He	3H	1H	
12	6.633E-01	-35.01	4He	4He	4He	3He	1n	
13	6.517E-01	-35.45	12C	1H	1H	1n	1n	
14	6.488E-01	-20.74	14N	2H				
15	4.966E-01	-26.98	12C	3H	1H			
16	4.961E-01	-33.51	13N	1H	1n	1n		
17	4.789E-01	-33.43	7Be	4He	4He	1n		
18	4.700E-01	-28.88	14O	1n	1n			
19	4.603E-01	-33.23	12C	2H	1H	1n		
20	4.534E-01	-27.74	12C	3He	1n			
21	4.464E-01	-28.29	13C	2H	1H			
22	4.411E-01	-34.57	10B	4He	1H	1n		
23	3.357E-01	-40.51	4He	4He	4He	2H	1H	1n
24	2.313E-01	-42.73	4He	4He	4He	1H	1H	1n 1n
25	2.183E-01	-22.80	13C	3He				
26	1.966E-01	-39.03	6Li	4He	4He	1H	1n	
27	1.875E-01	-34.35	10Be	4He	1H	1H		
28	1.549E-01	-31.29	13N	2H	1n			
29	1.111E-01	-32.35	10B	4He	2H			
30	9.613E-02	-25.04	13N	3H				
31	8.744E-02	-39.00	10C	4He	1n	1n		
32	7.272E-02	-36.81	6Li	4He	4He	2H		
33	6.866E-02	-33.45	9Be	4He	3He			
34	6.541E-02	-41.16	9Be	4He	1H	1H	1n	
35	5.585E-02	-31.01	12C	2H	2H			
36	4.666E-02	-41.77	6He	4He	4He	1H	1H	
37	3.727E-02	-35.34	6Li	6Li	4He			
38	3.667E-02	-38.94	9Be	4He	2H	1H		
39	3.400E-02	-38.29	4He	4He	4He	2H	2H	

#	PERCENT	Q VALUE	RESULTANT NUCLEI.....						
40	2.458E-02	-44.10	6Be	4He	4He	1n	1n		
41	2.220E-02	-45.70	11C	3H	1H	1n			
42	1.976E-02	-49.14	7Li	7Li	1H	1H			
43	1.926E-02	-43.70	11B	3He	1H	1n			
44	1.687E-02	-42.94	11B	3H	1H	1H			
45	1.225E-02	-30.88	10B	6Li					
46	1.197E-02	-49.19	11B	2H	1H	1H	1n		
47	1.173E-02	-40.33	12B	3He	1H				
48	9.771E-03	-51.95	11C	2H	1H	1n	1n		
49	8.793E-03	-31.86	9Be	7Be					
50	7.133E-03	-59.32	9C	6He	1n				
.									
.									
.									
175	5.612E-06	-63.63	6Li	6Li	1H	1H	1n	1n	
176	5.605E-06	-70.72	7Li	3He	3He	2H	1n		
177	4.489E-06	-61.72	7Be	4He	1H	1H	1n	1n	1n
178	3.787E-06	-66.48	6Be	6Li	2H	1n	1n		
179	3.048E-06	-64.68	6Be	4He	3He	1n	1n	1n	
180	2.765E-06	-69.96	7Li	3He	3H	2H	1H		
181	2.574E-06	-62.14	4He	4He	2H	2H	2H	2H	
182	2.189E-06	-61.74	9Be	3He	1H	1H	1n	1n	
183	1.986E-06	-70.95	6Li	3He	3H	3H	1H		
184	1.659E-06	-72.35	9Li	3He	2H	1H	1H		
185	1.491E-06	-65.62	6He	4He	2H	2H	1H	1H	
186	1.231E-06	-67.95	6Be	4He	2H	2H	1n	1n	
187	5.471E-07	-72.93	8B	3H	3H	1H	1n		
188	3.824E-07	-75.26	6Be	3H	3H	3H	1H		
189	3.357E-07	-63.31	4He	4He	3He	1H	1H	1n	1n 1n
190	2.144E-07	-62.88	6Li	4He	2H	2H	1H	1n	
191	1.948E-07	-74.45	6He	3He	3He	3H	1H		

BUILDLIST -- Given Z,A and E*, return all possible decay channels, with probability and Q value.

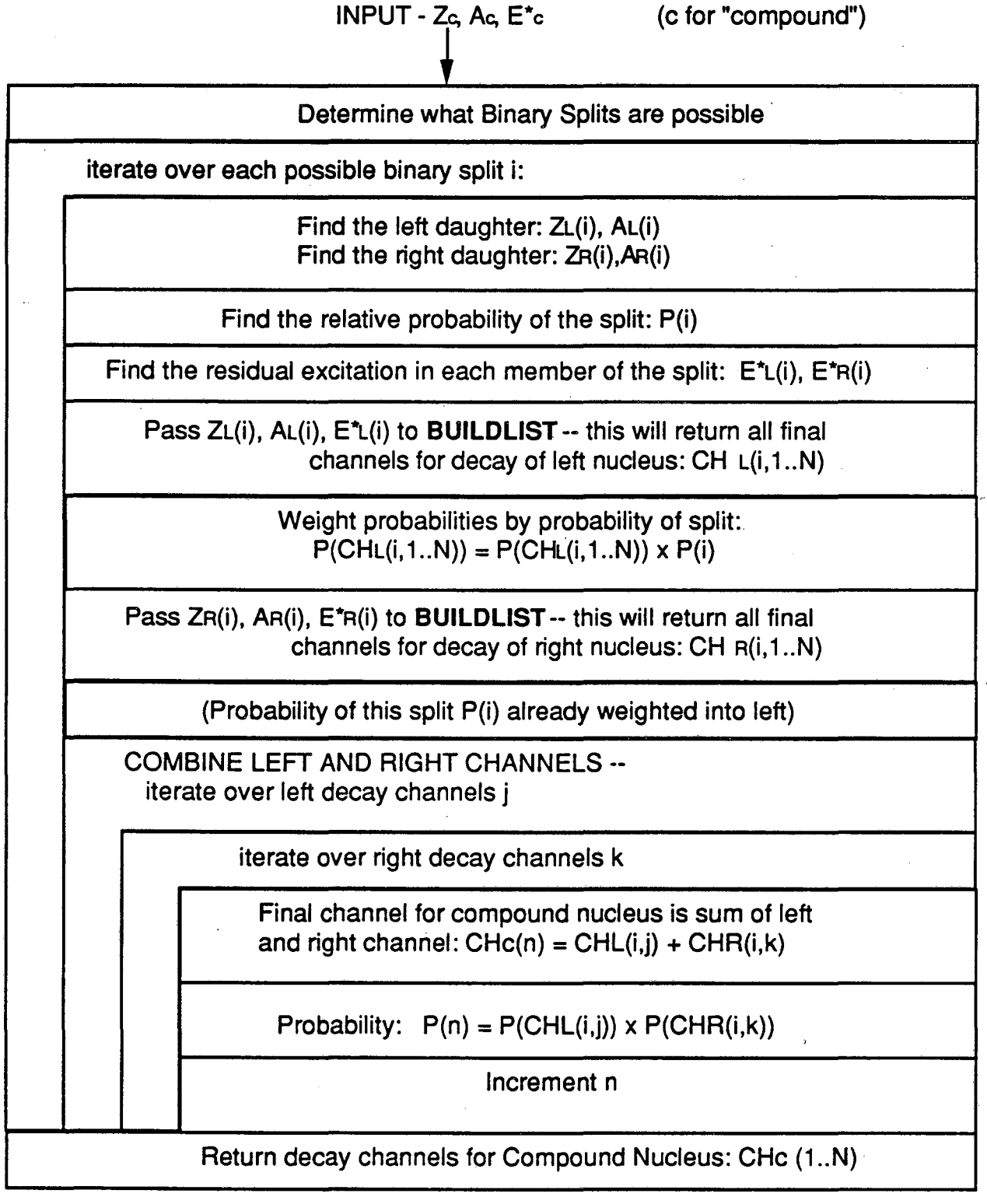


Figure 1: Flowchart summary of algorithm of BUILDLIST

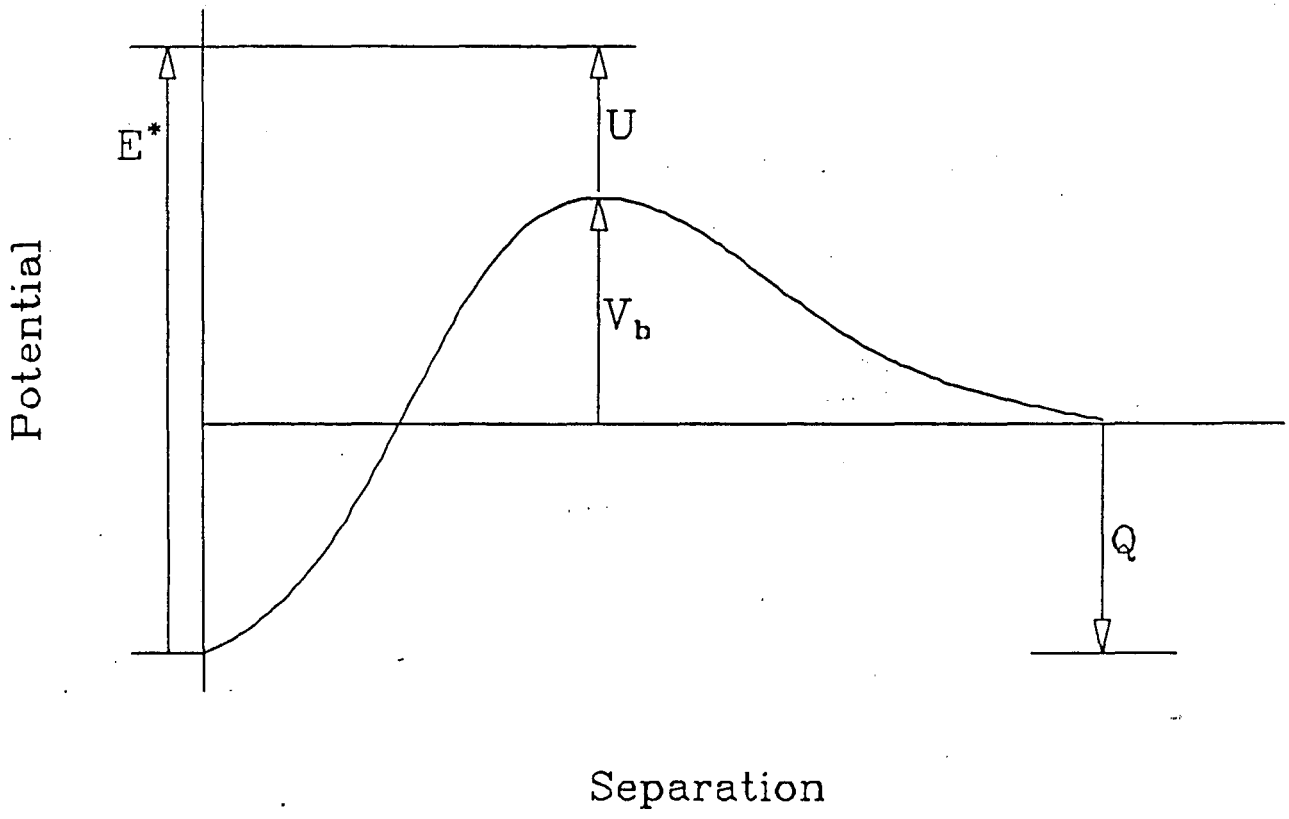
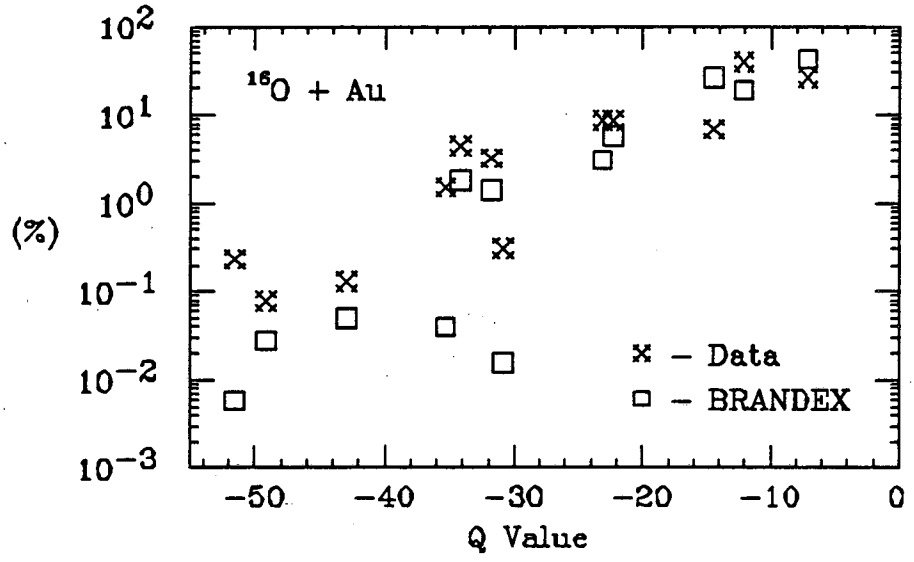


Figure 2: Nuclear potential diagram, with quantities as defined in BRANDEX.



^{16}O Channel	Q Value
C·He	-7.16
N·H	-12.13
He·He·He·He	-14.44
C·H·H	-22.34
B·He·H	-23.12
B·Li	-30.88
Li·He·He·H	-31.79
He·He·He·H·H	-34.25
Li·Li·He	-35.34
B·H·H·H	-42.94
Li·Li·H·H	-49.14
Li·He·H·H·H	-51.60

Figure 3: Comparison of BRANDEX coincidence channel yields with experimental data. BRANDEX output is for ^{16}O over the excitation curve found in Figure 4. The data is from the experiment described in *Performance*. In this case, all channels containing a Be are summed with the corresponding channel containing a He + He.

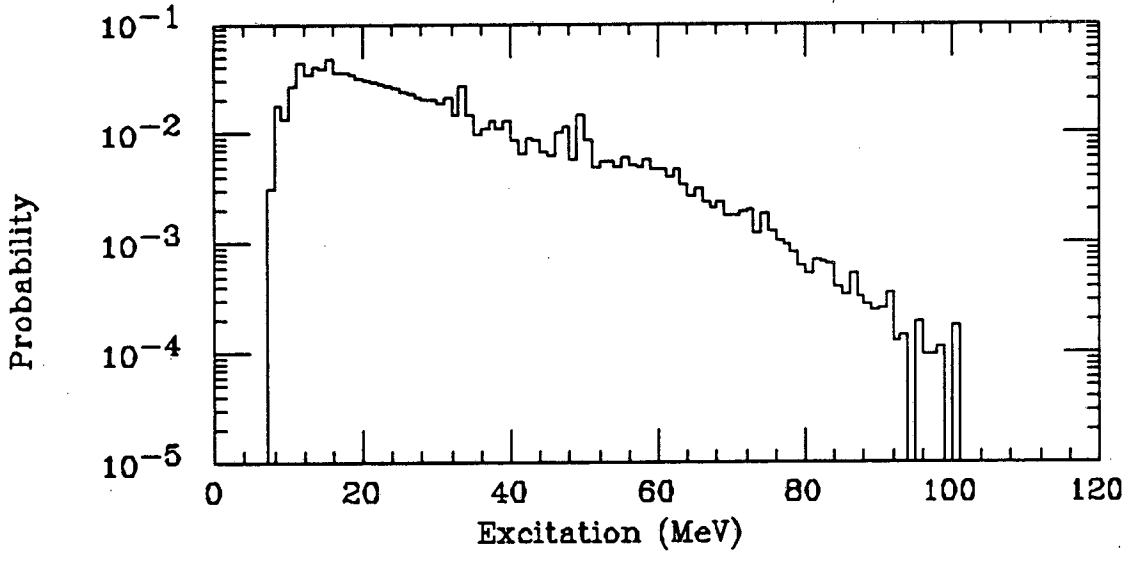


Figure 4: Primary excitation distribution measured from the same run from which the data in Figure 3 was taken. Used as input to BRANDEX for the results in Figure 3 and Appendix B.

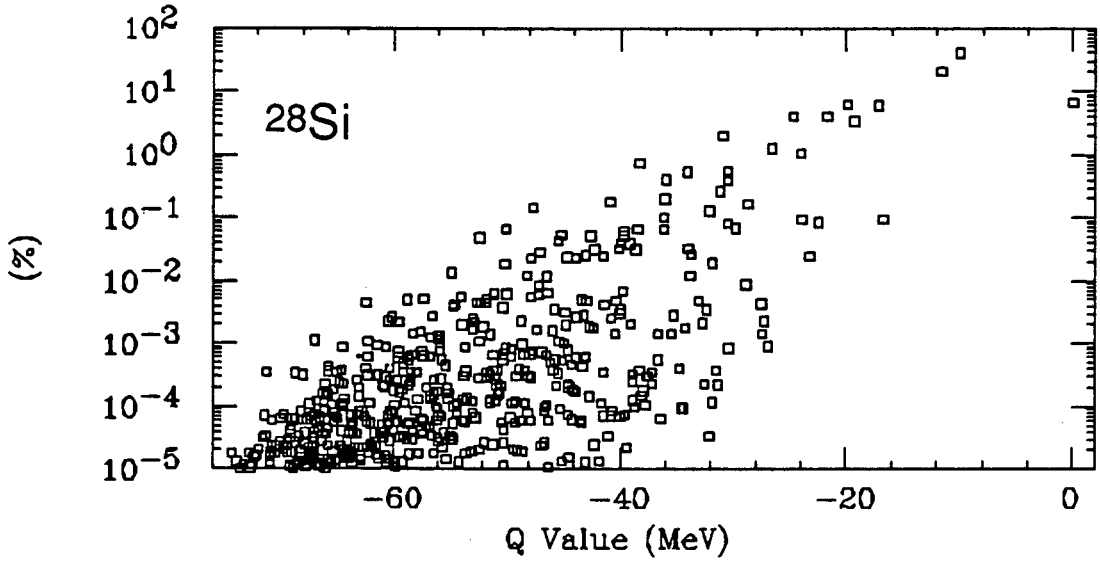


Figure 5: Q-value vs. percentage yield for all decay channels produced by BRANDEX for the splitting of ^{28}Si with an exponential primary excitation curve (Equation 6) between 9 MeV and 120 MeV. This run took about 2 hours of CPU time on a DEC VAXstation 2000.

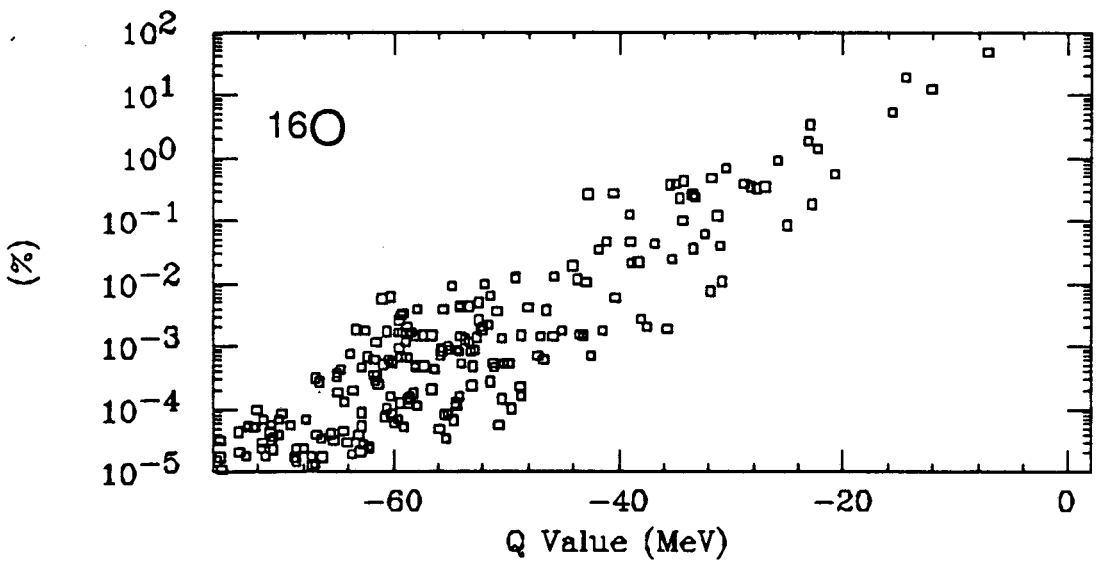


Figure 6: Q-value vs. percentage yield for all decay channels produced by Brandex for the splitting of ^{16}O with an exponential primary excitation curve (Equation 6) between 9 MeV and 120 MeV. This run took about 15 minutes of CPU time on a DEC VAXstation 2000.

REFERENCES

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