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HOW OFTEN DO RADIOISOTOPE AGES AGREE?
A PRELIMINARY STUDY OF 29,000 RADIOISOTOPE AGES
IN THE USGS NATIONAL GEOCHRONOLOGICAL DATABASE

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ABSTRACT

The USGS National Geochronological Database is a central repository for published radioisotope ages from across the United States. It contains 18,575 records with 29,043 age determinations using eight different radioisotope methods: potassium-argon (^{40}K-^{40}Ar), rubidium-strontium (^{87}Rb-^{87}Sr), samarium-neodymium (^{147}Sm-^{143}Nd), thorium-lead (^{232}Th-^{208}Pb), lead-lead (Pb-Pb), uranium-lead (^{235}U-^{207}Pb, ^{238}U-^{206}Pb), and fission tracks (FT). We created a "Concordance Metric" which measures a calculated "Concordance Score" for each record by looking at each pair of unique ages within the record, arriving at a score from 0.00 to 1.00, where 1.00 means total concordance within the record (all the age ranges overlap) and 0.00 means total discordance (none of the age ranges overlap). We adopted several approaches to identifying and quantifying the frequency of radioisotope age concordance in the database: (1) we calculated the frequency of "internal concordance" within each method; (2) we calculated the frequency of concordance where ages from two radioisotope methods were available for the same record; (3) we calculated the frequency of concordance where ages from three or more radioisotope methods, at least two of which were not in the U-Th-Pb decay chain, were available for the same record; and (4) we calculated the frequency of concordance where ages calculated using at least three of the four U-Th-Pb methods were available for the same record.

Overall, the average concordance score for the whole database is 0.64. Only 4,875 of the 18,575 records (26.2%) included more than one calculated age. Of these, 1,135 (23.3%) had a concordance score of 0.00 and 2,593 (53.2%) had a concordance score of 1.00. There were 998 records with age determinations using three or more U-Th-Pb methods. Concordance scores for these records ranged from 0.18 to 0.79, averaging 0.57. Only 34 records included ages using three or more different radioisotope methods where at least two were not U-Th-Pb, and only one of these (2.9%) had a concordance score of 1.00. We also found a systematic pattern in radioisotope discordances, somewhat similar to the pattern identified previously by the RATE (*R*adioisotopes and the *A*ge of *T*he *E*arth) group. RATE found that β-decaying isotopes tended to yield younger ages than α-decaying isotopes; in our study ^{40}K followed this pattern but ^{87}Rb did not. RATE also reported that within α- or β-decaying methods, the heavier isotope tended to yield older ages. In our study, we found the same pattern with the exception that 85.0% of ^{235}U-^{207}Pb ages were older than the corresponding ^{238}U-^{206}Pb ages.

KEYWORDS

radioisotope dating, geochronology, concordance, discordance, concordance metric, accelerated decay, USGS National Geochronological Database

I. INTRODUCTION

Radioisotope dating is in many ways the cornerstone of the modern geological synthesis, connecting rock units to absolute numerical ages. Young-earth creationists have highlighted several problems with radioisotope dating methods, one of which is the phenomenon of discordance. Kurt Wise summed it up well in his 2002 book *Faith, Form, and Time*: "If accurate, each radiometric method should produce the same radiometric age. In actuality, however, multiple methods usually yield multiple, non-overlapping ages" (p. 63). Other creationists have published detailed studies of specific rock units, revealing evidence of discordance and identifying systematic trends within those data. However, so far there has not been a large-scale study to confirm the prevalence of discordance. Wise (2002) supported his claim with a footnote that read: "The National Geochronological Database (USGS Digital Data Series DDS-14, 1995) contains thousands of rocks dated with multiple methods. A careful examination of these records shows that the methods rarely yield the same ages" (p. 256). We decided to interrogate the National Geochronological Database to examine Wise's claim and to extend the work of

other creationists.

II. PREVIOUS WORK

Several creationists have published on the phenomenon of radioisotope age discordance. Woodmorappe (1979) compiled about 350 radioisotope age determinations that were at least 20% too young or too old given their expected geologic age, along with some examples of discordant radioisotope age determinations. Numerous other instances of discordant radioisotope ages are described in Woodmorappe (1999) and Nethercott (2021). However, the most systematic creationist investigation of radioisotope discordance was carried out by the RATE (*R*adioisotopes and the *A*ge of *T*he *E*arth) research group, convened by the Institute for Creation Research and the Creation Research Society in 1997 (Vardiman et al. 2000, 2005). RATE published new radioisotope ages using the K-Ar, Rb-Sr, Sm-Nd, and Pb-Pb systems for ten rock units, including lava flows at Mt. Ngauruhoe, New Zealand; the Somerset Dam layered mafic intrusion, Queensland, Australia; the Beartooth andesitic amphibolite, Wyoming; and basalts and diabase sills of the Apache Group, central Arizona; in

addition to five rock units in the Grand Canyon region of Arizona (Austin and Snelling 1998; Snelling 1998, 2003a, 2003b; Snelling et al. 2003; Austin 2005; Snelling 2005). All but one of these rock units were derived from basaltic magmas generated in the mantle.

The results revealed that each radioisotope method yielded concordant ages internally (e.g. between whole-rock and mineral ages) but significant discordance between ages from different dating systems. Examples were found of all four categories of isochron discordance described by Austin (2000): (1) two or more discordant whole-rock isochron ages; (2) a whole-rock isochron age older than the associated mineral isochron ages; (3) two or more discordant mineral isochrons from the same rock; and (4) a whole-rock isochron age younger than the associated mineral isochron ages. Moreover, they identified systematic discordances between radioisotope dating systems, so that for the same rock unit Sm-Nd ages > U-Pb ages > Rb-Sr ages > K-Ar ages. In short, α-emitting radioisotopes (^{238}U, ^{235}U, ^{147}Sm) gave consistently older ages than β-emitting radioisotopes (^{87}Rb, ^{40}K), and isotopes with longer half-lives (and/or heavier atomic masses) tended to yield older ages than those with shorter half-lives (and/or lighter atomic masses). The RATE group explained these systematic trends by hypothesising one or more episodes of accelerated nuclear decay in the Earth's past, in which the amount of acceleration had depended on the type of decay involved (α versus β) and the length of the half-life of each parent isotope. However, the pattern is somewhat complicated by other factors such as the inheritance and mixing of radioisotopes from mantle and crustal sources. Snelling (2005, pp. 462-464) concluded that because the fundamental assumptions of radioisotope dating–known initial conditions, lack of contamination, and constant rates of decay–have been shown to be questionable, the resulting ages cannot be trusted as absolute ages but may still be applied, with caution, for relative dating.

III. METHODS

The National Geochronological Database (Zartman et al. 2003) was created by the United States Geological Survey (USGS) to provide a central repository for published radioisotope ages of rocks from across the United States. With over 18,000 records and almost 30,000 K-Ar, Rb-Sr, Sm-Nd, Th-Pb, Pb-Pb, U-Pb, and fission track ages, it is estimated to contain half of the radioisotope ages published through 1991. The data represent determinations on a wide variety of igneous and metamorphic rocks, as well as a few sedimentary rocks (322 records). Our study uses the 2003 version of the database; an update was released in 2011, but the changes were insignificant enough to make no difference to our analysis. Hillenbrand et al. (2023) published a major revision of the database after our analysis was completed and submitted for review.

The basic organizational unit of the database is "the record," each identifying a particular dated rock sample and containing location, rock description, and age information (Zartman et al. 2003). Record numbers link information contained in separate files for each method, a merged "allages" file, and a location file.

To determine whether two calculated ages from the same record agree, we used a standardized definition of concordance. If two such ages had uncertainty ranges that overlapped, then they were considered concordant with one another. If there was no overlap, the two ages were considered to be discordant. For cases in which no uncertainty range was given, we assumed a range of ±10% of the reported age. For comparison, the average uncertainty range in the database was ±6.3% of the corresponding age.

Using this definition of concordance, our first step was to calculate a "Concordance Metric" for each record or portion of a record containing two or more ages. Each unique pair of ages in a given record was labeled either 1.00 (concordant) or 0.00 (discordant). By dividing the number of concordant comparisons by the number of comparisons in the record, the metric yields a concordance score for the record. The concordance score can range from 1.00 to 0.00, where 1.00 means total concordance within the record (all the age ranges overlap) and 0.00 means total discordance (none of the age ranges overlap). This metric was directly applied to all records in the database, and this information was used to calculate the average concordance score of the records.

We used the concordance metric to find the overall concordance score of the database. After that we adopted three approaches to identifying and quantifying trends in the frequency of concordance and discordance in the database, all based on our concordance metric.

Our first approach was to isolate a particular method and the records with two or more ages calculated using that method. Using only the ages from that method, we calculated a new concordance score for each of these records. This was done for eight of the nine methods. We did not perform any analysis of the Sm-Nd ages because there were only 32 records in the database that included Sm-Nd ages.

Our second approach was to filter the database for any records that had ages calculated using at least two methods, referred to as the "Two Methods Comparison." We assembled the data for each unique pair of methods into a spreadsheet, which allowed us to directly compare one method to another. For each record, each calculated age by one method was compared to each calculated age by the other method to check for concordance. The proportion of concordant comparisons was then recorded.

Our third approach, called the "Three Methods Comparison" included records with ages calculated using at least three different methods, at least two of which were not in the U-Th-Pb decay chain. Of the 18,575 records in the database, only 34 met this criterion. These 34 records were compiled into a single spreadsheet and plots made of the radioisotope ages vs. present half-lives of the parent radioisotopes, along with atomic weight and type of decay.

Our fourth approach, called the "U-Th-Pb Comparison," was similar to the "Three Methods Comparison." It included records with ages calculated using three or more of the four U-Th-Pb methods. 998 records met this criterion. Concordance scores were calculated for each record and these were compared to the concordance scores of the database as a whole.

To perform our analysis, several pieces of software were used. Microsoft Excel was used to store and access data, perform general calculations, and generate preliminary charts. Processing, a programming language and environment, was used for searching, reformatting, and adding calculated values to the database. Grapher, a data visualization tool, was used to generate the charts used in this paper.

IV. RESULTS

The total number of unique records in the database is 18,575. For these records there are 29,043 distinct age calculations using eight different methods: ^{40}K-^{40}Ar, ^{87}Rb-^{87}Sr, ^{147}Sm-^{143}Nd, ^{232}Th-^{208}Pb, Pb-Pb, ^{235}U-^{207}Pb, ^{238}U-^{206}Pb, and fission tracks. Appendix A explains how the number of unique age determinations in the database was estimated and includes the source code used to generate our main data file. Six hundred and thirty-six (4.5%) of the ages included in the K-Ar category were actually some type of argon-argon (Ar-Ar) analysis, but we followed the organization of the database in grouping them together. For 12% of K-Ar and FT, 22% of Rb-Sr, 69% of Th-Pb, and 78% of Pb-Pb, ^{235}U-^{207}Pb, and ^{238}U-^{206}Pb ages, no uncer-

tainty range was given.

There are some noteworthy outliers within the database. Three K-Ar ages, one ^{235}U-^{207}Pb age, and eleven Pb-Pb ages are negative. One ^{235}U-^{207}Pb age and 647 Pb-Pb ages are given as zero. These zero ages make up 24.7% of the 2,621 Pb-Pb ages in the database. On the opposite end of the spectrum, there are nine K-Ar ages, four Rb-Sr ages, three ^{238}U-^{206}Pb ages, one Pb-Pb age, and three ^{232}Th-^{208}Pb ages that are greater than 4.5 billion years (Ga), the conventionally accepted age of the Earth. Two are over 10 Ga.

Of the 18,575 records in the database, only 4,875, or 26.2%, included more than one calculated age. These were the ones that could be analyzed using our "Concordance Metric," and thus relevant in our investigation of the frequency of concordance and discordance. Of these records, 1,135 (23.3%) had a concordance score of 0.00 (i.e. the reported ages were totally discordant) and 2,593 (53.2%) had a concordance score of 1.00. The average concordance score for the whole database is 0.64. Table 1 shows the concordance scores for all 4,875 records, along with a breakdown of the concordance scores for each radioisotope method. The distribution of concordance scores for all 4,875 records is shown as a histogram in Fig. 1. Appendix B provides pie charts representing all pairwise comparisons in our "Two Methods Comparison" dataset.

A scatterplot showing the number of ages involved in the calculation of the concordance score for each record is shown in Fig. 2. There is a slight negative correlation between the number of ages and the concordance score but this correlation is not statistically significant (R^2=0.0016).

Table 2 shows the proportion of concordant ages between specified pairs of radioisotope methods for each of our "Two Methods Comparisons." Table 3 shows how often the age calculated using one method was greater than the age calculated using another.

A. Individual methods

1. Lead-lead (Pb-Pb)

For all Pb-Pb age determinations for the same record, Pb-Pb has a 0.84 average concordance score with itself (that is, compared with other Pb-Pb determinations for the same records), which is the highest of all the methods. For "Three Methods Comparisons," the aver-

age score is significantly lower (0.62). Out of every record with a Pb-Pb concordance score, 77.9% (471 out of 605) are concordant (have a score of 1.00) and 9.3% (56) are discordant (have a score of 0.00).

When compared with other methods, Pb-Pb shows the highest concordance with ^{235}U-^{207}Pb (concordance score 0.54). Its score with FT is 0.00, meaning the two methods are never concordant with each other.

Pb-Pb yields consistently greater ages than every other method, ranging from Rb-Sr (where Pb-Pb ages are greater 54.4% of the time) to ^{232}Th-^{208}Pb (where Pb-Pb ages are greater 84.2% of the time).

2. Rubidium-strontium (Rb-Sr)

For all Rb-Sr age determinations for the same record, Rb-Sr has a 0.80 average concordance score with itself (that is, compared with other Rb-Sr determinations for the same records). For "Three Method Comparisons," the average score is much lower (0.61). Out of every record with a Rb-Sr concordance score, 73.0% (797 out of 1,092) are concordant (have a score of 1.00) and 12.6% (138) are discordant (have a score of 0.00).

When compared with other methods, Rb-Sr shows the highest degree of concordance with K-Ar (concordance score of 0.51), with the others ranging from 0.40 concordance (^{235}U-^{207}Pb) to 0.21 concordance (FT).

The percentage of Rb-Sr age determinations that are greater than those yielded by other methods ranges from 45.4% (Pb-Pb) to 70.8% (FT). Pb-Pb is the only method that gives consistently greater ages than Rb-Sr, suggesting that Rb-Sr most often overestimates ages in relation to other methods.

3. Uranium-lead (^{235}U-^{207}Pb)

For all ^{235}U-^{207}Pb age determinations for the same record, ^{235}U-^{207}Pb has a 0.80 average concordance score with itself (that is, compared with other ^{235}U-^{207}Pb determinations for the same records). For "Three Methods Comparisons," the average score is the same (0.80). Out of every record with a ^{235}U-^{207}Pb concordance score, 71.3% (347 out of 487) are concordant (have a score of 1.00) and 11.3% (55) are discordant (have a score of 0.00).

When compared with other methods, ^{235}U-^{207}Pb shows the high-

Table 1. The distribution of concordance scores for each method, as well as for the whole database. Also includes the average score and the percentage of concordant records.

	Pb-Pb	Rb-Sr	^{235}U-^{207}Pb	^{238}U-^{206}Pb	^{232}Th-^{208}Pb	K-Ar	FT	All Methods
Score = 0	708	138	68	55	56	43	108	1135
0 < Score < 0.50	119	84	53	47	41	13	27	638
0.50 ≤ Score < 1	76	73	47	38	37	14	19	509
Score = 1	1228	797	330	347	471	80	150	2593
Total Count	2131	1092	498	487	605	150	304	4875
Average Score	0.62	0.80	0.76	0.80	0.84	0.62	0.56	0.64
% Concordant (Score = 1)	58%	73%	66%	71%	78%	53%	49%	53%
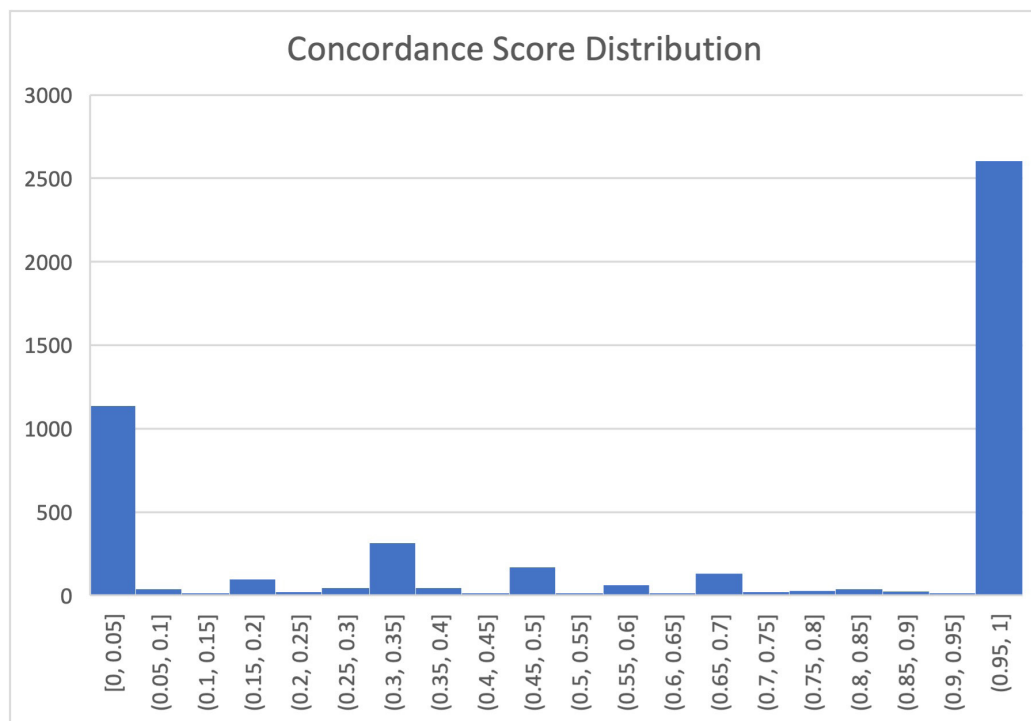
Table 2. The proportion of concordant pairwise age comparisons from our "Two Methods" dataset.

Method	Pb-Pb	Rb-Sr	^{235}U- ^{207}Pb	^{238}U- ^{206}Pb	^{232}Th-^{208}Pb	K-Ar	FT
Pb-Pb	X	0.40	0.54	0.43	0.18	0.14	0.00
Rb-Sr	0.40	X	0.40	0.32	0.26	0.51	0.21
^{235}U- ^{207}Pb	0.54	0.40	X	0.79	0.55	0.27	0.14
^{238}U- ^{206}Pb	0.43	0.32	0.79	X	0.55	0.24	0.07
^{232}Th-^{208}Pb	0.18	0.26	0.55	0.55	X	0.34	0.12
K-Ar	0.14	0.51	0.27	0.24	0.34	X	0.50
FT	0.00	0.21	0.14	0.07	0.12	0.50	X

Table 3. The percentage of pairs for which the age calculated using one method was greater than the age calculated using another. The method giving the older age is in the left-hand column; the method giving the younger age is along the top. Some pairs gave the same age, and so are not counted as being greater for either method.

Method (greater on left)	Pb-Pb	Rb-Sr	^{235}U- ^{207}Pb	^{238}U- ^{206}Pb	^{232}Th-^{208}Pb	K-Ar	FT
Pb- Pb	X	54.4%	84.7%	83.2%	84.2%	67.1%	54.9%
Rb-Sr	45.6%	X	55.1%	60.3%	55.4%	64.0%	70.8%
^{235}U- ^{207}Pb	14.6%	43.6%	X	85.0%	64.4%	77.5%	85.7%
^{238}U- ^{206}Pb	16.1%	38.1%	9.2%	X	56.0%	71.9%	87.1%
^{232}Th-^{208}Pb	15.4%	44.1%	33.9%	42.6%	X	69.6%	82.4%
K-Ar	32.9%	35.9%	21.7%	28.1%	30.4%	X	72.1%
FT	45.1%	29.2%	14.3%	12.9%	17.7%	26.5%	X
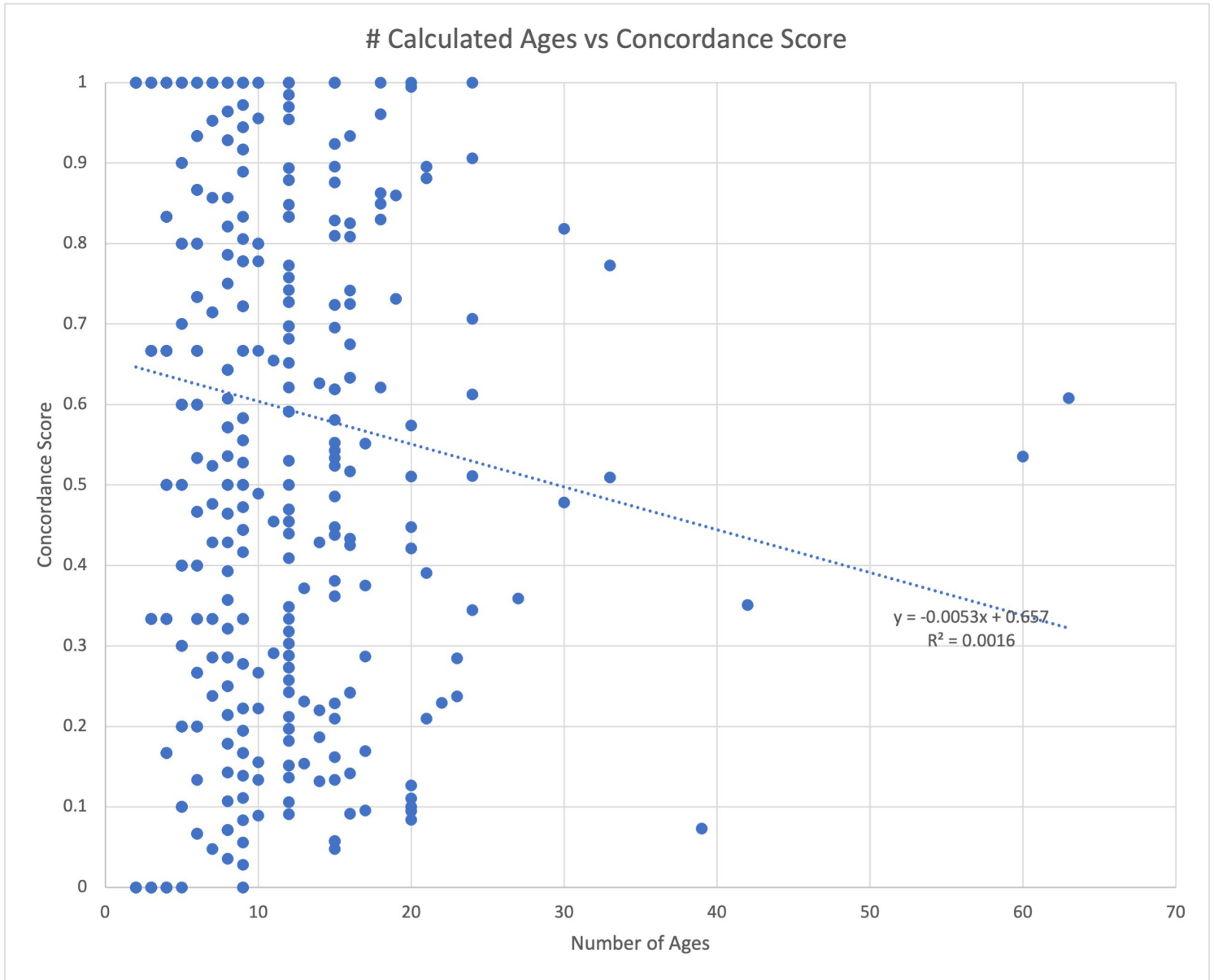
Figure 2. Scatterplot of the number of ages involved in the calculation of the concordance score for all 4,875 records, including the linear regression and R^2 value. Note that each datapoint may represent any number of records with the same concordance score and number of age determinations.

est concordance with ^{238}U-^{206}Pb (concordance score of 0.79). Like ^{238}U-^{206}Pb, its concordance scores with K-Ar (0.27) and FT (0.14) are extremely low, indicating very little agreement between these methods.

^{235}U-^{207}Pb yields consistently greater ages than K-Ar (77.5% of the time), ^{238}U-^{206}Pb (85.0%), and FT (85.7%), but consistently lower ages than Pb-Pb (84.7% of the time). Perhaps unsurprisingly it appears to be very similar to ^{238}U-^{206}Pb with respect to concordance scores.

4. Uranium-lead (^{238}U-^{206}Pb)

For all ^{238}U-^{206}Pb age determinations for the same record, ^{238}U-^{206}Pb has a 0.76 average concordance score with itself (that is, compared with other ^{238}U-^{206}Pb estimations for the same records). For "Three Methods Comparisons," the average score is similar (0.73). Out of every record with a ^{238}U-^{206}Pb concordance score, 66.3% (330 out of

498) are concordant (have a score of 1.00) and 13.7% (68) are discordant (have a score of 0.00).

When compared with other methods, ^{238}U-^{206}Pb shows the highest degree of concordance with ^{235}U-^{207}Pb (concordance score of 0.79), Its concordance scores with K-Ar and FT are extremely low (0.24 and 0.06 respectively), indicating very little agreement between these methods.

^{238}U-^{206}Pb yields consistently greater ages than K-Ar (greater 71.9% of the time) and FT (87.1%), but consistently lower ages than Pb-Pb (lower 85.0% of the time) and ^{235}U-^{207}Pb (83.2%).

5. Thorium-lead (^{232}Th-^{208}Pb)

For all ^{232}Th-^{208}Pb age determinations for the same record, ^{232}Th-^{208}Pb has a 0.62 average concordance score with itself (that is, compared with other ^{232}Th-^{208}Pb determinations for the same records). For "Three Methods Comparisons," the average score is similar (0.60).

Out of every record with a ^{232}Th-^{208}Pb concordance score, 53.3% (80 out of 150) are concordant (have a score of 1.00) and 28.7% (43) are discordant (have a score of 0.00).

When compared with other methods, ^{232}Th-^{208}Pb shows the highest degree of concordance with ^{238}U-^{206}Pb (concordance score 0.55). Its scores with Pb-Pb (0.18) and FT (0.12) are extremely low, indicating very little agreement between these methods.

^{232}Th-^{208}Pb typically yields the lowest ages of all the U-Th-Pb methods, and significantly lower ages than Pb-Pb (which gives lower ages only 15.4% of the time). However, it yields greater ages than FT 82.4% of the time. Thus, ^{232}Th-^{208}Pb tends to give lower ages than other methods, with the exception of FT.

6. Potassium-argon (K-Ar)

For all K-Ar age determinations for the same record, K-Ar has a 0.62 average concordance score with itself (that is, compared with other K-Ar determinations for the same records). For "Three Methods Comparisons," the average score is similar (0.63). Out of every record with a K-Ar concordance score, 57.6% (1,228 out of 2,131) are concordant (have a score of 1.00) and 33.2% (708) are discordant (have a score of 0.00).

When compared with other methods, K-Ar shows the highest degree of concordance with Rb-Sr (concordance score of 0.51). This is slightly higher than with FT (0.49 concordance). K-Ar has significantly less concordance with each U-Pb method, the highest being 0.34 (^{232}Th-^{208}Pb).

K-Ar yields consistently lower age estimations when compared with most other methods for the same records. K-Ar ages are lower than those given by every U-Th-Pb method at least 67.1% of the time. The only method that yields consistently lower ages than K-Ar is FT (72.1% of the time). This suggests that K-Ar typically underestimates ages in relation to other methods, with the exception of FT.

7. Fission track (FT)

For all FT age estimations for the same record, FT has a 0.56 average concordance score with itself (that is, compared with other FT estimations for the same records), which is the lowest of all the methods. For "Three Methods Comparisons," the average score is similar (0.33). Out of every record with an FT concordance score, 49.3% (150 out of 304) are concordant (have a score of 1.00) and 35.5% (108) are discordant (have a score of 0.00).

When compared with other methods, FT shows the highest degree of concordance with K-Ar (concordance score 0.49). The next highest score is with Rb-Sr (0.21), and the lowest is with Pb-Pb (0.00). The lack of concordance between FT and Pb-Pb ages is very striking, especially given that the FT ages are greater 45.1% of the time, which is far more often than in any of the other pairwise comparisons with FT.

FT typically yields the lowest ages of all the methods, giving significantly lower ages at least 54.9% of the time. This result is perhaps unsurprising given that fission tracks can be thermally reset and are therefore typically regarded as minimum ages.

8. Samarium-neodymium (Sm-Nd)

As noted previously, only 32 records included Sm-Nd ages. Interestingly, all came from five adjacent counties in north-central California and together yielded only three numerically unique ages (either 178.00, 314.00, or 575.00 million years). Moreover, only seven of the 32 records included age calculations for other methods. We omitted these records from our analysis since any conclusions drawn would be statistically insignificant.

B. "Three Methods Comparison"

Only 34 records in the database (0.18%) included ages calculated using three or more different methods (when all the U-Th-Pb methods are counted as one method). The distribution of concordance scores for this subset of records shows fewer extreme values but is concentrated toward lower values (Fig. 3). Appendix C provides the full data for all of our "Three Methods Comparisons." The concordance scores for this dataset are shown in Table 4.

The average concordance score for our "Three Methods Comparisons" is 0.39, with only one of the 34 records (2.9%) having a score of 1.00. This suggests that records with ages calculated by multiple methods tend to have lower concordance scores.
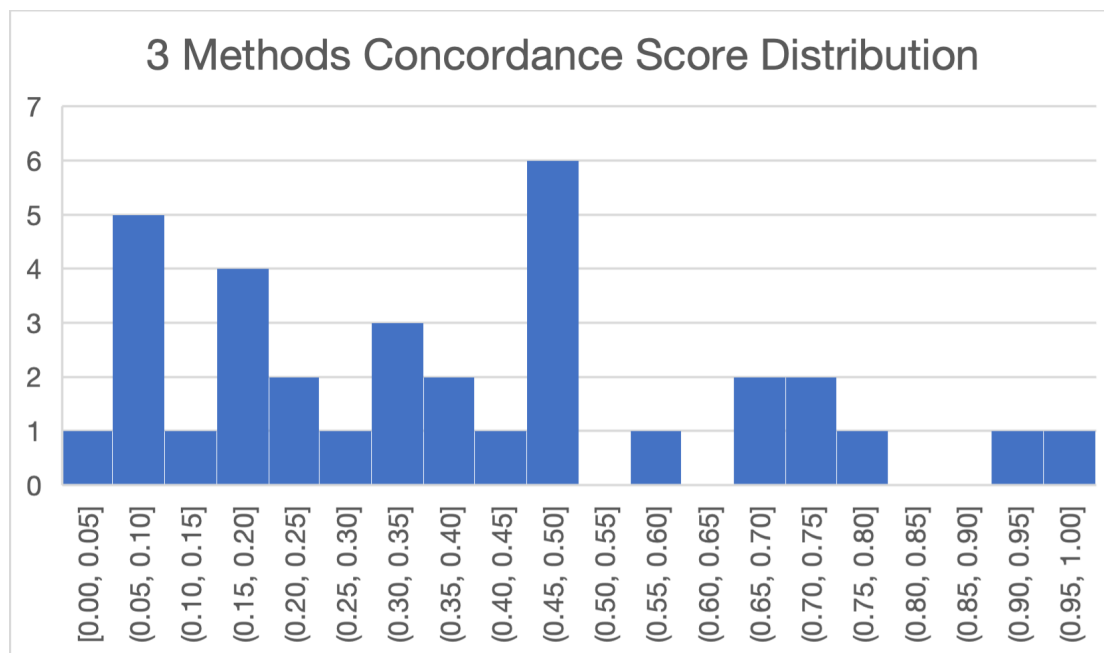

Figure 3. The distribution of concordance scores for all 34 records in the National Geochronological Database with ages determined using three or more radioisotope methods, at least two of which were not in the U-Th-Pb decay chain. This is the "Three Methods Comparison" dataset.

Table 4. The distribution of concordance scores for each method from the "Three Methods Comparisons" dataset. Also includes the average score and the percentage of concordant records.

|	K-Ar	Rb-Sr	^{238}U- ^{206}Pb	^{235}U- 207Pb	Pb-Pb	^{232}Th-^{208}Pb	FT	All Methods
Score = 0	4	3	0	0	1	1	2	1
0 < Score < 0.50	3	1	3	2	3	1	1	23
0.50 ≤ Score < 1	1	1	1	1	0	0	0	10
Score = 1	9	5	5	6	5	2	1	1
Total Count	17	10	9	9	9	4	4	34
Average Score	0.63	0.61	0.73	0.80	0.62	0.60	0.33	0.39
% Concordant (Score = 1)	53%	50%	56%	67%	56%	50%	25%	2.9%
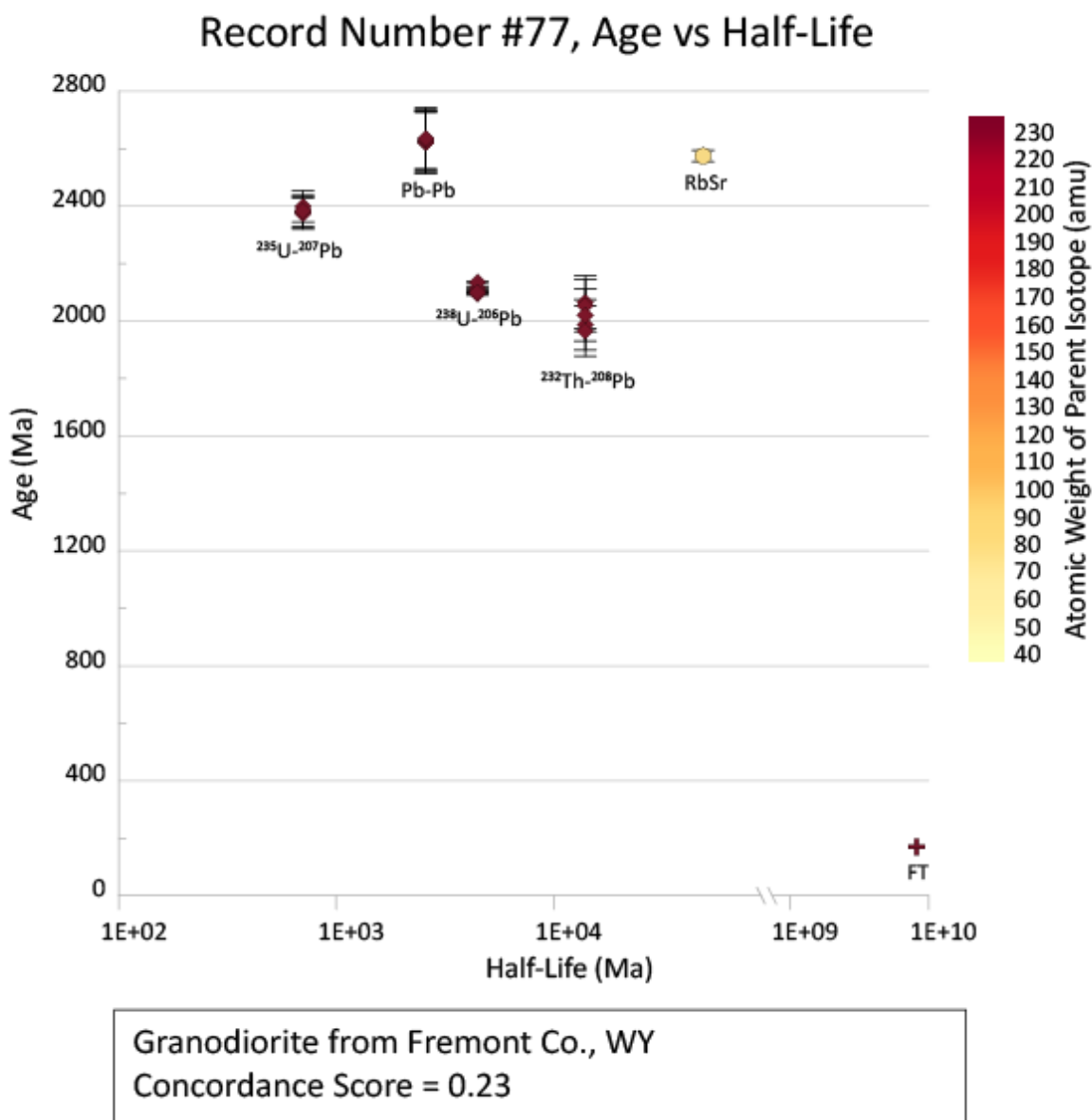
Figure 4. Scatterplot of radioisotope age determinations for Record #77. Radioisotope ages are plotted against the present half-lives of the parent radioisotopes, with any specified error bars shown. The color of each data point represents the atomic weight of each parent isotope, as given by the legend on the right-hand side of each plot. Diamond-shaped data points represent α-decay, circle-shaped data points represent β-decay, and plus-shaped points represent nuclear fission.

Record #77, shown in Fig. 4, is an example of a record dated by six methods, with up to five age determinations for each method. Note that ages are concordant within each method but mostly discordant between methods. The FT age is significantly lower than the ages yielded by the other methods. Consequently, this record has a concordance score of only 0.23.

By contrast, record #558, shown in Fig. 5, is one of only two records in the "Three Methods Comparisons" subset that displayed concordance. This record has an overall concordance score of 0.92 (33 out of 36 comparisons are concordant).

C. "U-Th-Pb Comparison"

The database contained 998 records (5.4%) with ages calculated using at least three of the four U-Th-Pb methods. The concordance scores for this dataset are shown in Table 5. The scores were calculated using all the U-Th-Pb and non-U-Th-Pb ages in each record included in the dataset. The distribution of concordance scores for this subset of records (Fig. 6) more closely matches the distribution of scores for the entire database than for the "Three Methods Comparisons." Many more "U-Th-Pb Comparisons" than "Three Methods Comparisons" had a concordance score of 1.00 (28.7% vs. 2.9%).

The average concordance score for our "U-Th-Pb Comparisons" is 0.57, which is lower than the database average of 0.64 but higher than the average of 0.39 for our "Three Methods Comparisons." The average concordance score was 0.46 for the 369 records that used all four U-Th-Pb methods; for the remaining 629 records using three out of the four methods the average concordance score was 0.64.

There is substantial variation in concordance between the U-Th-Pb methods, as shown in Table 2. The highest degree of concordance (0.79) is between ^{235}U-^{207}Pb and ^{238}U-^{206}Pb, and the lowest (0.18) is between Pb-Pb and ^{232}Th-^{208}Pb. The remaining four comparisons fall within the range 0.43-0.55. Overall, the U-Th-Pb methods are more concordant with each other than they are with the other methods (and generally than the other methods are to each other).

D. Systematic Discordances

The results of our "Two Methods Comparison" revealed a clear and systematic pattern of radioisotope age discordances. See the results in Table 3. For the same rock units, radioisotope dating methods tended to yield ages from oldest to youngest in the following order: Pb-Pb > Rb-Sr > ^{235}U-^{207}Pb > ^{238}U-^{206}Pb > ^{232}Th-^{208}Pb > K-Ar > FT. This compares to the pattern of systematic discordances reported by the RATE group, in which Sm-Nd > U-Pb > Rb-Sr > K-Ar (Austin 2005; Snelling 2005).

V. DISCUSSION
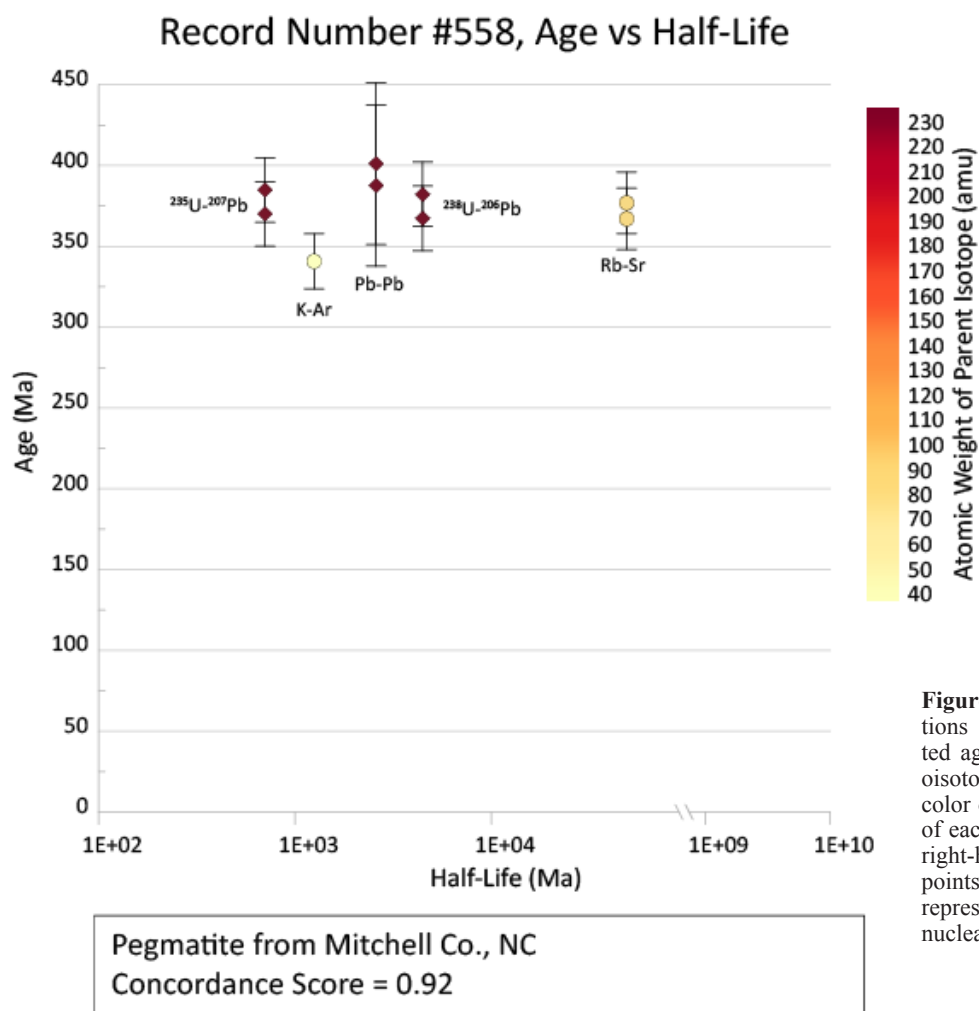
Figure 5. Scatterplot of radioisotope age determinations for Record #558. Radioisotope ages are plotted against the present half-lives of the parent radioisotopes, with any specified error bars shown. The color of each data point represents the atomic weight of each parent isotope, as given by the legend on the right-hand side of each plot. Diamond-shaped data points represent α-decay, circle-shaped data points represent β-decay, and plus-shaped points represent nuclear fission.

Table 5. The distribution of concordance scores for each U-Th-Pb method from the "U-Th-Pb Comparisons" dataset. Also includes the average score and the percentage of concordant records.

	Pb-Pb	$^{235}U - ^{207}Pb$	$^{238}U - ^{206}Pb$	$^{232}Th - ^{208}Pb$	All Methods
Score = 0	56	55	67	43	91
0 < Score < 0.50	40	47	52	13	316
0.50 ≤ Score < 1	35	37	47	14	305
Score = 1	363	347	324	80	286
Total Count	494	486	490	150	998
Average Score	0.80	0.80	0.76	0.62	0.57
% Concordant (Score = 1)	73%	71%	66%	53%	29%
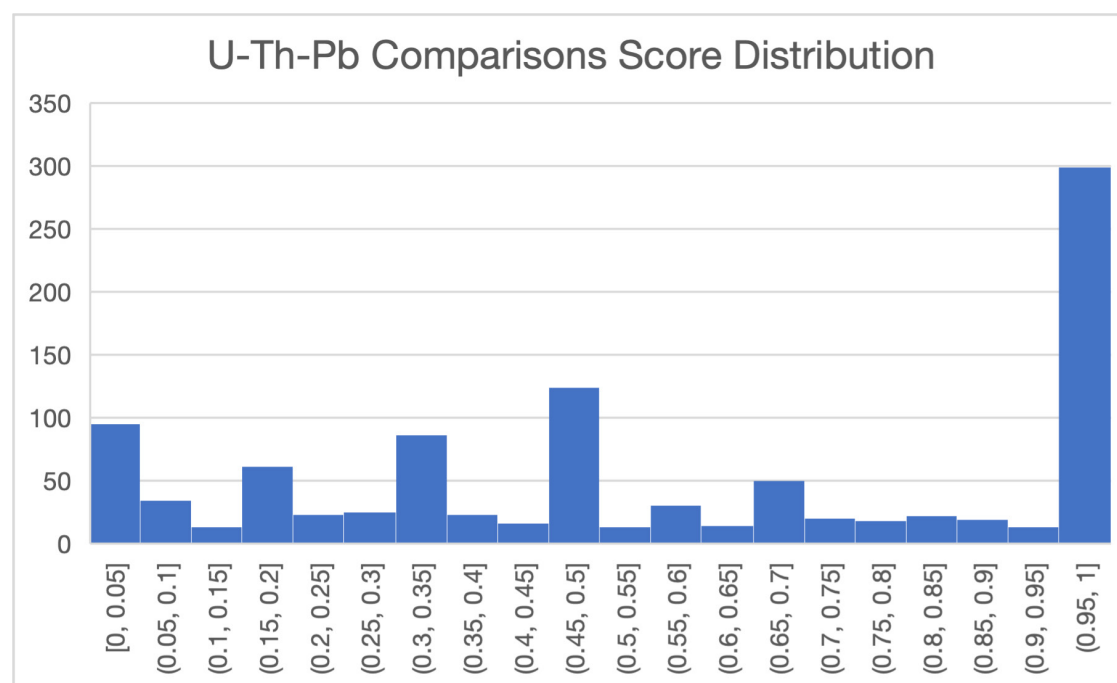
Figure 6. The distribution of concordance scores for all 998 records in the National Geochronological Database with ages determined using three or more U-Th-Pb methods. This is the "U-Th-Pb Comparisons" dataset.

One of the most striking features of our analysis of the USGS National Geochronological Database is how few of the 18,575 records included multiple age determinations using multiple methods. Only 4,875 (26.2%) of the records included two or more age determinations, only 998 (5.4%) included ages calculated using at least three of the four U-Th-Pb methods, and only 34 (0.2%) included age determinations using three or more methods where at least two were not U-Th-Pb. Of the 4,875 records with two or more age determinations, just over half (53.2%) had a concordance score of 1.00, meaning that all the age ranges overlapped, and 23.3% of the records had a concordance score of 0.00, meaning that none of the age ranges overlapped. Comparisons between two of the U-Th-Pb methods had concordance scores averaging 0.57, while comparisons between three of the methods averaged 0.64 and four of the methods averaged 0.46. Moreover, of the 34 records associated with three or more age determinations where at least two were not U-Th-Pb, only one (2.9%) had a concordance score of 1.00. Given how few records in this large database included multiple age determinations, there are clearly limits to what we can say with confidence about the prevalence of concordance. However, taken together, our results suggest that records with age determinations from more methods tend to have lower concord-

ance scores, and this should at least temper the claims sometimes made in the literature concerning "the vast amount of concordance" between radioisotope age determinations (e.g. Isaac 2007, p. 144).

One possible caveat concerns the way in which we treated each record as though it represented a separate rock unit, even though some rock units are represented in the database by multiple records and thus may have been dated by more radioisotope methods than is at first apparent. For instance, the Pikes Peak Granite of the central Front Range of Colorado is represented in the database by about 20 separate records with 90 age determinations between them. We are not certain what effect, if any, collating records that refer to the same rock units will have on our results, but this would seem to be an obvious next step. However, given that concordance scores tended to be lower when rock units were dated by multiple methods, we might expect that collating more age determinations for individual rock units would result in lower overall concordance scores.

Some interesting patterns emerge from our analysis. In cases where a single radioisotope method is used multiple times on a single rock unit, there is often significant "internal discordance" within the results from that one method. In our study, average "internal concord-

ance" scores ranged from 0.56 (for fission tracks) to 0.84 (for Pb-Pb). In other words, fission track ages were the least "internally consistent" and Pb-Pb ages were the most "internally consistent." When age determinations from two methods were compared, average concordance scores ranged from zero (fission tracks vs. Pb-Pb) to 0.79 (^{238}U-^{206}Pb vs. ^{235}U-^{207}Pb). The remainder had average concordance scores between 0.06 and 0.55. Thus, there is significantly less concordance between methods than within a single method.

It is noteworthy that the discordances in the database appear not to be random, but systematic. Systematic discordances were also described by the RATE group in their case studies. However, RATE found that β-decaying isotopes tended to yield younger ages than α-decaying isotopes while in our study ^{40}K followed this pattern but ^{87}Rb did not. RATE also reported that within α- or β-decaying methods, the heavier isotope tended to yield older ages. In our study, we found the same pattern with the exception that 85.0% of ^{235}U-^{207}Pb ages were older than the corresponding ^{238}U-^{206}Pb ages. However, ^{235}U and ^{238}U are probably too similar in atomic weights, valence as ions and geochemical behavior for this observation to have much significance. It should also be noted that ^{238}U-^{206}Pb and ^{235}U-^{207}Pb ages are the ones that overlapped the most, and only 22.5% of the 1,715 records in which the ^{235}U-^{207}Pb ages are older are discordant. Perhaps the differences between our results and those of the RATE group can be explained as stochastic effects or the result of confounding factors such as magma mixing, inheritance and isotopic fractionation in minerals but they warrant further investigation and might necessitate modification of some aspects of the RATE hypothesis of accelerated nuclear decay. Nevertheless, the fact that discordances appear to be systematic and not random is intriguing and seems to require some kind of explanation.

However, our analysis is a preliminary one and more detailed scrutiny of the database is required to confirm our results. The age data used in our analysis was taken from the "age" and "error" columns of the database but in some cases ages or error ranges were incorrectly reported in other parts of the database (e.g. the "comments" column) and were thus not included in our analysis. In other cases, the age information was incomplete, for example instances where the model ages used to construct an isochron were reported but not the actual isochron age. There was also a lack of consistency in how isochron ages were reported in the database, with some generated from multiple ages reported in a single record and others generated from ages reported in multiple records. In addition, there were some apparent errors in the database, for example the exact same "age" and "error range" reported multiple times for supposedly different age determinations. The task of identifying and fixing all of these problems was beyond the scope of this preliminary study and further work will be needed to explore whether these data quality issues, each of which is small, cumulatively affect our initial results and conclusions.

We propose several avenues of future research: (1) Given the availability of a newer, updated version of the database (Hillenbrand et al. 2023), as well as the data quality issues described above, our analysis should be re-run using the latest edition of the database, after a thorough audit has been carried out to identify and, where possible, correct any remaining errors.

(2) For this study, we devised and applied a simple concordance/discordance metric. However, a further analysis could measure degrees of discordance, for example noting by how many standard errors and/or by what percentage of the total age a discordant age is actually discordant. Such quantification may provide further insights into the systematic discordances that are observed and what might explain them.

(3) In this study, we did not compare ages generated by different types of radioisotope age determination (e.g. model ages vs. whole rock isochron ages vs. mineral isochron ages vs. concordia ages). A future study could compare ages from these different types of determinations to look for other patterns of concordance and discordance.

(4) In this study, we did not compare radioisotope age determinations on different minerals, but it would be instructive to see whether certain minerals systematically yield different ages than other minerals. The standard geological explanation for many discordant mineral ages involves the different blocking temperatures of minerals. For example, age determinations based on minerals with high closure temperatures might be expected to be older because they are more likely to reflect the original crystallization age and less likely to be affected by subsequent metamorphic reheating events. Future research could test this hypothesis by seeing whether there is a consistent correlation between the oldest ages and the highest blocking temperatures.

(5) Geoscience Australia (2021) has compiled an online database of radioisotope age determinations from Australia, called "Geochronology and Isotopes." This database is analogous in many ways to the USGS National Geochronological Database, and it may be useful as the subject of similar research in the future. It contains significantly fewer entries than the USGS database (6,036 records as of May 2023) but is more up-to-date and better maintained. It includes K-Ar, Rb-Sr, U-Pb, and FT ages. There are also some Ar-Ar ages and four rhenium-osmium (Re-Os) ages. As with the USGS database, however, the Australian database contains almost no Sm-Nd ages.

VI. ACKNOWLEDGEMENTS

REFERENCES

Austin, S.A. 2000. Mineral isochron method applied as a test of the assumptions of radioisotope dating. In L. Vardiman, A.A. Snelling, and E.F. Chaffin (editors), *Radioisotopes and the Age of the Earth: A Young-earth Creationist Research Initiative*, pp. 95-121. El Cajon, California: Institute for Creation Research, and St Joseph, Missouri: Creation Research Society.

Austin, S.A. 2005. Do radioisotope clocks need repair? Testing the assumptions of isochron dating using K-Ar, Rb-Sr, Sm-Nd, and Pb-Pb isotopes. In L. Vardiman, A.A. Snelling, and E.F. Chaffin (editors), *Radioisotopes and the Age of the Earth: Results of a Young-earth Creationist Research Initiative*, pp. 325-392. El Cajon, California: Institute for Creation Research, and Chino Valley, Arizona: Creation Research Society.

Austin, S.A., and A.A. Snelling. 1998. Discordant potassium-argon model and isochron "ages" for Cardenas Basalt (Middle Proterozoic) and associated diabase of eastern Grand Canyon, Arizona. In R.E. Walsh (editor), *Proceedings of the Fourth International Conference on Creationism*, pp. 35-52. Pittsburgh, Pennsylvania: Creation Science Fellowship.

Geoscience Australia. 2021. Geochronology and Isotopes Data Portal. Retrieved May 16, 2023, from https://portal.ga.gov.au/persona/geochronology. [For download options, select "Geochronology and Isotopes" > "Geochronology" > "Geochronology – All" > "About".]

Hillenbrand, I.W., K.D. Thomson, L.E. Morgan, A.K. Gilmer, A.D. Dombrowski, K.F. Warrell, J.R. Malone, A.K. Souders, A.M. Hudson, M.A. Cosca, J.B. Paces, R.A. Thompson, and A.J. Park. 2023. *USGS Geochron: A Database of Geochronological and Thermochronological Dates and Data.* United States Geological Survey data release. DOI: 10.5066/P9RZNPIF.

Isaac, R. 2007. Assessing the RATE project. *Perspectives on Science and Christian Faith* 59, no. 2 (June):143-146.

Nethercott, P. 2021. *Radiometric Dating Errors: A Rebuttal of Brent Dalrymple's Book "The Age of the Earth."* Longwood, Florida: Advantage Books.

Snelling, A.A. 1998. The cause of anomalous potassium-argon "ages" for recent andesite flows at Mt. Ngauruhoe, New Zealand, and the implications for potassium-argon "dating". In R.E. Walsh (editor), *Proceedings of the Fourth International Conference on Creationism*, pp. 503-525. Pittsburgh, Pennsylvania: Creation Science Fellowship.

Snelling, A.A. 2003a. The relevance of Rb-Sr, Sm-Nd and Pb-Pb isotope systematics to elucidation of the genesis and history of recent andesite flows at Mt Ngauruhoe, New Zealand, and the implications for radioisotopic dating. In R.L. Ivey, Jr. (editor), *Proceedings of the Fifth International Conference on Creationism*, pp. 285-303. Pittsburgh, Pennsylvania: Creation Science Fellowship.

Snelling, A.A. 2003b. Whole-rock K-Ar model and isochron, and Rb-Sr, Sm-Nd and Pb-Pb isochron, "dating" of the Somerset Dam layered mafic intrusion, Australia. In R.L. Ivey, Jr. (editor), *Proceedings of the Fifth International Conference on Creationism*, pp. 305-324. Pittsburgh, Pennsylvania: Creation Science Fellowship.

Snelling, A.A. 2005. Isochron discordances and the role of inheritance and mixing of radioisotopes in the mantle and crust. In L. Vardiman, A.A. Snelling, and E.F. Chaffin (editors), *Radioisotopes and the Age of the Earth: Results of a Young-earth Creationist Research Initiative*, pp. 393-524. El Cajon, California: Institute for Creation Research, and Chino Valley, Arizona: Creation Research Society.

Snelling, A.A., S.A. Austin, and W.A. Hoesch. 2003. Radioisotopes in the diabase sill (Upper Precambrian) at Bass Rapids, Grand Canyon, Arizona: an application and test of the isochron dating method. In R.L. Ivey, Jr. (editor), *Proceedings of the Fifth International Conference on Creationism*, pp. 269-284. Pittsburgh, Pennsylvania: Creation Science Fellowship.

Vardiman, L., A.A. Snelling, and E.F. Chaffin (editors). 2000. *Radioisotopes and the Age of the Earth: a Young-earth Creationist Research Initiative*. El Cajon, California: Institute for Creation Research, and St Joseph, Missouri: Creation Research Society.

Vardiman, L., A.A. Snelling, and E.F. Chaffin (editors). 2005. *Radioisotopes and the Age of the Earth: Results of a Young-earth Creationist Research Initiative*. El Cajon, California: Institute for Creation Research, and Chino Valley, Arizona: Creation Research Society.

Wise, K.P. 2002. *Faith, Form, and Time: What the Bible Teaches and Science Confirms about Creation and the Age of the Universe*. Nashville, Tennessee: Broadman and Holman Publishers.

Woodmorappe, J. 1979. Radiometric geochronology reappraised. *Creation Research Society Quarterly* 16, no. 2 (September):102-129, 147-148.

Woodmorappe, J. 1999. *The Mythology of Modern Dating Methods*. El Cajon, California: Institute for Creation Research.

Zartman, R.E., C.A. Bush, and C. Abston, revised by J. Sloan, C.D. Henry, M. Hopkins, and S. Ludington. 2003. *National Geochronological Database*. United States Geological Survey Open-File Report 03-236. DOI: 10.3133/ofr03326_rev.

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APPENDIX A: ESTIMATING THE NUMBER OF UNIQUE AGE DETERMINATIONS

The USGS National Geochronological Database comprises several files, including a separate file for each radioisotope method and a merged file called "allages." We used the "allages" file for the purposes of our study. However, because of the way this file is constructed, it included many duplicated ages, which we removed using the Processing software and the source code reproduced below. We called the resulting file our "reformatted allages" file, and we used it for any analyses using our Concordance Metric. However, for our "Two Methods Comparisons" and "U-Th-Pb Comparisons" we obtained data directly from the original "allages" file, removing records that did not contain ages determined by the methods in which we were interested.

It should be noted that there are some discrepancies between the "allages" file (and thus our "reformatted allages" file) and the separate files provided in the database for each method. For example:

- Record #45 is present in the K-Ar method file but not in the "allages" file. Instead, the "allages" file has a duplicated entry for Record #44.
- Record #16763, which contains a K-Ar age in the K-Ar method file, is omitted from the "allages" file.

Thus, the total number of unique age determinations in our "reformatted allages" file (29,043) is slightly different to the sum of the age determinations obtained from the separate method files (29,067). However, the difference of 24 ages is very small in comparison to the size of the database as a whole and should not significantly impact our results.

```
/////////////////////////////////////////////////////////////////////////////
//
// ConcordanceMetric_v1.pde
// Benjamin Kinard
//
// ConcordanceMetric_v1 creates the file "ConcordanceMetricOutput.csv"
// that reformats "allages.csv" such that each RecNo is contained
// in single row.
//
/////////////////////////////////////////////////////////////////////////////

Table allages; // table containing all samples
Table output = new Table(); // output table
int[] NumRecNo = new int[18670];
StringList columns = new StringList();
StringList genColumns = new StringList();
void setup() {
  allages = loadTable("allages.csv", "header, csv"); // 25359 rows
  // initialize output columns
  genColumns.append("RecNo");
  genColumns.append("LongDec");
  genColumns.append("LatDec");
  genColumns.append("State");
  genColumns.append("County");
  genColumns.append("QuadScale");
  genColumns.append("QuadName");
  genColumns.append("SampSour");
  genColumns.append("RockName");
  columns.append("ConcordanceScore");
  columns.append("TotalCount");
  columns.append("KArScore");
```

```
columns.append("KArCount");
columns.append("RbSrScore");
columns.append("RbSrCount");
columns.append("206_238Score");
columns.append("206_238Count");
columns.append("207_235Score");
columns.append("207_235Count");
columns.append("207_206Score");
columns.append("207_206Count");
columns.append("208_232Score");
columns.append("208_232Count");
columns.append("FTScore");
columns.append("FTCount");
// Add all the age and error columns to output
for (int i = 0; i < 6; i++) {
  columns.append("KArAge" + (i+1));
  columns.append("KArErr" + (i+1));
}
for (int i = 0; i < 24; i++) {
  columns.append("RbSrAge" + (i+1));
  columns.append("RbSrErr" + (i+1));
}
for (int i = 0; i < 21; i++) {
  columns.append("206_238Age" + (i+1));
  columns.append("206_238Err" + (i+1));
}
for (int i = 0; i < 21; i++) {
  columns.append("207_235Age" + (i+1));
  columns.append("207_235Err" + (i+1));
}
for (int i = 0; i < 33; i++) {
  columns.append("207_206Age" + (i+1));
  columns.append("207_206Err" + (i+1));
}
for (int i = 0; i < 15; i++) {
  columns.append("208_232Age" + (i+1));
  columns.append("208_232Err" + (i+1));
}
for (int i = 0; i < 5; i++) {
  columns.append("FTAge" + (i+1));
  columns.append("FTErr" + (i+1));
}
for (int i = 0; i < genColumns.size(); i++) {
  output.addColumn(genColumns.get(i));
}
for (int i = 0; i < columns.size(); i++) {
  output.addColumn(columns.get(i));
}
int rowCount = 0;
int prevRecNo = 1;
TableRow newRow;
newRow = output.addRow();
newRow.setInt("RecNo", 1);
for (TableRow row : allages.rows()) {
  rowCount++;
  int RecNo = row.getInt("RecNo");
  if (RecNo != prevRecNo) {
    prevRecNo = RecNo;
    newRow = output.addRow();
    newRow.setInt("RecNo", RecNo);
    for (int i = 1; i < genColumns.size(); i++) {
      String col = genColumns.get(i);
      String data = row.getString(col);
      newRow.setString(col, data);
    }
  }

  // get data from allages
  int KArRecNo = NaN(row.getInt("KArRecNo")); // MAX 6
```

```
  int RbSrRecNo = NaN(row.getInt("RbSrRecNo")); // MAX 24
  int UPbRecNo = NaN(row.getInt("UPbRecNo")); // MAX 33 (21, 21,
33, 15)
  int FTRecNo = NaN(row.getInt("FTRecNo")); // MAX 5
  float KArAge = row.getFloat("KArAge");
  float KArErr = row.getFloat("KArErr");
  float RbSrAge = row.getFloat("RbSrAge");
  float RbSrErr = row.getFloat("RbSrErr");
  float U206_238Age = row.getFloat("206_238Age");
  float U206_238Err = row.getFloat("Err206_238");
  float U207_235Age = row.getFloat("207_235Age");
  float U207_235Err = row.getFloat("Err207_235");
  float U207_206Age = row.getFloat("207_206Age");
  float U207_206Err = row.getFloat("Err207_206");
  float U208_232Age = row.getFloat("208_232Age");
  float U208_232Err = row.getFloat("Err208_232");
  float FTAge = row.getFloat("FTAge");
  float FTErr = row.getFloat("FTErr");

  // add data to output (if not already added)
  if (KArRecNo > 0 && !Float.isNaN(KArAge)) {
    newRow.setFloat("KArAge" + KArRecNo, KArAge);
    if (!Float.isNaN(KArErr)) {
      newRow.setFloat("KArErr" + KArRecNo, KArErr);
    } else {
      newRow.setFloat("KArErr" + KArRecNo, KArAge/10.0);
    }
  }
  if (RbSrRecNo > 0 && !Float.isNaN(RbSrAge)) {
    newRow.setFloat("RbSrAge" + RbSrRecNo, RbSrAge);
    if (!Float.isNaN(RbSrErr)) {
      newRow.setFloat("RbSrErr" + RbSrRecNo, RbSrErr);
    } else {
      newRow.setFloat("RbSrErr" + RbSrRecNo, RbSrAge/10.0);
    }
  }
  if (UPbRecNo > 0 && !Float.isNaN(U206_238Age)) {
    newRow.setFloat("206_238Age" + UPbRecNo, U206_238Age);
    if (!Float.isNaN(U206_238Err)) {
      newRow.setFloat("206_238Err" + UPbRecNo, U206_238Err);
    } else {
      newRow.setFloat("206_238Err" + UPbRecNo, U206_238Age/10.0);
    }
  }
  if (UPbRecNo > 0 && !Float.isNaN(U207_235Age)) {
    newRow.setFloat("207_235Age" + UPbRecNo, U207_235Age);
    if (!Float.isNaN(U207_235Err)) {
      newRow.setFloat("207_235Err" + UPbRecNo, U207_235Err);
    } else {
      newRow.setFloat("207_235Err" + UPbRecNo, U207_235Age/10.0);
    }
  }
  if (UPbRecNo > 0 && !Float.isNaN(U207_206Age)) {
    newRow.setFloat("207_206Age" + UPbRecNo, U207_206Age);
    if (!Float.isNaN(U207_206Err)) {
      newRow.setFloat("207_206Err" + UPbRecNo, U207_206Err);
    } else {
      newRow.setFloat("207_206Err" + UPbRecNo, U207_206Age/10.0);
    }
  }
  if (UPbRecNo > 0 && !Float.isNaN(U208_232Age)) {
    newRow.setFloat("208_232Age" + UPbRecNo, U208_232Age);
    if (!Float.isNaN(U208_232Err)) {
      newRow.setFloat("208_232Err" + UPbRecNo, U208_232Err);
    } else {
      newRow.setFloat("208_232Err" + UPbRecNo, U208_232Age/10.0);
    }
  }
  if (FTRecNo > 0 && !Float.isNaN(FTAge)) {
```

```
  newRow.setFloat("FTAge" + FTRecNo, FTAge);
  if (!Float.isNaN(FTErr)) {
    newRow.setFloat("FTErr" + FTRecNo, FTErr);
  } else {
    newRow.setFloat("FTErr" + FTRecNo, FTAge/10.0);
  }
}
// display progress
println();
println();
println();
println();
println();
println();
println();
println("Reformatting " + 100*rowCount/25359 + "% complete (" +
rowCount + "/25359)");/**/
}
/////////// CALCULATE CONCORDANCE SCORES
FloatList ages = new FloatList();
FloatList agesMethod = new FloatList();
FloatList error = new FloatList();
FloatList errorMethod = new FloatList();
int rowCount2 = 0;
for (TableRow row : output.rows()) {
  rowCount2++;
  ages = new FloatList();
  agesMethod = new FloatList();
  error = new FloatList();
  errorMethod = new FloatList();
  float methodScore;
  for (int i = 0; i < 6; i++) {
    if (!Float.isNaN(row.getFloat("KArAge" + (i+1)))) {
      ages.append(row.getFloat("KArAge" + (i+1)));
      agesMethod.append(row.getFloat("KArAge" + (i+1)));
      error.append(row.getFloat("KArErr" + (i+1)));
      errorMethod.append(row.getFloat("KArErr" + (i+1)));
    }
  }
  methodScore = calcScore(agesMethod, errorMethod);
  if (!(methodScore < 0)) {
    row.setFloat("KArScore", methodScore);
  }
  row.setInt("KArCount", agesMethod.size());
  agesMethod = new FloatList();
  errorMethod = new FloatList();
  for (int i = 0; i < 24; i++) {
    if (!Float.isNaN(row.getFloat("RbSrAge" + (i+1)))) {
      ages.append(row.getFloat("RbSrAge" + (i+1)));
      agesMethod.append(row.getFloat("RbSrAge" + (i+1)));
      error.append(row.getFloat("RbSrErr" + (i+1)));
      errorMethod.append(row.getFloat("RbSrErr" + (i+1)));
    }
  }
  methodScore = calcScore(agesMethod, errorMethod);
  if (!(methodScore < 0)) {
    row.setFloat("RbSrScore", methodScore);
  }
  row.setInt("RbSrCount", agesMethod.size());
  agesMethod = new FloatList();
  errorMethod = new FloatList();
  for (int i = 0; i < 21; i++) {
    if (!Float.isNaN(row.getFloat("206_238Age" + (i+1)))) {
      ages.append(row.getFloat("206_238Age" + (i+1)));
      agesMethod.append(row.getFloat("206_238Age" + (i+1)));
      error.append(row.getFloat("206_238Err" + (i+1)));
      errorMethod.append(row.getFloat("206_238Err" + (i+1)));
    }
  }
}

methodScore = calcScore(agesMethod, errorMethod);
if (!(methodScore < 0)) {
  row.setFloat("206_238Score", methodScore);
}
row.setInt("206_238Count", agesMethod.size());
agesMethod = new FloatList();
errorMethod = new FloatList();
for (int i = 0; i < 21; i++) {
  if (!Float.isNaN(row.getFloat("207_235Age" + (i+1)))) {
    ages.append(row.getFloat("207_235Age" + (i+1)));
    agesMethod.append(row.getFloat("207_235Age" + (i+1)));
    error.append(row.getFloat("207_235Err" + (i+1)));
    errorMethod.append(row.getFloat("207_235Err" + (i+1)));
  }
}
methodScore = calcScore(agesMethod, errorMethod);
if (!(methodScore < 0)) {
  row.setFloat("207_235Score", methodScore);
}
row.setInt("207_235Count", agesMethod.size());
agesMethod = new FloatList();
errorMethod = new FloatList();

for (int i = 0; i < 33; i++) {
  if (!Float.isNaN(row.getFloat("207_206Age" + (i+1)))) {
    ages.append(row.getFloat("207_206Age" + (i+1)));
    agesMethod.append(row.getFloat("207_206Age" + (i+1)));
    error.append(row.getFloat("207_206Err" + (i+1)));
    errorMethod.append(row.getFloat("207_206Err" + (i+1)));
  }
}
methodScore = calcScore(agesMethod, errorMethod);
if (!(methodScore < 0)) {
  row.setFloat("207_206Score", methodScore);
}
row.setInt("207_206Count", agesMethod.size());
agesMethod = new FloatList();
errorMethod = new FloatList();
for (int i = 0; i < 15; i++) {
  if (!Float.isNaN(row.getFloat("208_232Age" + (i+1)))) {
    ages.append(row.getFloat("208_232Age" + (i+1)));
    agesMethod.append(row.getFloat("208_232Age" + (i+1)));
    error.append(row.getFloat("208_232Err" + (i+1)));
    errorMethod.append(row.getFloat("208_232Err" + (i+1)));
  }
}
methodScore = calcScore(agesMethod, errorMethod);
if (!(methodScore < 0)) {
  row.setFloat("208_232Score", methodScore);
}
row.setInt("208_232Count", agesMethod.size());
agesMethod = new FloatList();
errorMethod = new FloatList();
for (int i = 0; i < 5; i++) {
  if (!Float.isNaN(row.getFloat("FTAge" + (i+1)))) {
    ages.append(row.getFloat("FTAge" + (i+1)));
    agesMethod.append(row.getFloat("FTAge" + (i+1)));
    error.append(row.getFloat("FTErr" + (i+1)));
    errorMethod.append(row.getFloat("FTErr" + (i+1)));
  }
}
methodScore = calcScore(agesMethod, errorMethod);
if (!(methodScore < 0)) {
  row.setFloat("FTScore", methodScore);
}
row.setInt("FTCount", agesMethod.size());
float score = calcScore(ages, error);
if (!(score < 0)) {
  row.setFloat("ConcordanceScore", score);
```

```
    }
    row.setInt("TotalCount", ages.size());

    // display progress
    println();
    println();
    println();
    println();
    println();
    println();
    println();
    println("Calculating " + 100*rowCount2/output.getRowCount() + "%
complete (" + rowCount2 + "/"+output.getRowCount()+")");/**/
   }
   // create file
   String fileName = "ConcordanceMetricOutput.csv";
   println("RowCount: " + rowCount);
   saveTable(output, "output/" + fileName);
   println("File \"" + fileName + "\" created with " + output.getRowCount()
+ " rows");
   println("Program terminated");
 }
 // determine if an integer value is valid
 int NaN(int n) {
  if (n > 0) {
   return n;
  }
  return -1;
 }
 // determine if a float value is valid
 float NaN(float n) {
  if (n >= 0) {
   return n;
  }
  return -1;
 }
 // calculate the concordance score given lists of ages and errors
 float calcScore(FloatList input, FloatList error) {
  if (input.size() != error.size()) {
   return -1;
  }
  int total = 0;
  int concordant = 0;
  int count = input.size();
  if (count < 2) {
   return -1;
  }
  for (int i = 0; i < count-1; i++) {
   for (int j = i+1; j < count; j++) {
    total++;
    int prev = concordant;
    float in1 = input.get(i);
    float in2 = input.get(j);
    float err1 = error.get(i);
    float err2 = error.get(j);
    if (err1 < 0) {
     err1 = in1/10.0;
    }
    if (err2 < 0) {
     err2 = in2/10.0;
    }
    if (in1 > in2) {
     if (in1-err1 <= in2+err2) {
      concordant++;
     }
    } else if (in2 > in1) {
     if (in2-err2 <= in1+err1) {
      concordant++;
     }
    } else {
     concordant++;
    }
   }
  }

  return float(concordant)/total;
 }
```

APPENDIX B: FULL TWO METHODS COMPARISON
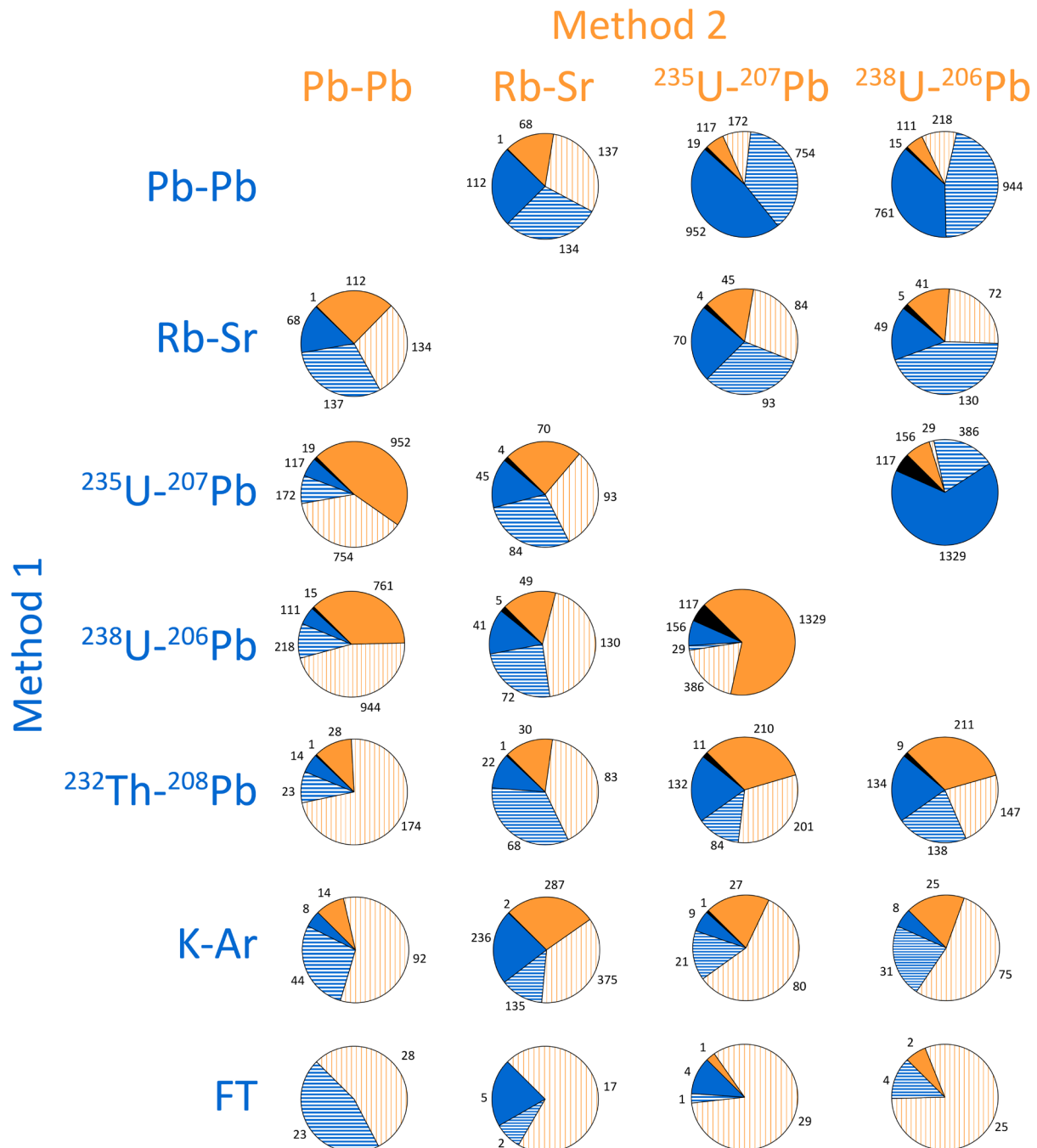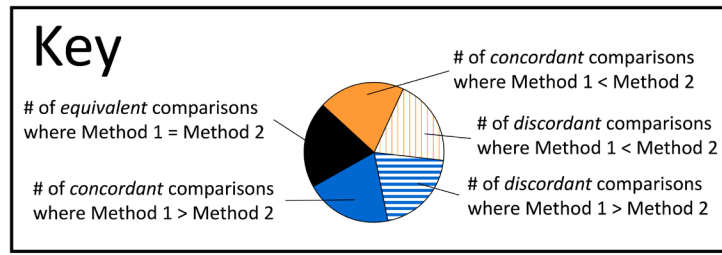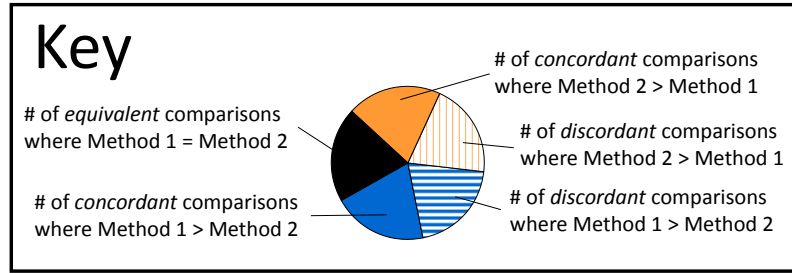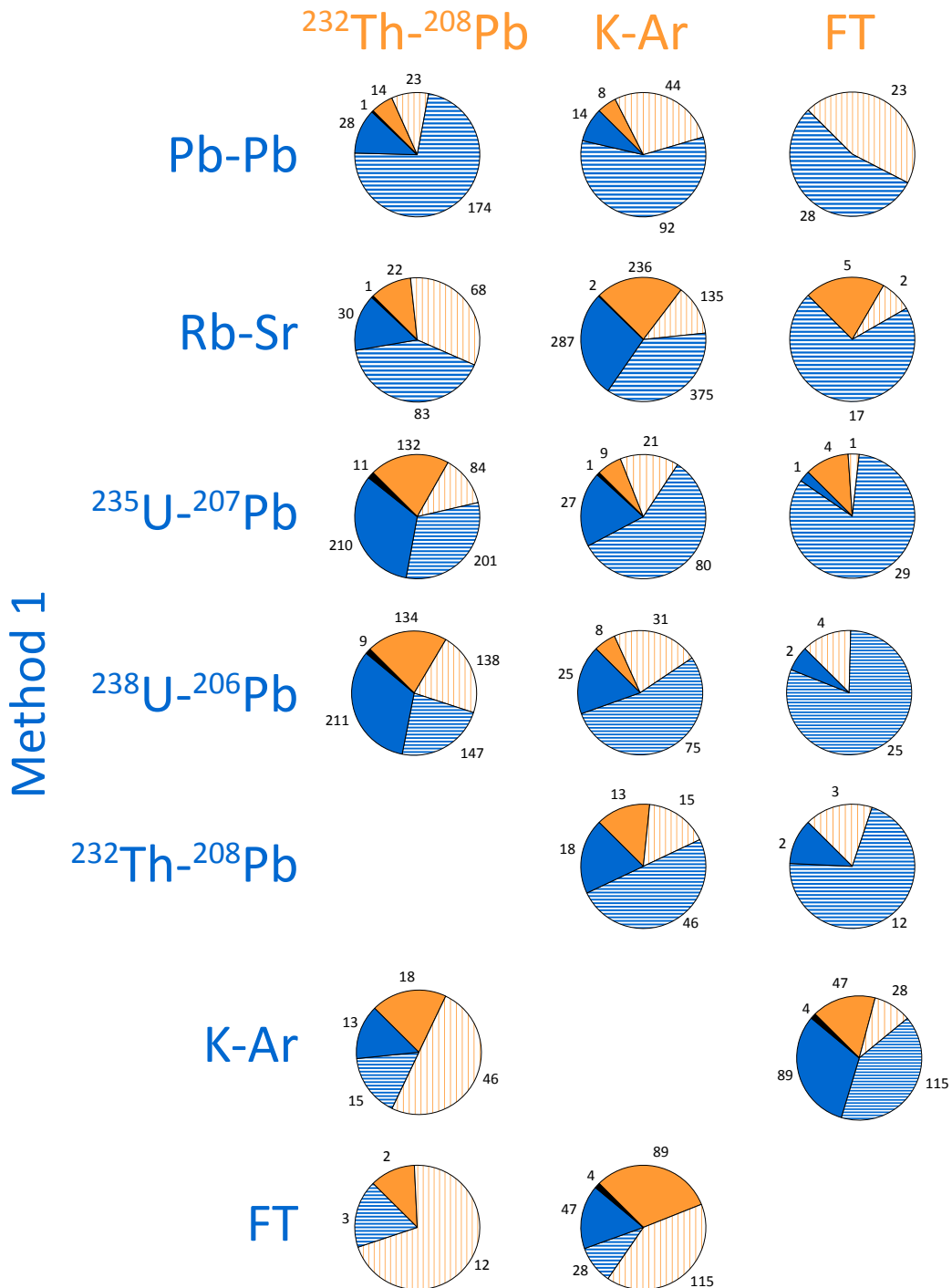
APPENDIX C: FULL THREE METHODS COMPARISON

Record Number #77, Age vs Half-Life
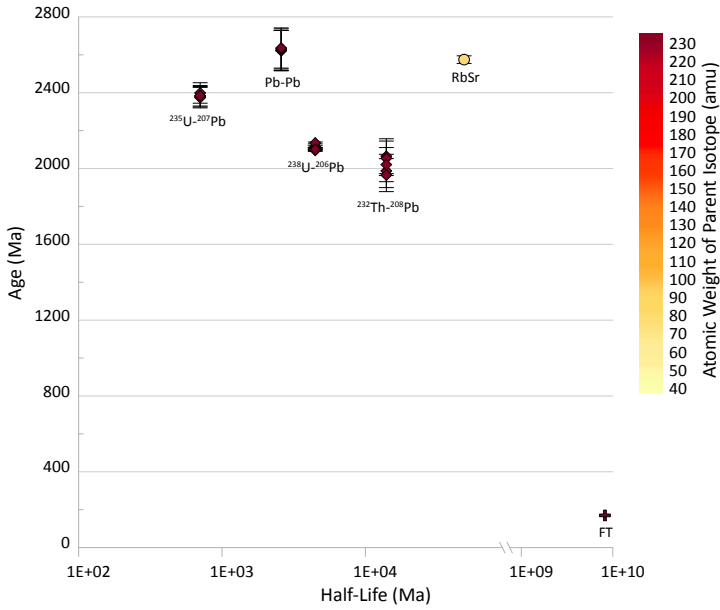
Granodiorite from Fremont Co., WY
Concordance Score = 0.23

Record Number #559, Age vs Half-Life
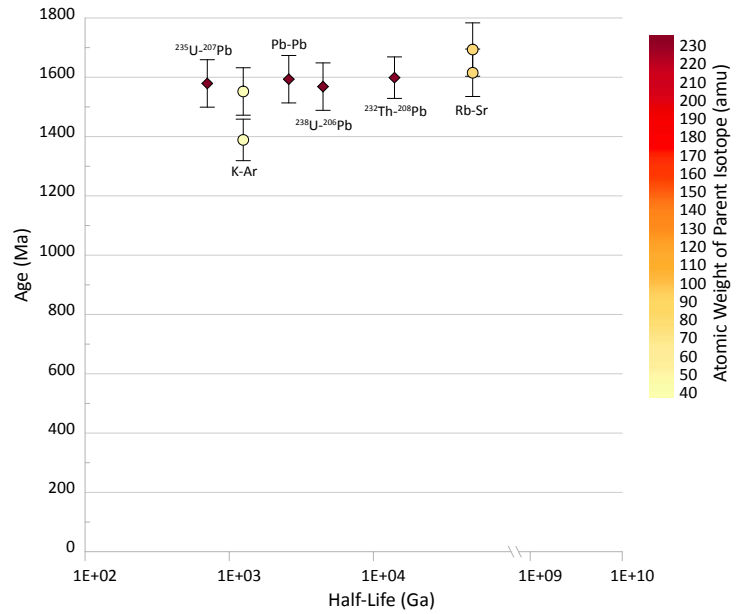
Pegmatite from Pennington Co., SD
Concordance Score = 0.75

Record Number #558, Age vs Half-Life
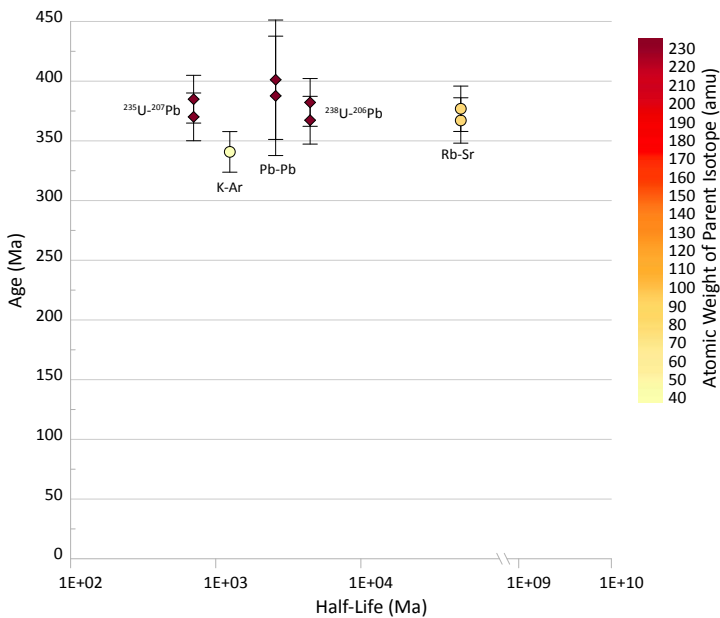
Pegmatite from Mitchell Co., NC
Concordance Score = 0.92

Record Number #560, Age vs Half-Life
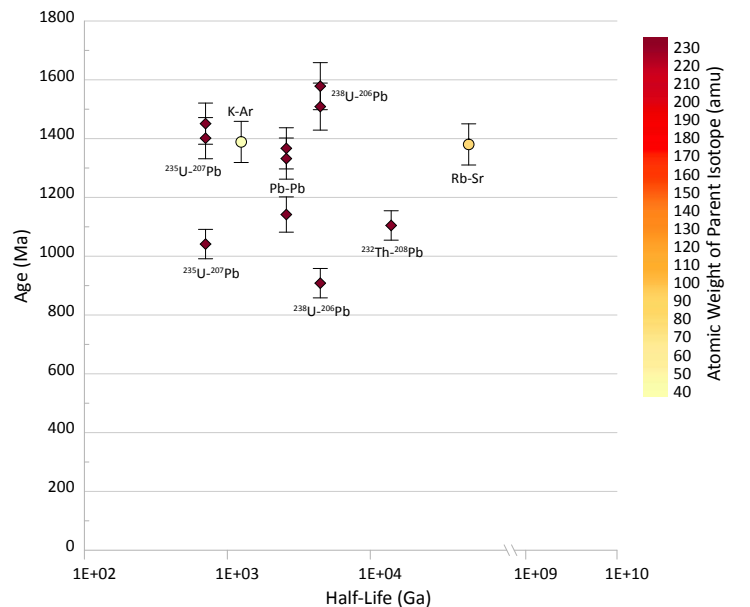
Pegmatite from Gunnison Co., CO
Concordance Score = 0.35

Record Number #561, Age vs Half-Life
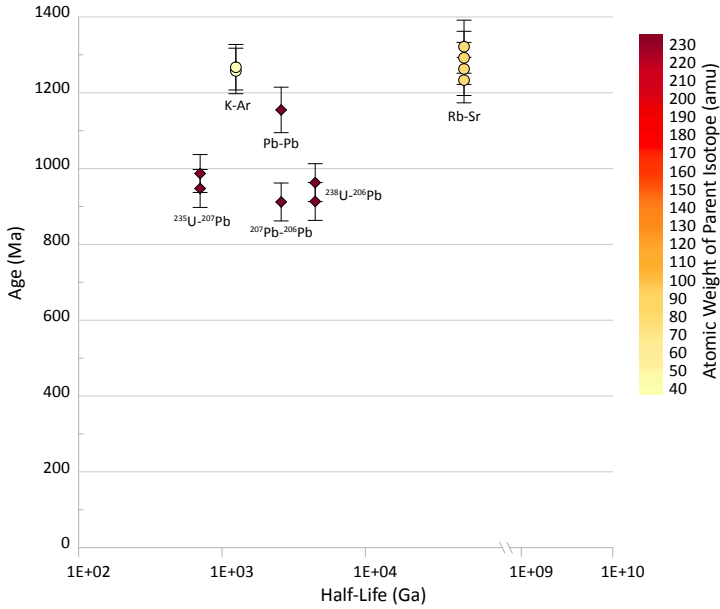
Pegmatite from Taos Co., NM
Concordance Score = 0.44

Record Number #563, Age vs Half-Life
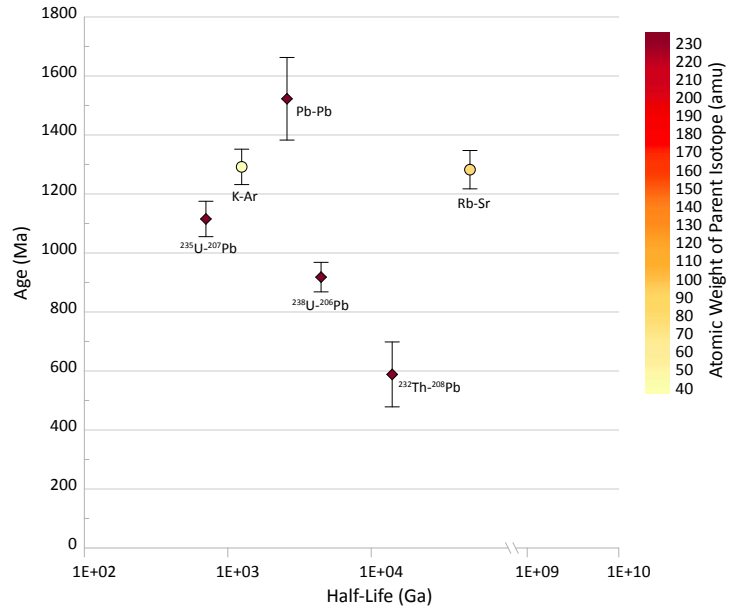
Granite from Gunnison Co., CO
Concordance Score = 0.07

Record Number #562, Age vs Half-Life
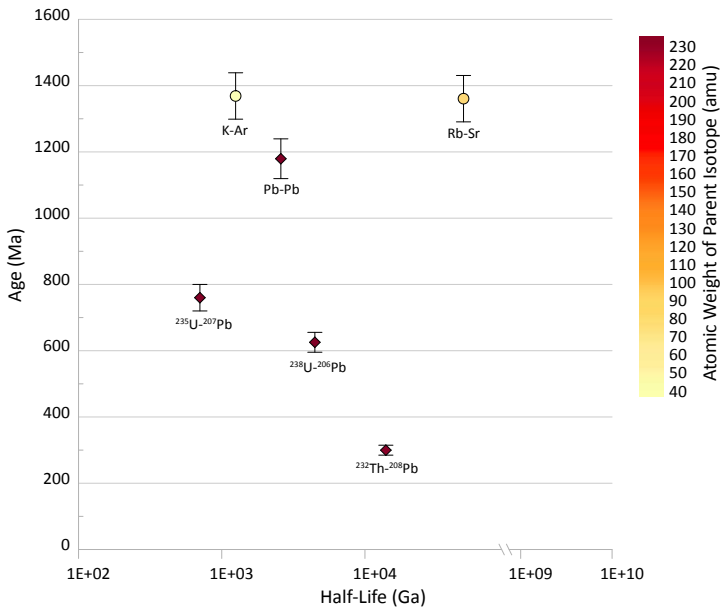
Granite from Yavapai Co., AZ
Concordance Score = 0.07

Record Number #564, Age vs Half-Life
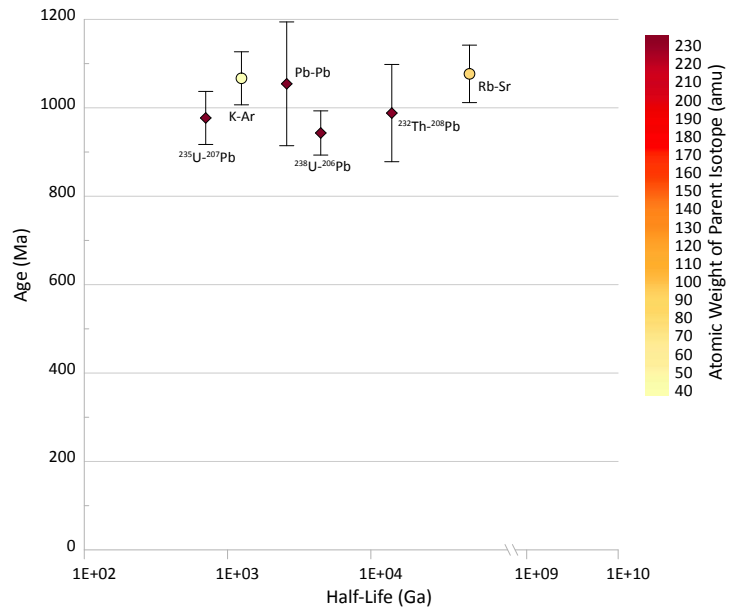
Granite from Llano Co., TX
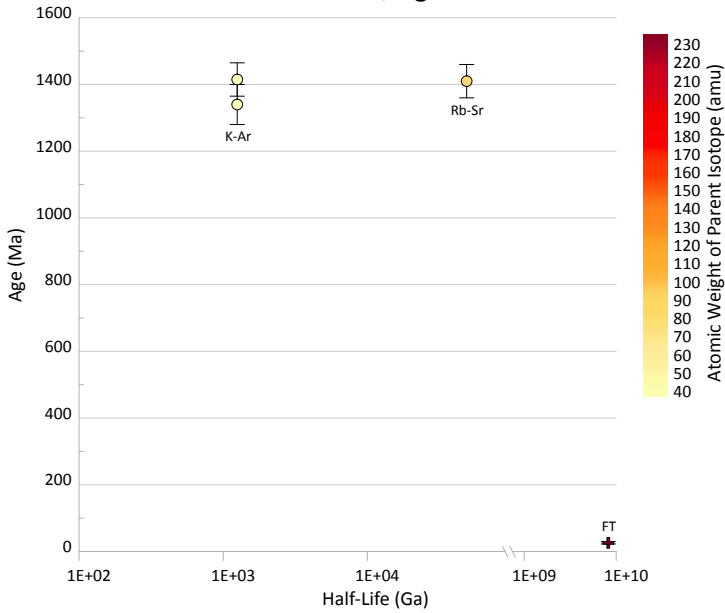Concordance Score = 0.80

Record Number #565, Age vs Half-Life
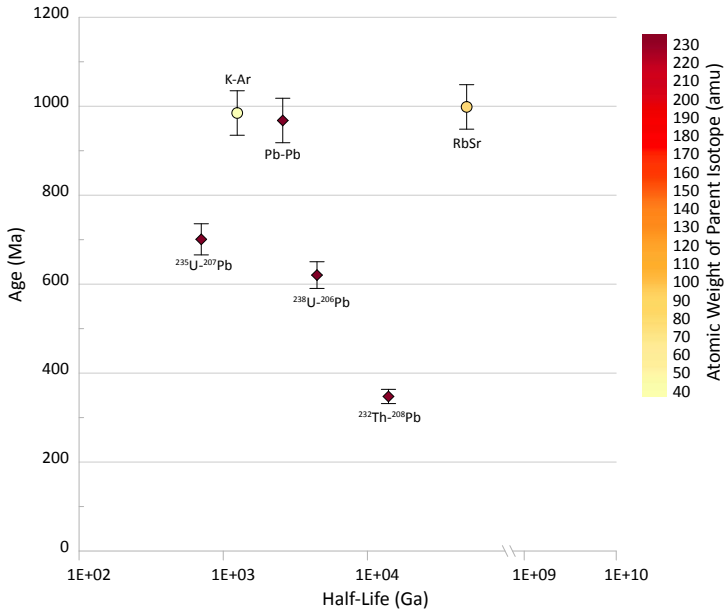
Granite from El Paso Co., CO
Concordance Score = 0.20

Record Number #1658, Age vs Half-Life
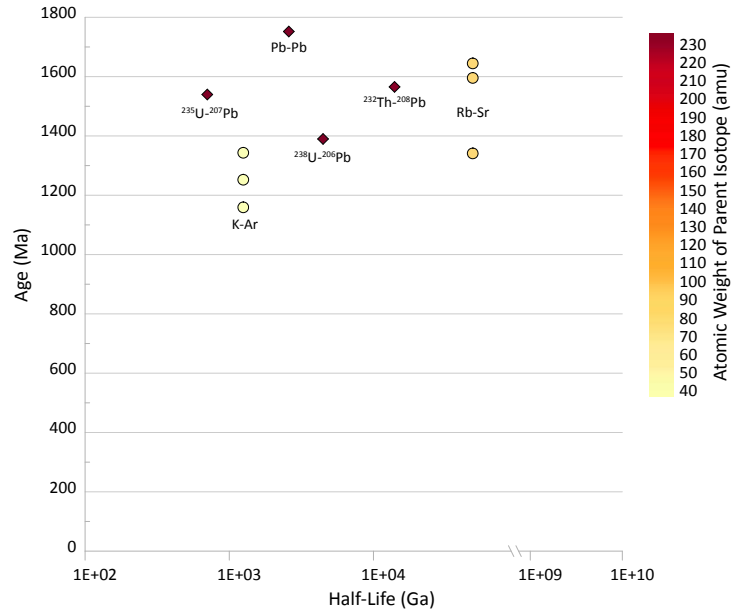
Granite from Iron Co., MI
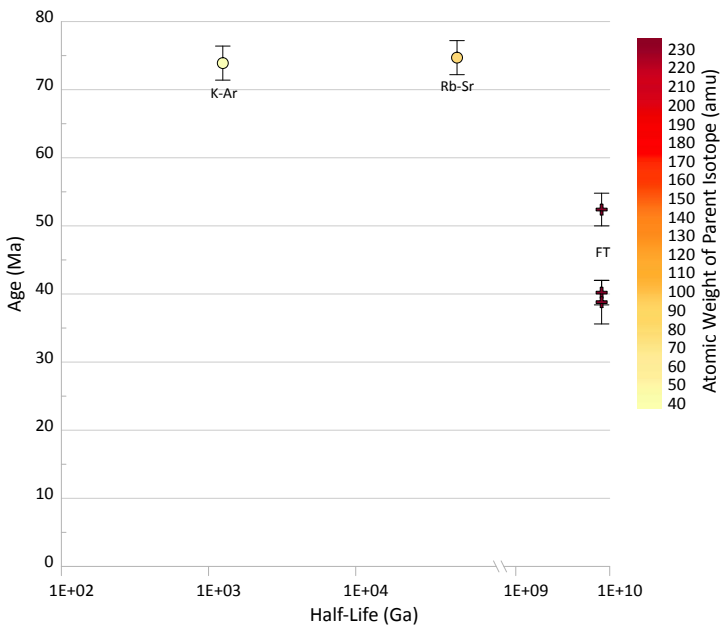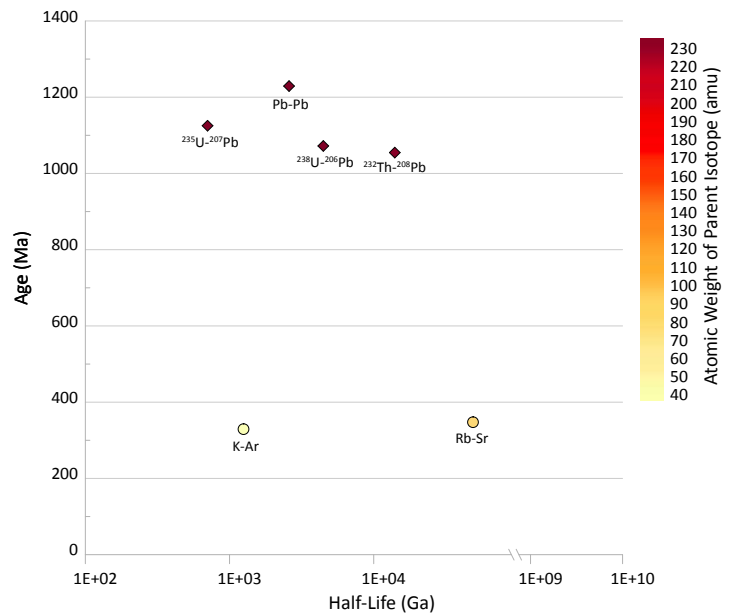Concordance Score = 0.67

Record Number #566, Age vs Half-Life
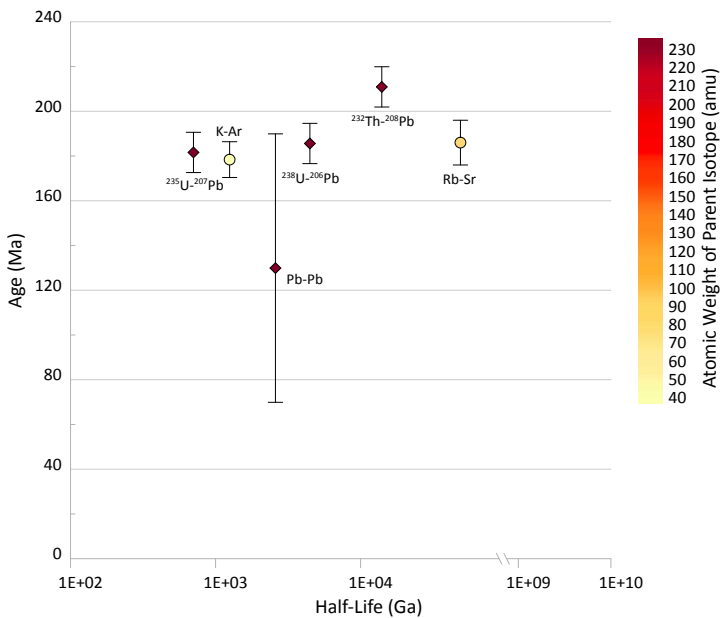
Hastingsite granite from Conway Co., NH
Concordance Score = 0.67

Record Number #1665, Age vs Half-Life
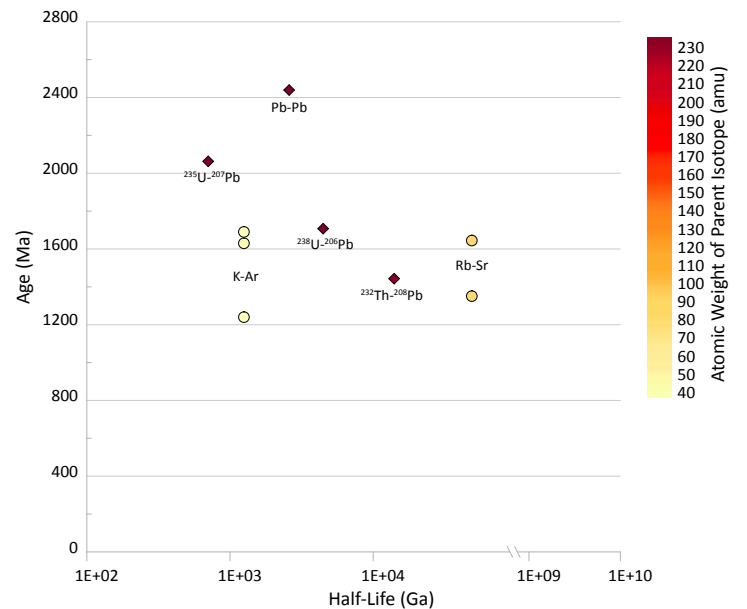
Gneiss from Dickinson Co., MI
Concordance Score = 0.50

Record Number #1681, Age vs Half-Life
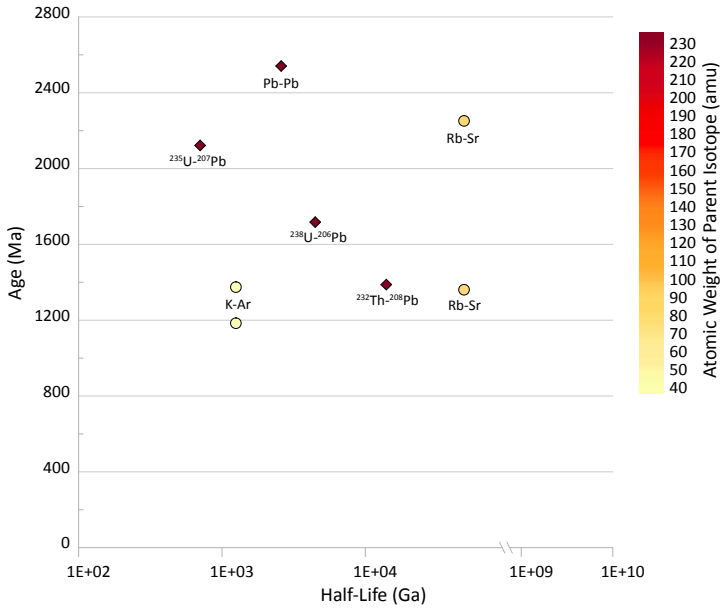
Granite from Dickinson Co., MI
Concordance Score = 0.32

Record Number #1684, Age vs Half-Life
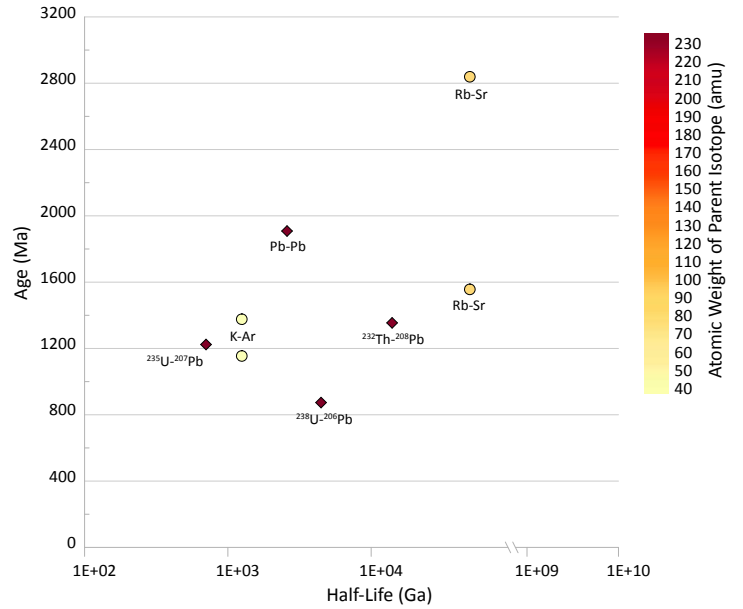
Granite from Iron Co., MI
Concordance Score = 0.29

Record Number #1682, Age vs Half-Life
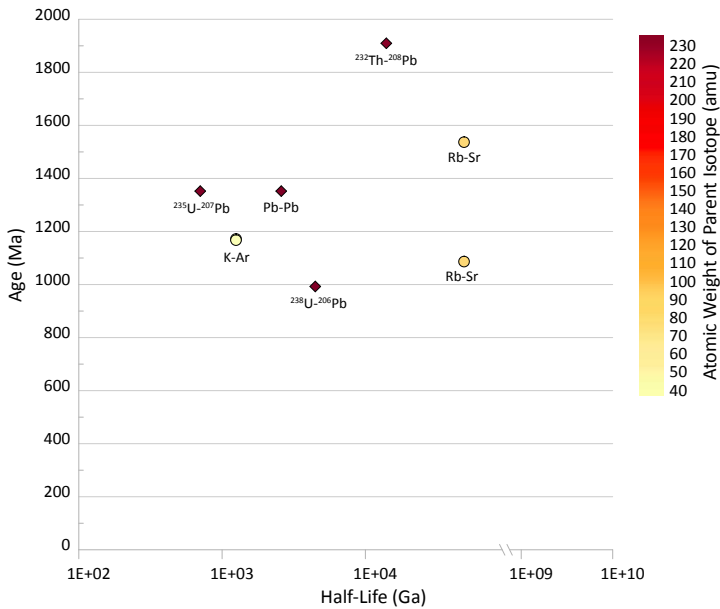
Granite from Dickinson Co., MI
Concordance Score = 0.36

Record Number #1694, Age vs Half-Life
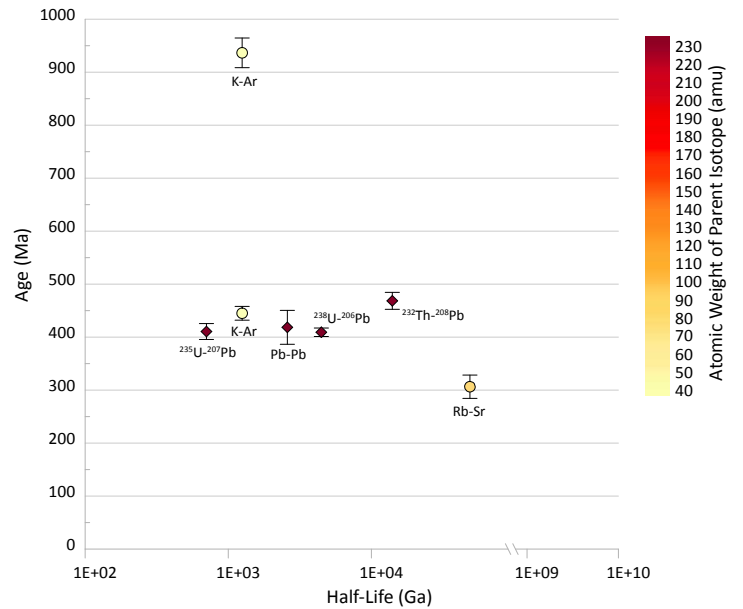
Granite from Norfolk Co., MA
Concordance Score = 0.24

Record Number #1708, Age vs Half-Life
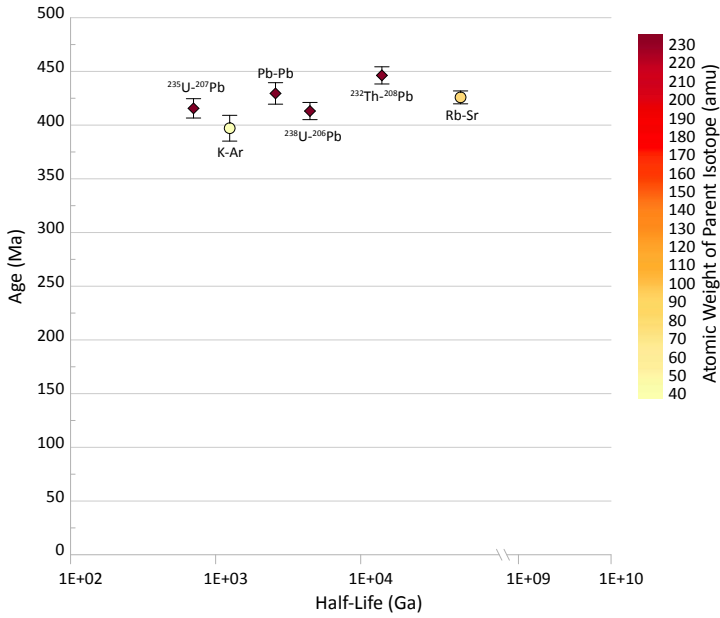
Granite from Essex Co., MA
Concordance Score = 0.60

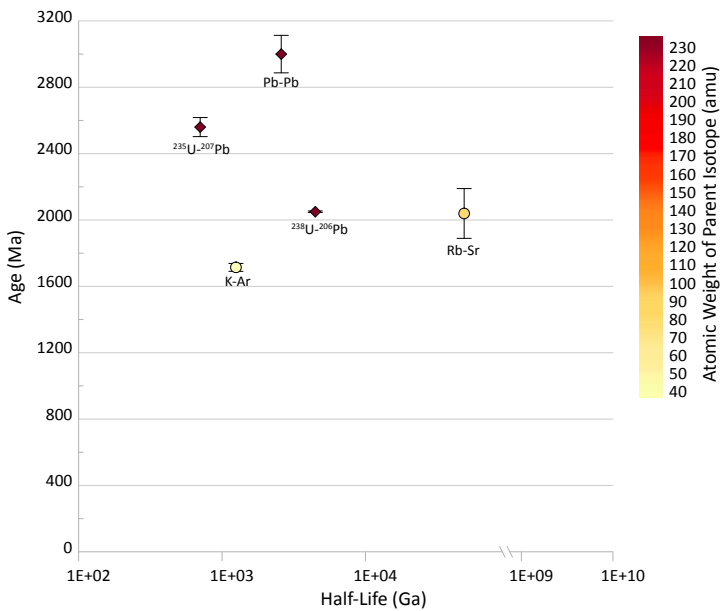Record Number #1724, Age vs Half-Life
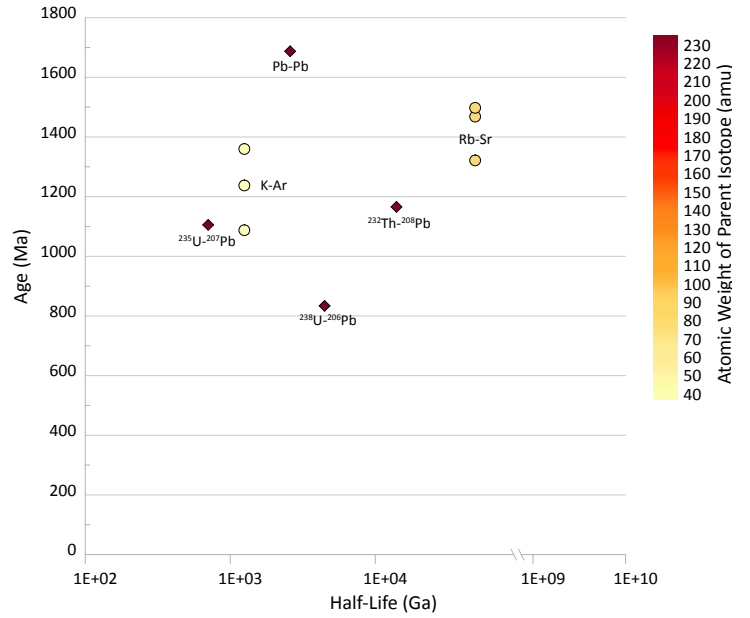
Granite from Marinnete Co., WI
Concordance Score = 0.49

Record Number #1714, Age vs Half-Life
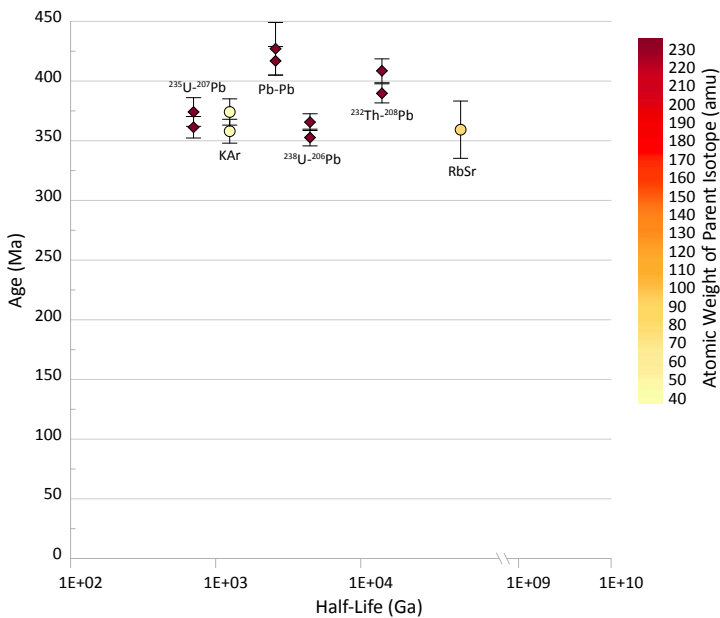
Granite from Essex Co., MA
Concordance Score = 0.45

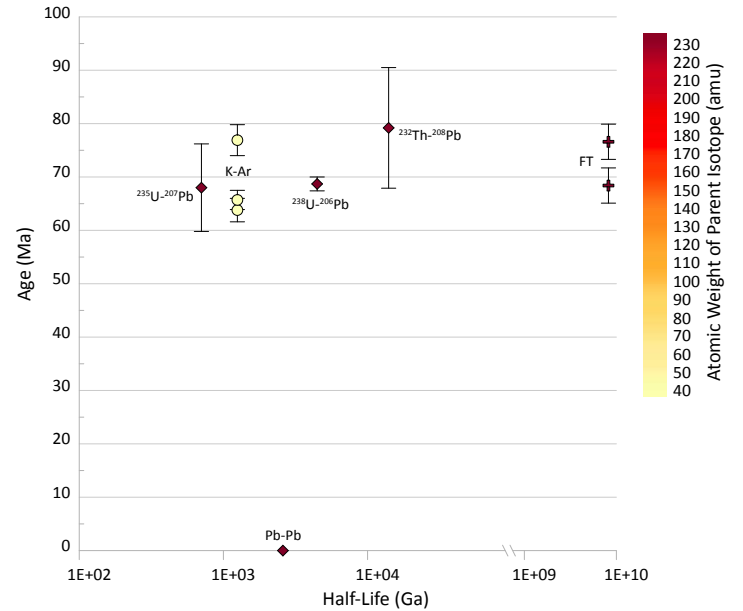Record Number #1725, Age vs Half-Life
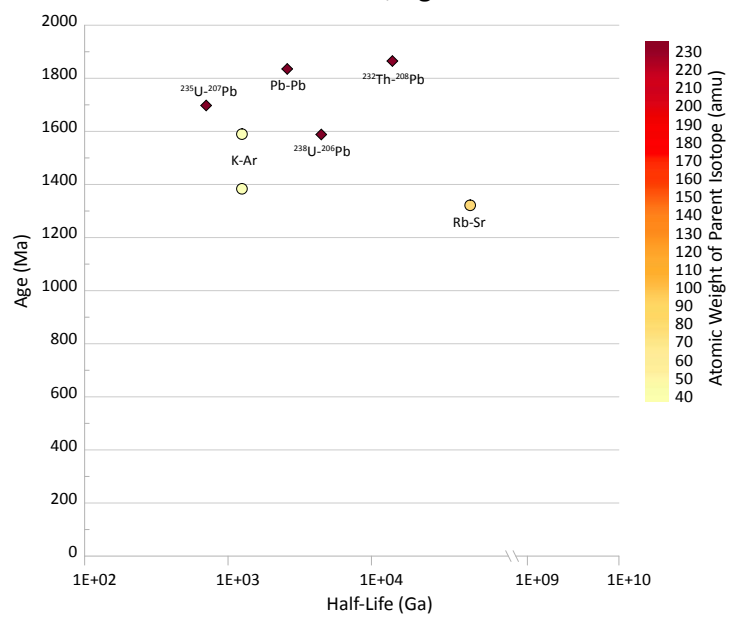
Quartz diorite from Marinnete Co., WI
Concordance Score = 0.71

Record Number #4469, Age vs Half-Life

Granodiorite from Pima Co., AZ
Concordance Score = 0.50

Record Number #5489, Age vs Half-Life
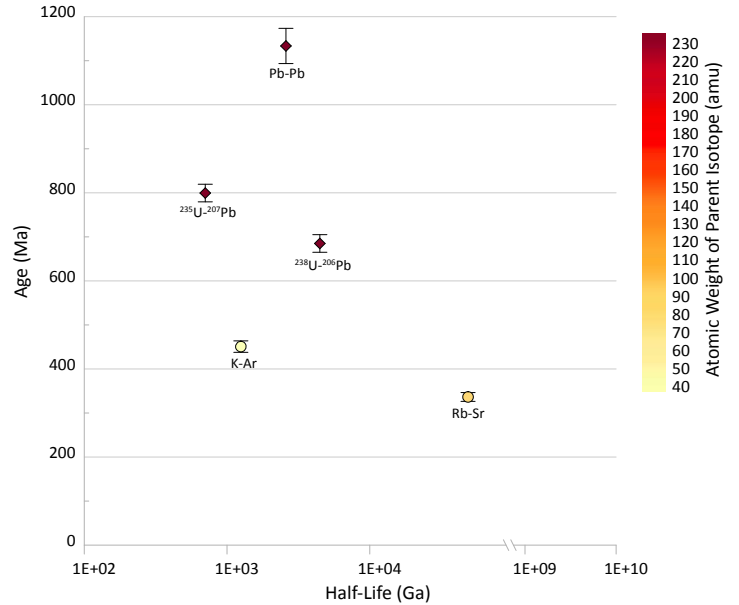
Schist from Westchester Co., NY
Concordance Score = 0.00

Record Number #5051, Age vs Half-Life

Quartz monzonite from Custer Co., ID
Concordance Score = 0.20

Record Number #5683, Age vs Half-Life

Gneiss from Yancey Co., NC
Concordance Score = 0.47

Record Number #6555, Age vs Half-Life
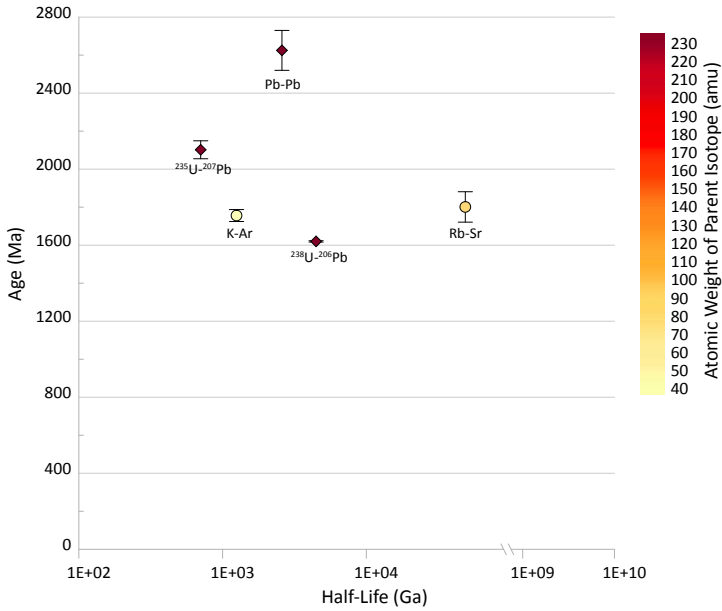
Schist from Park Co., MT
Concordance Score = 0.10

Record Number #6559, Age vs Half-Life
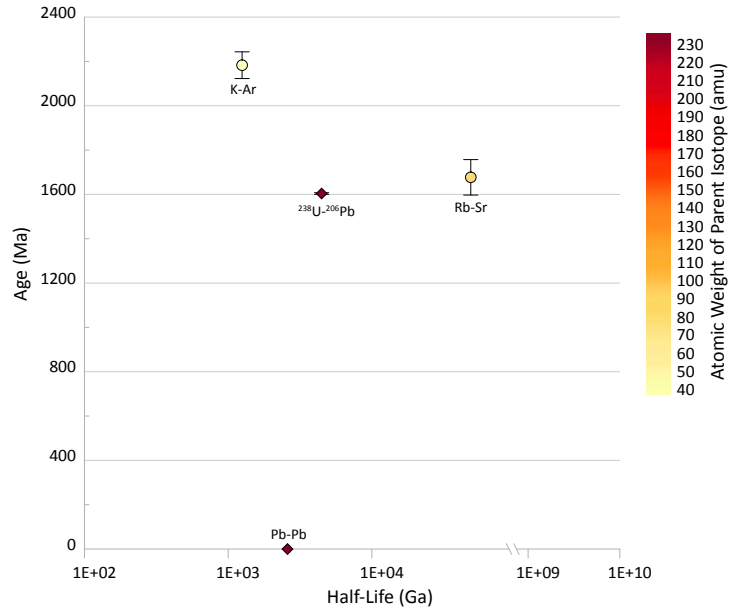
Gneiss from Park Co., MT
Concordance Score = 0.17

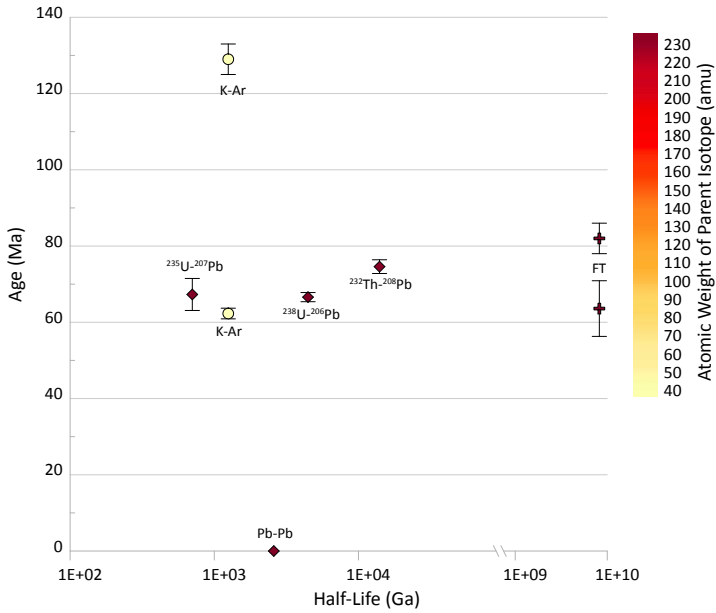### Record Number #6557, Age vs Half-Life

Gneiss from Park Co., MT
Concordance Score = 0.10

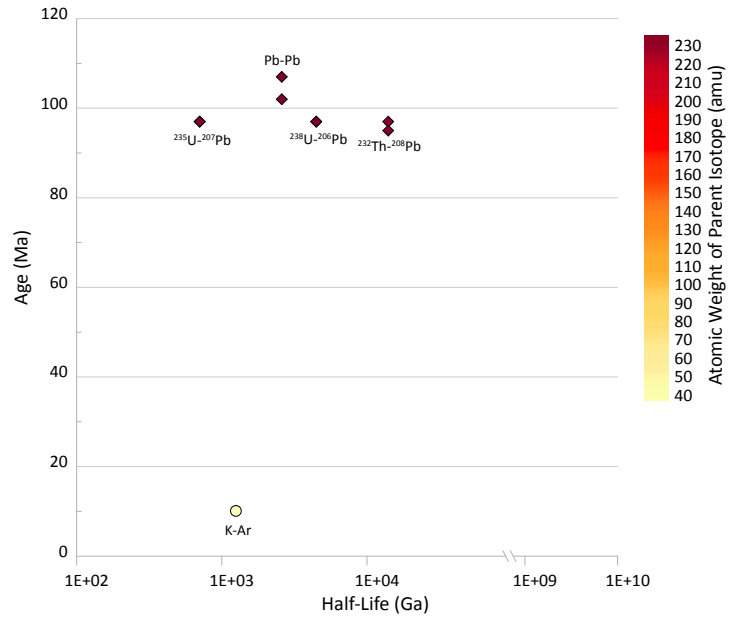### Record Number #9177, Age vs Half-Life

Quartz Monzonite from Fergus Co., MT
Concordance Score = 0.47

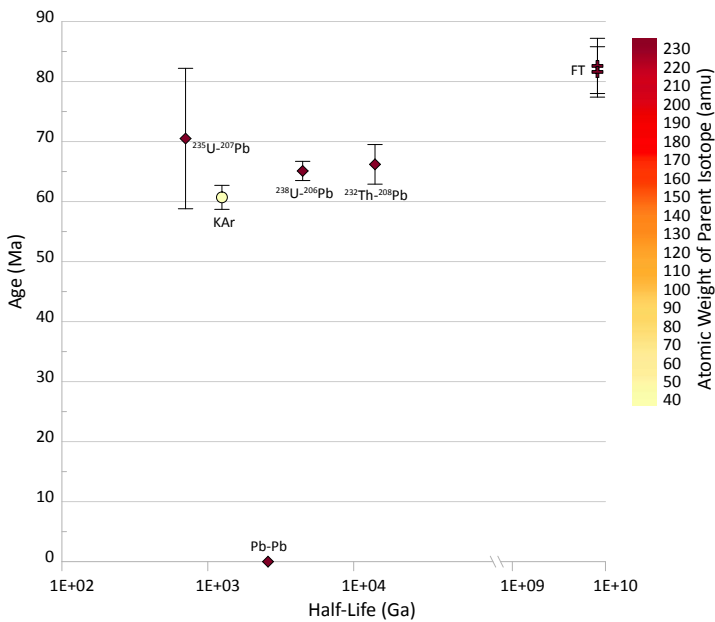### Record Number #9178, Age vs Half-Life

Monzonite from Fergus Co., MT
Concordance Score = 0.18

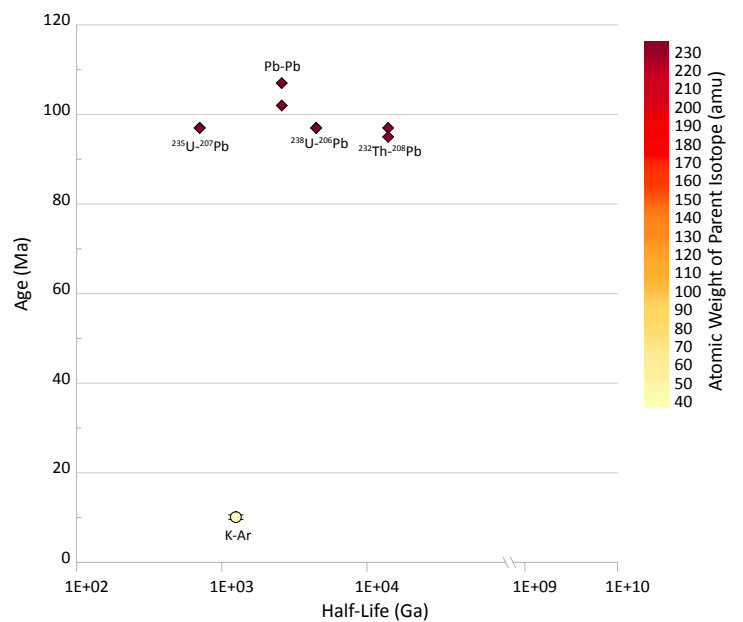### Record Number #14949, Age vs Half-Life

Granite from San Bernardino Co., CA
Concordance Score = 0.36
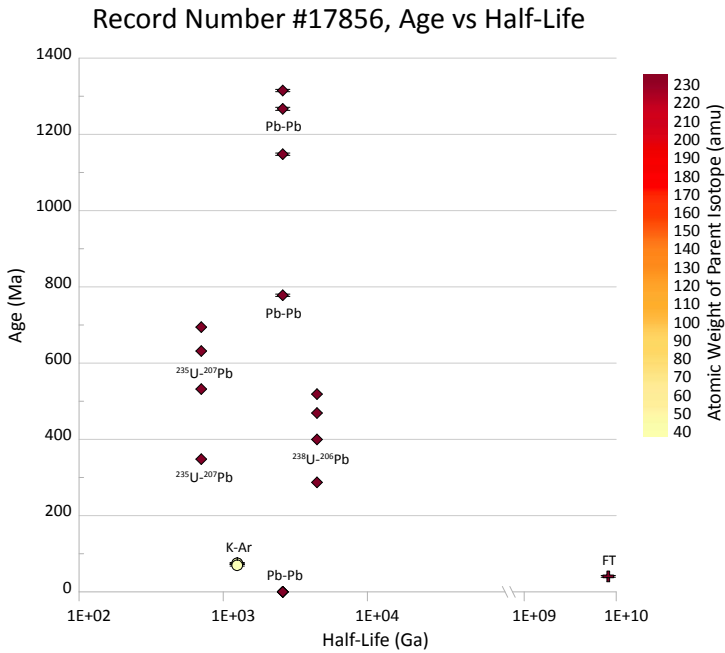
Record Number #9180, Age vs Half-Life

Syenite from Fergus Co., MT
Concordance Score = 0.33

Record Number #14969, Age vs Half-Life

Quartz Monzonite from San Bernardino Co., CA
Concordance Score = 1.00

Record Number #17856, Age vs Half-Life

Megaporphyry from San Bernardino Co., CA
Concordance Score = 0.08

Record Number #17857, Age vs Half-Life

Megaporphyry from Los Angeles Co., CA
Concordance Score = 0.11