**Abstract** The Kolmogorov–Smirnov (KS) test is a nonparametric statistical test used to test for differences between univariate probability distributions. The versatility of the KS test has made it a cornerstone of statistical analysis across many scientific disciplines. However, the test proposed by Kolmogorov and Smirnov does not easily extend to multidimensional distributions. Here we present the `fasano.franceschini.test` package, an R implementation of a multidimensional two-sample KS test described by Fasano and Franceschini (1987). The `fasano.franceschini.test` package provides a test that is computationally efficient, applicable to data of any dimension and type (continuous, discrete, or mixed), and that performs competitively with similar R packages.

**Introduction**

The Kolmogorov–Smirnov (KS) test is a nonparametric, univariate statistical test designed to assess whether a sample of data is consistent with a given probability distribution (or, in the two-sample case, whether the two samples came from the same underlying distribution). First described by Kolmogorov and Smirnov in a series of papers (Kolmogorov, 1933a; Smirnov, 1936, 1937, 1939, 1944, 1948), the KS test is a popular goodness-of-fit test that has found use across a wide variety of scientific disciplines (e.g., Atasoy et al., 2017; Chiang et al., 2018; Hahne et al., 2018; Wong and Collins, 2020; Kaczanowska et al., 2021).

Due to its popularity, several multivariate extensions of the KS test have been described in literature. Justel et al. (1997) proposed a multivariate test based on Rosenblatt’s transformation, which reduces to the KS test in the univariate case. While the test statistic is distribution-free, it is difficult to compute in more than two dimensions, and an approximate test with reduced power must be used instead. Furthermore, the test is only applicable in the one-sample case. Heuchenne and Mordant (2022) proposed to use the Hilbert space-filling curve to define an ordering in $\mathbb{R}^2$. The preimage of both samples is computed under the space-filling curve map, and the two-sample KS test is performed on the preimages. While it is theoretically possible to extend this approach to higher dimensions, the authors note that this would be computationally challenging and leave it as an open problem. Naaman (2021) derived a multivariate extension of the DKW inequality and used it to provide estimates of the tail properties of the asymptotic distribution of the KS test statistic in multiple dimensions. While an important theoretical result, practical usage is limited absent a method for computing exact $p$-values.

Peacock (1983) proposed a test which addresses the fact that there are multiple ways to order points in higher dimensions, and thus multiple ways of defining a cumulative distribution function. In one dimension, probability density can be integrated from left to right, resulting in the canonical CDF $P(X < x)$; or from right to left, resulting in the survival function $P(X > x)$. However, since $P(X < x) = 1 - P(X > x)$ (for continuous random variables), the KS test statistic is independent of this choice. In two dimensions, there are four ways of ordering points, and thus four possible cumulative distribution functions: $P(X < x, Y < y)$, $P(X > x, Y < y)$, $P(X < x, Y > y)$, and $P(X > x, Y > y)$. Since any three are independent, the KS test statistic will depend on which is used. To address this, Peacock (1983) proposed to compute a KS statistic using each possible cumulative distribution function, and to take the test statistic to be the maximum of those.

Peacock (1983) suggested that for a sample $\{(X_i, Y_i) : 1 \leq i \leq n\}$, each KS statistic be maximized over the set of all coordinate-wise combinations $\{(X_i, Y_j) : 1 \leq i, j \leq n\}$. The complexity of computing Peacock’s test statistic thus scales cubically with sample size, which is expensive and can become intractable for large sample sizes. Fasano and Franceschini (1987) proposed a simple change to Peacock’s test: instead of maximizing each KS statistic over all coordinate-wise combinations of points in the sample, they are maximized over just the points in the sample itself. This slight change greatly reduces the computational complexity of the test while maintaining a similar power across a variety of alternatives (Fasano and Franceschini, 1987; Lopes et al., 2007).

In this article we present the `fasano.franceschini.test` package, an R implementation of the two-sample Fasano–Franceschini test. Our implementation can be applied to continuous, discrete, or mixed datasets of any size and of any dimension. We first introduce the test by detailing how the test statistic is computed, how we compute it efficiently, and how we compute $p$-values. We then describe the package structure and provide several basic examples illustrating its usage. We conclude...
by comparing our package to three other CRAN packages implementing multivariate two-sample goodness-of-fit tests.

**Fasano–Franceschini test**

**Two-sample test statistic**

Let

\[ S_1 = \{X_1, \ldots, X_{n_1}\}, \quad S_2 = \{Y_1, \ldots, Y_{n_2}\} \]

be samples of i.i.d. \(d\)-dimensional random vectors drawn from unknown distributions \(F_1\) and \(F_2\), respectively. The two-sample Fasano–Franceschini test evaluates the null hypothesis

\[ H_0 : F_1 = F_2 \]

against the alternative

\[ H_1 : F_1 \neq F_2. \]

In their original paper, Fasano and Franceschini (1987) only considered two- and three-dimensional random vectors, although their test naturally extends to arbitrary dimensions as follows.

For a given point \(x \in \mathbb{R}^d\), we define the \(i\)th open orthant with origin \(x\) as

\[ O_i(x) = \left\{ x' \in \mathbb{R}^d \mid e_{ij}(x_j - x'_j) > 0, \; j = 1, \ldots, d \right\} \]

where \(e_i \in \{-1, 1\}^d\) is a length \(d\) combination of \(\pm 1\). For example, in two dimensions, the four combinations \(e_1 = (1, 1), e_2 = (-1, 1), e_3 = (-1, -1),\) and \(e_4 = (1, -1)\) correspond to quadrants one through four in the plane, respectively. In general there are \(2^d\) such combinations, corresponding to the \(2^d\) orthants that divide \(\mathbb{R}^d\).

Using the indicator function

\[ I_j(x \mid p) = \begin{cases} 1, & x \in O_j(y) \\ 0, & x \notin O_j(y) \end{cases} \]

we define the distance

\[ D(p) = \max_{1 \leq i \leq 2^d} \left\{ \frac{1}{n_1} \sum_{k=1}^{n_1} I_j(X_k \mid p) - \frac{1}{n_2} \sum_{k=1}^{n_2} I_j(Y_k \mid p) \right\}, \quad (1) \]

This is similar to the distance used in the two-sample KS test, but takes into account all possible ways of ordering points in \(\mathbb{R}^d\). Note that this distance does not depend on the enumeration of the orthants. The distance is then maximized over each sample separately, leading to the difference statistics

\[ D_1 = \max_{1 \leq i \leq n_1} D(X_i) \]

and

\[ D_2 = \max_{1 \leq i \leq n_2} D(Y_i). \]

The two-sample Fasano–Franceschini test statistic is then defined as the average of the difference statistics scaled by the sample sizes:

\[ D = \sqrt{\frac{n_1 n_2}{n_1 + n_2} \left( \frac{D_1 + D_2}{2} \right)}, \quad (2) \]

**Computational complexity**

The bulk of the time required to compute the two-sample Fasano–Franceschini test statistic (Eq. 2) is spent evaluating sums of the form

\[ \sum_{x \in S} I_j(x \mid y), \]

which count the number of points in a set \(S\) that lie in a given \(d\)-dimensional region. The simplest approach to computing such sums is brute force, where every point \(x \in S\) is checked independently. The orthant a point lies in can be determined using \(d\) binary checks, resulting in a time complexity of \(O(N^2)\) (where \(N = \max(n_1, n_2)\)) to evaluate Eq. (2) for fixed \(d\).

Alternatively, we can consider each sum as a single query rather than a sequence of independent
**Figure 1:** Illustration of the computation of the difference statistic $D_1$ in two dimensions. Each point in the first sample is used to divide the plane into four quadrants, and both samples are cumulated in each of the four quadrants. The fraction of each sample in each quadrant is shown in the corresponding plot corner, and the maximum difference over all four quadrants is shown above each plot. $D_1$ is taken as the maximum of these differences. To compute the Fasano–Franceschini test statistic, the same procedure would need to be repeated, but using points in the second sample to divide the plane instead.

The $D_1$ statistic is defined as:

$$D_1 = \max_i D(X_i) = 0.5$$

where $D(X_i)$ represents the maximum difference in the $i$-th quadrant. This statistic is then used to test for differences between two samples.

Specifically, both sums in Eq. (1) are orthogonal range counting queries, which ask how many points in a set $S \subseteq \mathbb{R}^d$ lie in an axis-aligned box $(x_1, x_1') \times \cdots \times (x_d, x_d')$. Range counting is an important problem in the field of computational geometry, and as such a variety of data structures have been described to provide efficient solutions (de Berg et al., 2008). One solution, first introduced by Bentley (1979), is a multi-layer binary search tree termed a range tree. Other slightly more efficient data structures have been proposed for range counting, but range trees are well suited for our purposes, particularly because their construction scales easily to arbitrary dimensions (Bentley, 1979; de Berg et al., 2008).

A range tree can be constructed on a set of $n$ points in $d$-dimensional space using $O(n \log^{d-1} n)$ space in $O(n \log^{d-1} n)$ time. The number of points that lie in an axis-aligned box can be reported in $O(\log^d n)$ time, and this time can be further reduced to $O(\log^{d-1} n)$ (when $d > 1$) using fractional cascading (de Berg et al., 2008). To compute the two-sample Fasano–Franceschini test statistic, we construct one range tree for each of the two samples, and then query each tree $2^d$ times. Thus the total time complexity to compute the test statistic using range trees for fixed $d$ is $O(N \log^{d-1} N)$, where again $N = \max(n_1, n_2)$.

As the range tree method has a better asymptotic time complexity than the brute force method, we expect it to perform better for larger sample sizes. However, for smaller sample sizes, the cost of building the range trees can outweigh the benefit gained by more efficient querying. For each dimension, we sought to determine the sample size $N^*$ at which the range tree method becomes more efficient than the brute force method (Figure 2). For $d = 2$, $N^* \approx 25$; for $d = 3$, $N^* \approx 200$; for $d = 4, 5$, and presumably all higher dimensions, $N^* > 5000$. As goodness-of-fit tests are generally applied to samples of much smaller sizes than this, we stopped benchmarking here.

Based on these benchmarking results, our package automatically selects which of the two methods is likely faster based on the dimension and samples sizes of the supplied data. However, as we used equal sample sizes during benchmarking, and since computation time can vary depending on the geometry of the samples, the selected method may not actually be fastest. If users are interested in performing benchmarking for their specific dataset, the argument `nPermute` can be set equal to 0, which bypasses the permutation test and only computes the test statistic.

### Significance testing

To the best of our knowledge, no results have been published concerning the distribution of the Fasano–Franceschini test statistic. Any analysis would likely be complicated by the fact that, unlike the KS test statistic, the Fasano–Franceschini test statistic is not distribution free (Fasano and Franceschini, 1987). In their original paper, Fasano and Franceschini (1987) did not attempt any analytical analysis.
and instead performed Monte Carlo simulations to estimate critical values of their test statistic for various two- and three-dimensional distributions. By fitting a curve to their results, Press et al. (2007) proposed an explicit formula for \( p \)-values in the two-dimensional case. However, this formula is only approximate, and its accuracy degrades as sample sizes decrease or the true \( p \)-value becomes large (greater than 0.2). While this will still allow a simple rejection decision at any common significance level, it is sometimes useful to quantify large \( p \)-values more exactly (such as if one was to do a cross-study concordance analysis comparing \( p \)-values between studies as in Ness-Cohn et al. (2020)). Effort could be made to improve this approximation, however it is still only valid in two dimensions, and thus an alternative method would be needed in higher dimensions.

To allow the fasano.franceschini.test package to be applicable to as broad a class of problems as possible, we compute \( p \)-values using a permutation test. Under the null hypothesis, the two samples were drawn from the same underlying distribution, and a permutation test leverages this to compute the null distribution of the test statistic. Permutation tests are distribution free, and can be applied to continuous, discrete, or mixed data of any dimension. The test procedure is as follows:

1. Compute the test statistic \( D \) for the original samples \( S_1 \) and \( S_2 \).
2. Pool the two samples, and label each element according to which sample it belongs to.
3. Permute the labels, and split the pooled sample into two new samples \( S_1' \) and \( S_2' \) according to the new labels.
4. Compute the test statistic \( D_i \) for \( S_1' \) and \( S_2' \).
5. Repeat steps (3-4) for every permutation of the labels.
6. The \( p \)-value is fraction of test statistics \( D_i \) at least as large as \( D \).

However, as the sample sizes increase to even modest values, the total number of permutations of the labels increases rapidly, and it quickly becomes computationally infeasible to compute the test statistic for every permutation. Thus instead of considering all permutations, we select a fixed number of permutations \( M \) with replacement and compute a Monte Carlo approximation of the \( p \)-value, given by

\[
\hat{p} = \frac{1 + \sum_{i=1}^{M} I(D_i \geq D)}{1 + M}
\]
where
\[
I(x \geq y) = \begin{cases} 
1, & x \geq y \\
0, & x < y.
\end{cases}
\]

If permutations are selected without replacement, this estimator is exact. However, if permutations are selected with replacement, this estimator is slightly more conservative than the exact estimator (Phipson and Smyth, 2010). Unless sample sizes are small, the loss of power will be minimal as the likelihood of selecting the same permutation multiple times will be negligible.

We select permutations with replacement primarily to circumvent the computationally expensive step of ensuring that repeated permutations are not selected. An additional benefit is that we are easily able compute a confidence interval for the true permutation \( p \)-value, as the number of test statistics for permuted samples at least as large as \( D \) is distributed binomially with a probability of success equal to the true permutation test \( p \)-value (Good, 2005). We compute the confidence interval using the \texttt{binom.test} function from the \texttt{stats} package, which computes an exact binomial confidence interval as given in Clopper and Pearson (1934).

**Package overview**

The \texttt{fasano.franceschini.test} package is written primarily in C++, and interfaces with R using \texttt{Rcpp} (Eddelbuettel et al., 2022). The permutation test is parallelized using \texttt{RcppParallel} (Allaire et al., 2022). The package consists of one function, \texttt{fasano.franceschini.test}, for performing the two-sample Fasano–Franceschini test. The arguments of this function are described below.

- \texttt{S1} and \texttt{S2}: the two samples to compare. Both should be either numeric \texttt{matrix} or \texttt{data.frame} objects with the same number of columns.
- \texttt{nPermute}: the number of permuted samples to generate when estimating the permutation test \( p \)-value. The default is 100. If set equal to 0, the permutation test is bypassed and only the test statistic is computed.
- \texttt{threads}: the number of threads to use when performing the permutation test. The default is one thread. This parameter can also be set to "auto", which uses the value returned by \texttt{RcppParallel::defaultNumThreads()}.
- \texttt{seed}: an optional seed for the pseudorandom number generator (PRNG) used during the permutation test.
- \texttt{p.conf.level}: the confidence level for the confidence interval of the permutation test \( p \)-value. The default is 0.95.
- \texttt{verbose}: whether to display a progress bar while performing the permutation test. The default is \texttt{TRUE}. This functionality is only available when \texttt{threads} = 1.
- \texttt{method}: an optional character indicating which method to use to compute the test statistic. The two methods are ‘\texttt{Var}’ (range tree) and ‘\texttt{b}’ (brute force). Both methods return the same results but may vary in computation speed. If this argument is not passed, the sample sizes and dimension of the data are used to infer which method is likely faster.

The output is an object of the class \texttt{htest}, and consists of the following components:

- \texttt{statistic}: the value of the test statistic \( D \).
- \texttt{estimate}: the value of the difference statistics \( D_1 \) and \( D_2 \).
- \texttt{p.value}: a Monte-Carlo approximation of the permutation test \( p \)-value.
- \texttt{conf.int}: a binomial confidence interval for the permutation test \( p \)-value.
- \texttt{method}: the name of the test (i.e. 'Fasano-Franceschini Test').
- \texttt{data.name}: the names of the original data objects.

**Examples**

Here we demonstrate the basic usage and features of the \texttt{fasano.franceschini.test} package. We begin by loading the necessary libraries and setting a seed for reproducibility.

```r
> library(fasano.franceschini.test)
> library(MASS)
> set.seed(1)
```
Note that to produce reproducible results, we need to set two seeds: the set.seed function sets the seed in R, ensuring we draw reproducible samples; and the seed passed as an argument to the fasano.franceschini.test function sets the seed for the C++ PRNG, ensuring we compute reproducible $p$-value estimates.

As a first example, we draw two samples from a bivariate standard normal distribution. The Fasano–Franceschini test fails to reject the null hypothesis — that the samples were drawn from the same distribution — at an $\alpha = 0.05$ significance level.

```r
> S1 <- mvrnorm(n = 100, mu = c(0,0), Sigma = diag(2))
> S2 <- mvrnorm(n = 150, mu = c(0,0), Sigma = diag(2))
> fasano.franceschini.test(S1, S2, seed = 2, verbose = FALSE)
Fasano-Franceschini Test
data: S1 and S2
D = 0.85206, p-value = 0.8416
95 percent confidence interval:
 0.7555271 0.9066534
sample estimates:
  D1  D2
0.11 0.11
```

We next draw two samples from bivariate normal distributions with identical covariance matrices but different locations. The Fasano–Franceschini test rejects the null hypothesis at an $\alpha = 0.05$ significance level.

```r
> S3 <- mvrnorm(n = 225, mu = c(0,0), Sigma = diag(2))
> S4 <- mvrnorm(n = 152, mu = c(0.2,0.2), Sigma = diag(2))
> fasano.franceschini.test(S3, S4, seed = 3, verbose = FALSE)
Fasano-Franceschini Test
data: S3 and S4
D = 2.0212, p-value = 0.009901
95 percent confidence interval:
 0.00025064 0.05393235
sample estimates:
  D1  D2
0.2109649 0.2134503
```

However, we note that $\alpha = 0.05$ is contained in the $p$-value confidence interval. To be careful, we rerun the test with 200 permutations instead of the default 100, in which case both the $p$-value estimate and the right endpoint of its confidence interval are strictly less than $\alpha = 0.05$.

```r
> fasano.franceschini.test(S3, S4, nPermute = 200, seed = 3, verbose = FALSE)
Fasano-Franceschini Test
data: S3 and S4
D = 2.0212, p-value = 0.004975
95 percent confidence interval:
 0.0001259513 0.0274064298
sample estimates:
  D1  D2
0.2109649 0.2134503
```

### Comparison with other R packages

In this section, we compare the fasano.franceschini.test package with three other CRAN packages that perform multivariate two-sample goodness-of-fit tests.
We denote the $d$-dimensional distribution with standard normal marginals joined by a Clayton copula with parameter $\rho$. Both distributions are sampled from using the \texttt{MASS} package (Ripley, 2021). The $d$-dimensional normal distribution with mean $\mu \in \mathbb{R}^d$ and covariance matrix $\Sigma \in \mathbb{R}^{d \times d}$ by $N_d(\mu, \Sigma)$, and sample from it using the \texttt{MASS} package (Ripley, 2021). The $d \times d$ identity matrix, which is sometimes used as a covariance matrix, is denoted as $I_d$. For copula alternatives, we consider the Gaussian copula with correlation matrix

$$[P(\rho)]_{ij} = \begin{cases} \rho, & i \neq j \\ 1, & i = j \end{cases}$$

and the Clayton copula with parameter $\theta \in [-1, \infty) \setminus \{0\}$. We denote the $d$-dimensional distribution with standard normal marginals joined by a Gaussian copula with correlation matrix $P(\rho)$ by $G_d(\rho)$. We denote the $d$-dimensional distribution with standard normal marginals joined by a Clayton copula with parameter $\theta$ by $C_d(\theta)$. Both distributions are sampled from using the \texttt{copula} package (Hofert et al., 2022). For all power analyses performed, power was approximated using 1000 replications, a significance level of $\alpha = 0.05$ was used, all samples were of size 50, and all R functions implementing tests were called using their default arguments.

We first examined the power of the tests on various bivariate alternatives. All three tests had similar power across location alternatives, although the Cramér and DiProPerm tests did tend to slightly outperform the Fasano–Franceschini test. Across dispersion alternatives, the Cramér and Fasano–Franceschini tests had very similar powers. On both copula alternatives, the Fasano–Franceschini test had a consistently higher power than the Cramér test. The DiProPerm test was unable to achieve a
**Figure 3:** Visualization of the distributions used in power analyses. Each plot shows two samples consisting of 10000 points each. The first sample $S_1$ is shown in blue, and the second sample $S_2$ is shown in red. (a) $S_1 \sim N_2(0, I_2)$ and $S_2 \sim N_2(0.4, I_2)$. (b) $S_1 \sim N_2(0, I_2)$ and $S_2 \sim N_2(0, I_2 + 1.5)$. (c) $S_1 \sim G_2(0)$ and $S_2 \sim G_d(0.6)$. (d) $S_1 \sim C_2(1)$ and $S_2 \sim C_2(8)$.

**Figure 4:** Comparison of power of the Fasano–Franceschini, Cramér, and DiProPerm tests on various bivariate alternatives. (a) Location alternatives, with $S_1 \sim N_2(0, I_2)$ and $S_2 \sim N_2(\mu, I_2)$. (b) Dispersion alternatives, with $S_1 \sim N_2(0, I_2)$ and $S_2 \sim N_2(0, I_2 + \epsilon)$. (c) Gaussian copula alternatives, with $S_1 \sim G_2(0)$ and $S_2 \sim G_2(\rho)$. (d) Clayton copula alternatives, with $S_1 \sim C_2(1)$ and $S_2 \sim C_2(\theta)$. 
power above the significance level of $\alpha = 0.05$ on any of the dispersion or copula alternatives. This is likely due to the fact that in these instances, there is significant overlap between the high density regions of the two distributions, making it difficult to find a separating hyperplane between samples drawn from them.

Figure 5: Comparison of power of the Fasano–Franceschini, Cramér, and DiProPerm tests on fixed alternatives as the dimension of the data increases. (a) Location alternative, with $S_1 \sim N_d(0, I_d)$ and $S_2 \sim N_d(0.4, I_d)$. (b) Dispersion alternative, with $S_1 \sim N_d(0, I_d)$ and $S_2 \sim N_d(0, I_d + 1.5)$. (c) Gaussian copula alternative, with $S_1 \sim G_d(0)$ and $S_2 \sim G_d(0.6)$. (d) Clayton copula alternative, with $S_1 \sim C_d(1)$ and $S_2 \sim C_d(8)$.

We next examined how the power of the three tests varied when the two sampling distributions were kept fixed but the dimension of the data increased. On the location alternative, the power of the Cramér and DiProPerm tests was quite similar, monotonically increasing to one as dimension increased. The power of the Fasano–Franceschini increased until $d = 5$ and then monotonically decreased to $\alpha = 0.05$ by $d = 20$. We see similar results for the Cramér and Fasano–Franceschini tests on the dispersion alternative. On copula alternatives, both the Cramér and Fasano–Franceschini tests have monotonically increasing power as dimension is increased. However, whereas the Fasano–Franceschini test is able to achieve a power of nearly one near $d = 10$ on both alternatives, the Cramér test’s power grows at a much slower rate. The DiProPerm test is still unable to attain a power above $\alpha = 0.05$ on the dispersion alternatives or either of the copula alternatives.

Overall, the Cramér and DiProPerm tests perform better than the Fasano–Franceschini test on location alternatives, especially as dimension increases. On dispersion alternatives, the Fasano–Franceschini and Cramér tests have comparable performance for low dimensions, but the Cramér test maintains a higher power for high dimensions. However, in these cases the marginal distributions differ, and thus a multivariate test is not strictly necessary as univariate tests could be applied to the marginals independently (with a multiple testing correction) to detect the difference between the multivariate distributions. On copula alternatives, where a multivariate test is required, the Fasano–Franceschini test consistently outperformed both the Cramér and DiProPerm tests.

Summary

This paper introduces the fasano.franceschini.test package, an R implementation of the multidimensional two-sample goodness-of-fit test described by Fasano and Franceschini (1987). We provide users with a computationally efficient test that is applicable to data of any dimension and of any type (continuous, discrete, or mixed), and that demonstrates competitive performance with similar R packages. Complete package documentation and source code are available via the Comprehensive R Archive Network.
Network (CRAN) at https://cran.r-project.org/web/packages/fasano.franceschini.test and the package website at https://nesscoder.github.io/fasano.franceschini.test.

Computational details

The results in this paper were obtained using R 4.1.1 with the packages fasano.franceschini.test 2.1.1, diproperm 0.2.0, cramer 0.9-3, MASS 7.3-54, and copula 1.1-0. All computations were done using the Quest high performance computing facility at Northwestern University. R itself and all package dependencies are available from CRAN at https://cran.r-project.org.

Acknowledgments

This research was supported in part through the computational resources and staff contributions provided for the Quest high performance computing facility at Northwestern University which is jointly supported by the Office of the Provost, the Office for Research, and Northwestern University Information Technology.

Funding for this work was provided by the Simons Foundation/SFARI (597491-RWC01), the National Science Foundation (1764421-01), and the National Institute of Health/National Institute of Aging (1R01AG068579-01).

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