

An Exact Nonparametric Method for Inferring Mosaic Structure in Sequence Triplets

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ABSTRACT

Statistical tests for detecting mosaic structure or recombination among nucleotide sequences usually rely on identifying a pattern or a signal that would be unlikely to appear under clonal reproduction. Dozens of such tests have been described, but many are hampered by long running times, confounding of selection and recombination, and/or inability to isolate the mosaic-producing event. We introduce a test that is exact, nonparametric, rapidly computable, free of the infinite-sites assumption, able to distinguish between recombination and variation in mutation/fixation rates, and able to identify the breakpoints and sequences involved in the mosaic-producing event. Our test considers three sequences at a time: two parent sequences that may have recombined, with one or two breakpoints, to form the third sequence (the child sequence). Excess similarity of the child sequence to a candidate recombinant of the parents is a sign of recombination; we take the maximum value of this excess similarity as our test statistic $\Delta_{m,n,b}$. We present a method for rapidly calculating the distribution of $\Delta_{m,n,b}$ and demonstrate that it has comparable power to and a much improved running time over previous methods, especially in detecting recombination in large data sets.

MOSAIC structure exists in a nucleotide sequence if different segments of the sequence descend from different ancestors. A nucleotide sequence can be a mosaic of other sequences as a result of recombination or gene conversion; mosaic structure in bacterial DNA can also result from transduction, transformation, or conjugation, which are collectively referred to as horizontal gene transfer. The detection of mosaic structure has received much attention over the past two decades as a result of both a proliferation of sequence data and leaps in computing power, which together have allowed for the inference of multiple ancestral contributions to a nucleotide sequence. The biological questions at the source of this recent attention range from interest in the evolution of pathogens (AWADALLA 2003; MOYA *et al.* 2004; WILSON *et al.* 2005) and the characterization of linkage disequilibrium in large genomes (PRITCHARD and PRZEWORSKI 2001; ARDLIE *et al.* 2002; GABRIEL *et al.* 2002) to theoretical questions about clonality and the definitions of clonal and nearly clonal organisms (MAYNARD SMITH *et al.* 1993; HALKETT *et al.* 2005). For reviews on the methods and results in this field, see POSADA *et al.* (2002) and STUMPF and McVEAN (2003).

MAYNARD SMITH (1999) recognized that the continuum between completely clonal and freely recombining organisms naturally gives rise to two distinct problems:

determining whether recombination occurs and measuring its frequency. In this investigation, we focus on the former. Detecting recombination usually involves searching groups of sequences for candidate recombinants or recombination signals and testing whether these represent statistically significant departures from expectation under a null hypothesis of no recombination. Dozens of statistical tests have been developed (STEPHENS 1985; SAWYER 1989; BALDING *et al.* 1992; KARLIN and BRENDEL 1992; MAYNARD SMITH 1992; TAKAHATA 1994; SNEATH 1995; GOSS and LEWONTIN 1996; JAKOBSEN and EASTEAL 1996; GRASSLY and HOLMES 1997; MAYNARD SMITH and SMITH 1998; SNEATH 1998; AWADALLA *et al.* 1999; CRANDALL and TEMPLETON 1999; HOLMES *et al.* 1999; MAYNARD SMITH 1999; WALL 1999; GIBBS *et al.* 2000; MARTIN and RYBICKI 2000; WOROBEY 2001; BRUEN *et al.* 2006) and evaluated (WALL 2000; BROWN *et al.* 2001; POSADA and CRANDALL 2001; WIUF *et al.* 2001; POSADA 2002) in this endeavor, none of which has yet emerged as the single standard test to be used for identifying recombination. In addition to testing for the existence of recombination, certain methods are also able to locate recombination breakpoints and, sometimes, the parent sequences involved in the recombination event, although the latter can be quite difficult. Methods that do not focus on parent sequences and breakpoints usually rely on detecting a recombination signal—for example, a phylogenetic incongruence or an excess of homoplasies—but may have trouble isolating the actual recombination event,

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which entails identifying particular parent sequences that recombined at particular breakpoints to form a recombinant offspring sequence.

Some methods (TAKAHATA 1994; ROBERTSON *et al.* 1995; CRANDALL and TEMPLETON 1999; HOLMES *et al.* 1999; GIBBS *et al.* 2000; MARTIN and RYBICKI 2000; MARTIN *et al.* 2005) perform tests on three sequences at a time, which allows them to posit candidate parent sequences and candidate breakpoints. The proposed arrangement is then tested with a likelihood analysis, by visual detection of similarity in different sequence regions, or against a null distribution that would be expected under clonal evolution. The most common among these triplet tests—the Chimaera method (POSADA and CRANDALL 2001; POSADA 2002), which is based on a χ^2 -statistic (MAYNARD SMITH 1992), and the Martin–Rybicki (MR) binomial distribution test (MARTIN and RYBICKI 2000)—identify unusually high levels of sequence similarity inside a predefined window or on either side of a candidate breakpoint. We also take this approach by introducing a simple and intuitive statistic describing how identity varies along a sequence within a sequence triple. Our test statistic $\Delta_{m,n,b}$ is discrete and nonparametric. Describing its distribution, in principle, would require a computing time that grows exponentially with the number of informative sites (a subset of the polymorphisms) in the given sequence triple; to avoid this costly brute-force computation, we introduce a method for computing probabilities and *P*-values in polynomial time. Our method is memory intensive but very fast: computation of exact *P*-values takes seconds on a personal computer when there are <250 informative sites in the proposed sequence triple.

Our triplet test represents an advance over Chimaera and the MR method in that we eliminate the need for a sliding window, use a nonparametric statistic, and introduce a computation scheme that is exact and orders of magnitude faster. In evaluating our method's power to detect recombination in sequence triplets, we find that we always have higher power than the MR method and comparable power to Chimaera. In repeated applications of our triplet test to data sets with more than three sequences, we show that our method is among the most powerful of 16 previously tested methods.

STATISTICAL TESTS

We begin with three homologous sequences of the same length. The relationship among these three sequences is similar in practice to the relationship formulated by CRANDALL and TEMPLETON (1999, pp. 166–167) among networks of sequences. From our three sequences, we designate one as the child sequence and investigate whether it could be a recombinant of the other two sequences, which we call parent sequences. We first present the simple case of a single-breakpoint recombinant but later focus on the more interesting and realistic

case of a double-breakpoint recombinant. Considering our sequence triple, we ask whether one can reject the null hypothesis that the evolutionary history among the three sequences was completely clonal.

We call our parent sequences **p** and **q** and our child sequence **c**. For sequence length *L*, we can represent our three sequences as vectors of nucleotides: **p** = (*p*₁, *p*₂, ..., *p*_{*L*}), **q** = (*q*₁, *q*₂, ..., *q*_{*L*}), and **c** = (*c*₁, *c*₂, ..., *c*_{*L*}). A single-breakpoint recombinant between the parent sequences at position *l* can be denoted

$$(\mathbf{pq})_l = (p_1, \dots, p_l, q_{l+1}, \dots, q_L),$$

with $0 \leq l \leq L$.

Writing $|\mathbf{p} - \mathbf{q}|$ as the number of nucleotide differences between sequences **p** and **q**, we say that the most likely recombination breakpoint *l* minimizes $|\mathbf{pq}_l - \mathbf{c}|$, the number of differences between the observed child sequence and a possible recombinant of the parent sequences. If this candidate recombinant is much closer (than either parent) to the child sequence, then we may have reason to believe that the evolutionary history of sequence **c** is better explained by a recombination or a gene conversion than by strictly clonal reproduction. If the candidate recombinant $(\mathbf{pq})_l$ is only slightly closer than the parents to the child sequence, then the candidate recombinant's additional sequence similarity may simply be an accident of how mutations accumulated on either side of the breakpoint *l*. Assessing whether the locations of the mutations (relative to the breakpoint) are significantly nonrandom is the foundation for the maximum χ^2 -test (MAYNARD SMITH 1992), the Chimaera method (POSADA and CRANDALL 2001; POSADA 2002), the exact test based on the binomial distribution suggested by MARTIN and RYBICKI (2000), and the heuristic test suggested by CRANDALL and TEMPLETON (1999); it is also the focus of our analysis.

We introduce a nonparametric statistic slightly different from the ones above, but one that is more direct at detecting potential mosaics. Let

$$d_{\text{NoRec}} = \min\{|\mathbf{p} - \mathbf{c}|, |\mathbf{q} - \mathbf{c}|\} \quad (1)$$

be the minimum distance from the child to either of the parents, and let

$$d_{\text{Rec},1} = \min_{0 \leq l \leq L} \{ |(\mathbf{pq})_l - \mathbf{c}| \} \quad (2)$$

be the minimum distance from the child to a candidate recombinant of the parents (including the boundary case recombinants, which are just the parents themselves); the subscript "1" indicates that there is just one breakpoint in the recombinant. Then, we define

$$\Delta_1 = d_{\text{NoRec}} - d_{\text{Rec},1}. \quad (3)$$

The quantity Δ_1 describes the difference, between clonal evolution and nonclonal evolution, in the number of mutations needed to describe the evolutionary

history between the child and the closer parent; by nonclonal evolution we mean, here, an evolutionary history that allows for a single recombination event with a single breakpoint. Clearly $\Delta_1 \geq 0$, and even if there had truly been no recombination or gene conversion among the sequences, a particular sequence triple could give the appearance of recombination with a high value of Δ_1 if, by chance, the pattern of mutations was such that the left side of the child sequence appeared to be more closely related to parent **p** and the right side appeared to be closer to parent **q**. The distribution of this recombination signal Δ_1 under the null hypothesis of clonal reproduction can be easily computed (see next section).

The difference in (3) is affected only by informative sites of the sequence triple (**p**, **q**, **c**). For our purposes, we define informative sites as those where the child's nucleotide matches exactly one of the parents' nucleotides. Uninformative sites are sites where (i) all three sequences agree, (ii) all three sequences differ, or (iii) the parents have matching (*i.e.*, identical) nucleotides that differ from the child's. Our definition of informative sites is identical to that used in the Chimaera method and to the sister groups defined by TAKAHATA (1994).

Suppose that there are m informative sites where **p** and **c** match and n informative sites where **q** and **c** match. The quantity Δ_1 in (3) is then more precisely defined as $\Delta_{m,n,1}$. Under the null hypothesis of clonal evolution among sequences **p**, **q**, and **c**, $\Delta_{m,n,1}$ is a random variable that describes the maximum number of mutation events one could "explain away" by recombining **p** with **q** at a single breakpoint.

A two-breakpoint recombinant of sequences **p** and **q** can be described by

$$(\mathbf{pqp})_{ij} = (p_1, \dots, p_i, q_{i+1}, \dots, q_j, p_{j+1}, \dots, p_L),$$

where $i \leq j$. Letting

$$d_{\text{Rec},2} = \min_{0 \leq i \leq j \leq L} \{ |(\mathbf{pqp})_{ij} - \mathbf{c}| \}, \tag{4}$$

we define

$$\Delta_{m,n,2} = d_{\text{NoRec}} - d_{\text{Rec},2}, \tag{5}$$

where m and n are again the numbers of the two types of informative sites.

$\Delta_{m,n,1}$ and $\Delta_{m,n,2}$ are random variables that describe single-breakpoint and double-breakpoint recombination signals, respectively, under the null hypothesis of no recombination. They are discrete random variables with range $0 \leq \Delta_{m,n,b} \leq \min\{m, n\}$, where b is the number of breakpoints. Observed Δ -quantities can be quickly calculated [in $\mathcal{O}(L)$ -time, for any b] from sequence data, and the null hypothesis of clonal evolution can be rejected if they are too high. In the next two sections, we review what is already known about the distribution of $\Delta_{m,n,1}$ and present a method for calculating the distribution of $\Delta_{m,n,2}$.

Single-breakpoint recombinant: Consider a sequence triple (**p**, **q**, **c**) with m informative sites where **p** and **c** match and n informative sites where **q** and **c** match. Moving left to right across the informative sites on the child sequence, we can assign each informative site a letter based on probable ancestry (determined by the parent to which it is identical) and obtain a sequence such as PPPQPPQQQQ, where a P denotes an informative site at which the child sequence and parent **p** share a nucleotide, and Q denotes an informative site at which the child sequence and parent **q** share a nucleotide. Under the null hypothesis of clonal reproduction, the placement of P's and Q's in the sequence should be completely random; *i.e.*, each of the $(m+n)!/(m!n!)$ possibilities has equal probability. In the example sequence above, it appears that the P's cluster toward the left side of the sequence and the Q's to the right side; therefore, this sequence may be a true (statistically significant) recombinant.

This sequence of P's and Q's is most easily visualized as a random walk on a set of axes where P is a step up and Q is a step down. This is not a traditional random walk since the number of up steps is known to be m , the number of down steps is known to be n , and the only randomness is the order in which they appear. After s steps, the height X_s of the random walk is distributed quasi-hypergeometrically [the quantity $(X_s + s)/2$ is distributed hypergeometrically]. The probability of being at height h after s steps, when $|h| \leq s$ and $0 \leq s \leq m+n$, is

$$P(X_s = h) = \binom{m}{\frac{s+h}{2}} \binom{n}{\frac{s-h}{2}} \binom{m+n}{s}^{-1}$$

if $h+s$ is even; $P(X_s = h) = 0$ if $h+s$ is odd. This type of finite stochastic process can be called a hypergeometric random walk (HGRW). HGRWs have been previously analyzed in the probability literature in the form of ballot problems (FELLER 1957), wherein one candidate in an election receives m votes, the second candidate receives n votes, and the order in which the votes are counted is of interest. We denote a hypergeometric random walk with m up steps and n down steps by the random variable $\mathbf{H}_{m,n}$. Given data, we refer to an observed walk diagrammed from the informative sites of a sequence triple; examples of observed walks diagrammed from real data are in Figure 1.

Given our sequence triple with $m+n$ informative sites and allowing only one breakpoint in a putative recombinant, the observed value $\Delta_{m,n,1}$ is related to the maximum height of the walk diagrammed from the informative sites of sequences **p**, **q**, and **c**, by the relation

$$\Delta_{m,n,1} = \max \mathbf{H}_{m,n} + \min\{0, n-m\}.$$

Using results from ballot theory (BARTON and MALLOWS 1965) and gambling problems (WHITWORTH 1901, prop. 39, pp. 116–117), it can be shown that

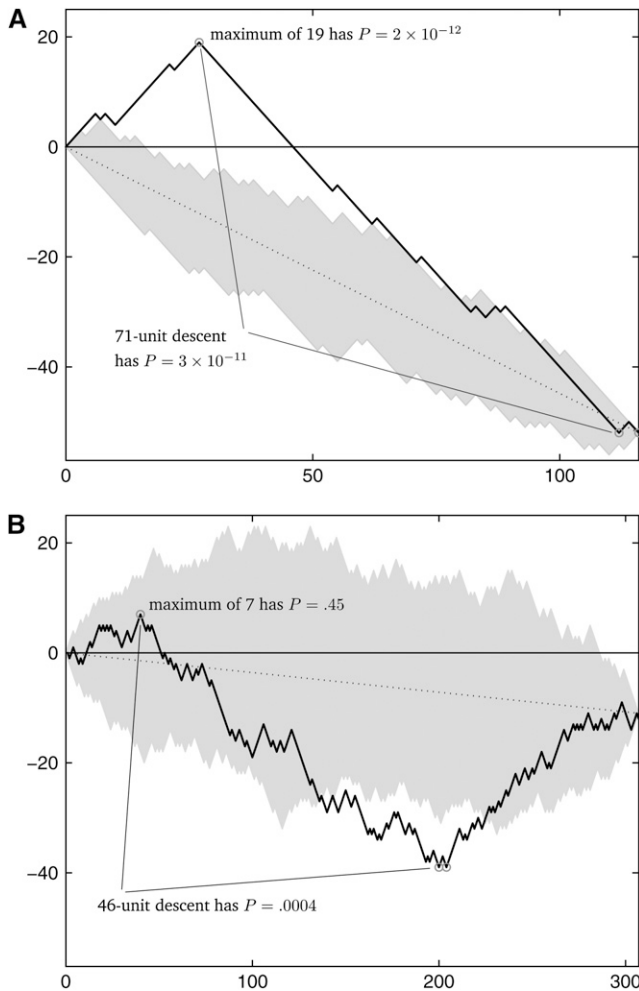


FIGURE 1.—Observed walks diagrammed from the informative sites of sequence triples. (A) The walk is diagrammed from *Neisseria* data (from the fourth row of Table 1). (B) The walk is diagrammed from influenza data (from the first row of Table 2). The circles indicate the beginning and end of the maximum descent in each walk, and in both cases the beginning of the maximum descent is also the maximum height of the walk. The dotted line in each diagram denotes the expected location of the hypergeometric random walk. The shaded areas in each diagram show the range of 100 simulated HGRWs.

$$P(\Delta_{m,n,1} \geq k) = \begin{cases} \binom{m+n}{n+k} / \binom{m+n}{n} & \text{when } m \leq n \\ \binom{m+n}{m+k} / \binom{m+n}{n} & \text{when } m > n \end{cases}, \tag{6}$$

or equivalently that

$$P(\max \mathbf{H}_{m,n} \geq k) = \binom{m+n}{n+k} / \binom{m+n}{n}. \tag{7}$$

From the observed maximum height of the diagrammed walk of the informative sites of a sequence triple, the null hypothesis of clonal reproduction can be

rejected at the level P as calculated in (6) or (7). This is implicitly a one-tailed test with rejection of the null hypothesis of clonal evolution when the observed $\Delta_{m,n,1}$ (or the maximum height of the observed walk) is large relative to m and n . An HGRW with a statistically improbable maximum height will have its up steps clustered toward the beginning (left side) of the walk and its down steps clustered toward the end (right side) of the walk. This is precisely a mosaic pattern in a nucleotide sequence: a child sequence having ancestry in \mathbf{p} in the left-hand side of its sequence and ancestry in \mathbf{q} in the right-hand side of its sequence.

Double-breakpoint recombinant: Identifying mosaics with two breakpoints is the more relevant and interesting problem since in long sequence regions, converted tracts of DNA or horizontally transferred segments will usually have both breakpoints present. Identification of two breakpoints also allows for the removal of the horizontally acquired segment; the remaining segment(s) can then be tested again for clonal evolution, and multi-breakpoint mosaics could be inferred by repeating such a process. Note that the two-breakpoint case subsumes the one-breakpoint case since a one-breakpoint recombinant can be viewed as having two breakpoints where one breakpoint is on the end of the sequence.

Again, considering only the informative sites of the sequence triple $(\mathbf{p}, \mathbf{q}, \mathbf{c})$ and viewing their ordering in the context of a hypergeometric random walk, the quantity $\Delta_{m,n,2}$ can be calculated by identifying the *maximum descent* (md) of the walk constructed from the arrangement of informative sites. Letting X_s be the height of $\mathbf{H}_{m,n}$ at step s , the maximum descent is defined as

$$\text{md } \mathbf{H}_{m,n} = \max_{0 \leq s \leq t \leq m+n} (X_s - X_t),$$

and it can be shown that

$$P(\Delta_{m,n,2} = k) = \begin{cases} P(\text{md } \mathbf{H}_{m,n} = k) & \text{when } m \geq n \\ P(\text{md } \mathbf{H}_{m,n} = k + n - m) & \text{when } m < n \end{cases}.$$

Statistical theory underlying a general class of statistics based on partial sum processes (SIEGMUND 1988; KARLIN *et al.* 1990), change-point problems (SIEGMUND 1986), and maximal segmental sums (KARLIN and DEMBO 1992) provides asymptotic approximations that could be applied to calculate the probability that $\text{md } \mathbf{H}_{m,n}$ is large relative to m and n . Notably, Lemmas 3 and 4 in SIEGMUND (1988) and Theorems 2 and 3 in HOGAN and SIEGMUND (1986) contain the appropriate constructions to approximate probabilities of maximum descents in HGRWs. In the theory on ballot problems, the maximum descent of an HGRW represents the maximum lead change (in one direction only) when counting ballots in a two-candidate election; as far as we are aware, this distribution has not been calculated with the combinatorial methods and reflection techniques usually applied

in ballot problems. Below, we provide a method for calculating this distribution exactly.

We use the shorthand $\mathbf{x}_{m,n,k} = P(\text{md } \mathbf{H}_{m,n} = k)$, and for $j, k \geq 0$, we define

$$\mathbf{y}_{m,n,k,j} = P(\text{md } \mathbf{H}_{m,n} = k \cap \min \mathbf{H}_{m,n} = -j).$$

Then,

$$\mathbf{x}_{m,n,k} = \sum_{j=0}^k \mathbf{y}_{m,n,k,j}, \tag{8}$$

and the \mathbf{y} -probabilities can be obtained by solving the recursions

$$j = 0: \quad \mathbf{y}_{m,n,k,0} = \left(\frac{m}{m+n}\right) [\mathbf{y}_{m-1,n,k,1} + \mathbf{y}_{m-1,n,k,0}] \tag{9}$$

$$j > k \geq 0: \quad \mathbf{y}_{m,n,k,j} = 0 \tag{10}$$

$$j = k > 0: \quad \mathbf{y}_{m,n,j,j} = \left(\frac{n}{m+n}\right) [\mathbf{y}_{m,n-1,j-1,j-1} + \mathbf{y}_{m,n-1,j,j-1}] \tag{11}$$

$$k > j > 0: \quad \mathbf{y}_{m,n,k,j} = \left(\frac{m}{m+n}\right) \mathbf{y}_{m-1,n,k,j+1} + \left(\frac{n}{m+n}\right) \mathbf{y}_{m,n-1,k,j-1}, \tag{12}$$

with boundary conditions

$$\mathbf{y}_{m,0,k,j} = \begin{cases} 1 & \text{for } k = j = 0 \\ 0 & \text{otherwise} \end{cases} \tag{13}$$

$$\mathbf{y}_{0,n,k,j} = \begin{cases} 1 & \text{for } k = j = n \\ 0 & \text{otherwise} \end{cases} \tag{14}$$

$$\mathbf{y}_{m,n,0,0} = \begin{cases} 1 & \text{for } n = 0 \\ 0 & \text{otherwise} \end{cases} \tag{15}$$

$$\mathbf{y}_{m,n,k,j} = 0 \quad \text{when } k > n \text{ or } k < n - m \tag{16}$$

$$\mathbf{y}_{m,n,k,j} = 0 \quad \text{when } j > n \text{ or } j < n - m. \tag{17}$$

All of the above recursions can be proved with a simple but careful first-step analysis of the random walk $\mathbf{H}_{m,n}$. Below, the random variables $\mathbf{H}_{m-1,n}$ and $\mathbf{H}_{m,n-1}$ refer to the subwalk of $\mathbf{H}_{m,n}$ that starts after the first step of $\mathbf{H}_{m,n}$.

As an example, recursion (11) can be proved by noting that the event $\{\text{md } \mathbf{H}_{m,n} = j \cap \min \mathbf{H}_{m,n} = -j\}$ implies that the first step of $\mathbf{H}_{m,n}$ must be down ($X_1 = -1$) and that $\text{md } \mathbf{H}_{m,n-1}$ must be either j or $j - 1$. Thus,

$$\begin{aligned} &P(\text{md } \mathbf{H}_{m,n} = j \cap \min \mathbf{H}_{m,n} = -j) \\ &= P(\text{md } \mathbf{H}_{m,n} = j \cap \min \mathbf{H}_{m,n} = -j \\ &\quad \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j) \\ &\quad + P(\text{md } \mathbf{H}_{m,n} = j \cap \min \mathbf{H}_{m,n} = -j \\ &\quad \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j - 1). \end{aligned} \tag{18}$$

In both summands of the right-hand side of (18), the last three events imply the first. We can rewrite the right-hand side of (18) as

$$\begin{aligned} &P(\min \mathbf{H}_{m,n} = -j \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j) \\ &\quad + P(\min \mathbf{H}_{m,n} = -j \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j - 1). \end{aligned} \tag{19}$$

The events

$$\begin{aligned} &\{\min \mathbf{H}_{m,n} = -j \cap X_1 = -1\} \\ &\equiv \{\min \mathbf{H}_{m,n-1} = -(j-1) \cap X_1 = -1\} \end{aligned} \tag{20}$$

are identical; one occurs if and only if the other occurs. Using this identity, we substitute into (19) and obtain

$$\begin{aligned} &P(\min \mathbf{H}_{m,n-1} = -(j-1) \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j) \\ &\quad + P(\min \mathbf{H}_{m,n-1} = -(j-1) \cap X_1 = -1 \cap \text{md } \mathbf{H}_{m,n-1} = j - 1). \end{aligned} \tag{21}$$

By independence of the first step $X_1 = -1$ from the subwalk $\mathbf{H}_{m,n-1}$, this becomes

$$\begin{aligned} &P(X_1 = -1) \cdot P(\min \mathbf{H}_{m,n-1} = -(j-1) \cap \text{md } \mathbf{H}_{m,n-1} = j) \\ &\quad + P(X_1 = -1) \cdot P(\min \mathbf{H}_{m,n-1} = -(j-1) \cap \text{md } \mathbf{H}_{m,n-1} = j - 1), \end{aligned} \tag{22}$$

which is

$$\left(\frac{n}{m+n}\right) [\mathbf{y}_{m,n-1,j,j-1} + \mathbf{y}_{m,n-1,j-1,j-1}].$$

The other recursions can be proven similarly, and the boundary cases (13)–(17) are easily verifiable.

The computation time for any $\mathbf{y}_{m,n,k,j}$ is bounded above by mn^3 , which is the maximum table size required in memory to solve recursions (9)–(12); $k + 1$ \mathbf{y} -values must be computed to calculate $\mathbf{x}_{m,n,k}$ via Equation 8. On a single 3-GHz processor with access to 2 GB RAM, the worst-case \mathbf{x} -calculations for 250 informative sites take <3 sec; most \mathbf{x} -probabilities can be calculated in <1 min for up to 400 informative sites. All calculations presented in this article (except where noted) were done on a 3.2-GHz Linux laptop with 1 GB of RAM and 750 MB of virtual memory. C++ source code for calculating the \mathbf{x} - and \mathbf{y} -variables is available from the authors.

For a given sequence triple in which we observe a $\Delta_{m,n,2} = k$, with a P -value of $\sum_{j=k}^n \mathbf{x}_{m,n,j}$ we can reject the null hypothesis of completely clonal reproduction in favor of an evolutionary history that includes a two-breakpoint recombination event.

APPLICATIONS

The following are two simple examples that use the distributions $\Delta_{m,n,1}$ and $\Delta_{m,n,2}$ to test for mosaic structure among three sequences.

TABLE 1
Mosaic structure in *Neisseria argF* gene

| p | q | c | Null | Observed maximum | P-value | Observed maximum descent | P-value |
|----------------|----------------|----------------|--------------------|------------------|------------------------|--------------------------|------------------------|
| <i>N. men.</i> | <i>N. cin.</i> | <i>N. gon.</i> | H _{84,6} | 78 | 1 | 2 | 0.30 |
| <i>N. cin.</i> | <i>N. men.</i> | <i>N. gon.</i> | H _{6,84} | 0 | 1 | 78 | 1 |
| <i>N. gon.</i> | <i>N. cin.</i> | <i>N. men.</i> | H _{84,32} | 52 | 1 | 19 | 8.93×10^{-11} |
| <i>N. cin.</i> | <i>N. gon.</i> | <i>N. men.</i> | H _{32,84} | 19 | 1.42×10^{-12} | 71 | 2.50×10^{-11} |
| <i>N. gon.</i> | <i>N. men.</i> | <i>N. cin.</i> | H _{6,32} | 0 | 1 | 26 | 1 |
| <i>N. men.</i> | <i>N. gon.</i> | <i>N. cin.</i> | H _{32,6} | 26 | 1 | 2 | 0.60 |

The first three columns show a candidate parent–parent–child configuration that is tested for recombination; the fourth column shows the null distribution for the ordering of informative sites in the given sequence triple. The 1-breakpoint recombinant in the fourth row can be achieved with three different breakpoints, at positions 201, 202, and 203 (a breakpoint at position 201 indicates a breakpoint after the 201st nucleotide). The 2-breakpoint recombinant in the fourth row can be achieved with 66 different pairs of breakpoints: the first is always one of 202–204 while the second is one of 742–759/784–787. The 2-breakpoint recombinant in the third row can be achieved with 21 different pairs of breakpoints: the first is always one of 0–6 while the second is one of 202–204. *N. men.*, *N. meningitidis*; *N. cin.*, *N. cinerea*; *N. gon.*, *N. gonorrhoeae*.

Neisseria: We considered a classic example from the genus *Neisseria* and applied our tests to its *argF* gene, which is widely believed to have mosaic structure as a result of horizontal gene transfer among different species (ZHOU and SPRATT 1992; GRASSLY and HOLMES 1997; HUSMEIER and MCGUIRE 2003). ZHOU and SPRATT (1992) found regions of clustered polymorphism in a comparison between the *argF* genes of a *Neisseria meningitidis* isolate and a *N. gonorrhoeae* isolate and deduced that this region of clustered polymorphisms had likely ancestry in the species *N. cinerea* (since *N. meningitidis* and *N. cinerea* were nearly identical in this region). The authors noted that there were two regions in *N. meningitidis* that could have arisen by horizontal gene transfer, one of which might have been the result of variation in mutation rates or fixation rates (usually called “rate variation”). Further studies (GRASSLY and HOLMES 1997; HUSMEIER and MCGUIRE 2003) suggested that additional regions in the *argF* gene may have arisen by recombination.

We used three of the *Neisseria* sequences, one of each species, from the studies mentioned above (GenBank accession nos. X64860, X64866, and X64869; 787 nt in length) and tested whether there is any parent–parent–child relationship among them that lends support to one sequence being a mosaic of the other two. Table 1 shows that of the six possible arrangements, one has a highly significant ($P = 10^{-12}$) single-breakpoint recombination signal, while the other five have none. This occurs because the first 202 nucleotides of *N. meningitidis* cluster significantly with *N. cinerea* (3.5% divergent, while *N. meningitidis* and *N. gonorrhoeae* are 13% divergent in this region) and the final 585 nucleotides of *N. meningitidis* cluster significantly with *N. gonorrhoeae* (2.9% divergent, while *N. meningitidis* and *N. cinerea* are 15% divergent in this region). This indicates that the first 202 nucleotides of *N. meningitidis* have probable ancestry in *N. cinerea* while the final 585 nucleotides of *N. meningitidis* have probable ancestry in *N. gonorrhoeae*, a

view that is supported by the last two columns of Table 1, which allow for two breakpoints in the child sequence’s composition but support a mosaic structure almost identical to the one-breakpoint case.

Influenza A: GIBBS *et al.* (2001) found evidence for recombination in the hemagglutinin gene of the 1918 “Spanish” influenza strain, but their results were later refuted by WOROBEY *et al.* (2002) and STRIMMER *et al.* (2003). We reanalyzed the five sequences presented by Gibbs that were the candidate recombiners and recombinants: two swine sequences (A/swine/Iowa/15/30 and A/swine/Wisconsin/1/61) and three human sequences (A/South Carolina/1/18, A/Kiev/59/79, and A/Alma Ata/1417/84), where the last two numbers in the sequence names indicate the year the sequence was isolated. In Table 2 we show the results obtained using our Δ -method on the significant relationships presented in Figure 1 of GIBBS *et al.* (2001).

With any type of analysis, detecting recombination in ancient influenza sequences is a challenge because of the high mutation rates in RNA viruses. A recombination that occurred 90 years ago would have its recombination signal obscured by mutations that accumulated after the recombination event. The relationship specified by the first two rows in Table 2, for example, requires a minimum of 104 years of evolution after the posited recombination event (61 years between the South Carolina and the Kiev strains and 43 years between the South Carolina and Wisconsin strains). Our five influenza sequences are on average 10% divergent (range: 2.4–18.3%), which means that detecting recombination events should be easy if the events were recent but difficult if they were ancient. On the timescale of influenza evolution, the hypothesized recombination events in Table 2 would be quite ancient.

Nevertheless, our method does detect weak recombination signals in the 1918 and 1984 human influenza strains. It is important to note that we are performing

TABLE 2
Mosaic structure in influenza A hemagglutinin gene

| p | q | c | Null | Observed maximum | P-value | Observed maximum descent | P-value | Dunn-Šidák | |
|-------|-------|-------|---------------|------------------|-----------------------|--------------------------|-----------------------|------------|------|
| | | | | | | | | Maximum | md |
| 1979h | 1961s | 1918h | $H_{148,159}$ | 7 | 0.45 | 46 ^a | 4.00×10^{-4} | | 0.03 |
| 1961s | 1979h | 1918h | $H_{159,148}$ | 39 ^b | 7.85×10^{-4} | 30 ^c | 5.22×10^{-3} | 0.05 | NS |
| 1979h | 1961s | 1930s | $H_{94,218}$ | 0 | 1 | 124 | 1 | | |
| 1961s | 1979h | 1930s | $H_{218,94}$ | 124 | 1 | 10 ^d | 9.06×10^{-3} | | NS |
| 1979h | 1961s | 1984h | $H_{92,220}$ | 0 | 1 | 128 | 1 | | |
| 1961s | 1979h | 1984h | $H_{220,92}$ | 128 | 1 | 12 ^e | 8.88×10^{-4} | | 0.06 |

The first three columns refer to the five influenza sequences mentioned in the *Influenza A* section. Here, the sequences are referred to by year and whether the sequence is human (h) or swine (s). The last two columns show the Dunn-Šidák corrected *P*-values given that without any knowledge about which sequences are recombinant, 60 comparisons would have to be made to test all parent-parent-child combinations. The breakpoint descriptions listed in footnotes *a-e* refer to a gapped alignment of length 1778 nt; 80 positions are gapped.

^aThere are 90 pairs of breakpoints that result in a maximum descent of 46 units in the diagrammed walk from these three sequences. The first breakpoint is in position 242–247, while the second one is in 953–955/971–982.

^bThe maximum height of 39 for this triple can be attained by 15 different breakpoints, at positions 952–954/970–981.

^cThere are 30 pairs of breakpoints that result in a maximum descent of 30 for this sequence triple. The first breakpoint is in position 953–955/971–982; the second breakpoint is either in position 1653 or in position 1654.

^dThere are 45 pairs of breakpoints that result in a maximum descent of 10 for this sequence triple. The first breakpoint is in position 953–955/971–982; the second breakpoint is in position 1049–1051.

^eThere are 9 pairs of breakpoints that result in a maximum descent of 12 for this sequence triple. The first breakpoint is in position 953–955; the second breakpoint is in position 1049–1051.

post hoc tests on previously analyzed sequences for which GIBBS *et al.* (2001) obtained statistically significant recombination signals. Given these same five sequences without any *a priori* knowledge about their relationships, we might compute *P*-values for all 60 possible parent-parent-child relationships among these sequences. The last two columns of Table 2 show which of these comparisons would still be significant after a Dunn-Šidák correction for 60 comparisons. The Dunn-Šidák correction is, of course, extremely conservative, especially since the Δ -values from our comparisons are positively correlated. A more accurate correction for multiple comparisons would take into account that we have multiple significant results. Using an exact binomial test, the probability under H_0 that ≥ 3 of 60 comparisons would be significant at the 10^{-3} level is $P = 3.3 \times 10^{-5}$. To be slightly more conservative, we could say that the two *P*-values in rows 1 and 2 of Table 2 that are $< 10^{-3}$ are in fact manifestations of the same arrangement of strains (Kiev, Wisconsin, and South Carolina); then, the probability that ≥ 2 of 60 comparisons would be significant at the 10^{-3} level is $P = 1.7 \times 10^{-3}$.

Although it has been long believed that intragenic (homologous) recombination does not occur in influenza (KILBOURNE 1978), the occurrence of nonhomologous recombination (KHATCHIKIAN *et al.* 1989; ORLICH *et al.* 1994; SUAREZ *et al.* 2004) together with the data presented by Gibbs suggests that homologous recombination in influenza may be possible. However, as pointed out by WOROBAY *et al.* (2002), the observed substitution

pattern in the influenza hemagglutinin can also be explained by within-sequence rate variation that varies across the different branches of the phylogeny (lineage-specific rate variation). Using pairwise comparisons among human sequences of the influenza A hemagglutinin, WOROBAY *et al.* described the HA1 region (nucleotide sites 151–920) as evolving more quickly than the HA2 region (sites 1–150 and 921–1695) in humans. If the opposite can be shown to be true for swine hemagglutinin sequences—that the HA2 evolves more quickly than the HA1—then the detected mosaicism in the 1918 human influenza hemagglutinin would be best explained by lineage-specific rate variation. This type of rate variation has also been called heterotachy (LOPEZ *et al.* 2002), and it was first introduced in the context of a changing set of concomitantly variable codons by FITCH and MARKOWITZ (1970). It has been suggested that, for influenza A viruses, heterotachous or lineage-specific rate variation is a more likely evolutionary history than an intragenic recombination event (E. C. HOLMES, personal communication).

SIMULATIONS

In addition to our Δ -method's theoretical appeal of being exact and nonparametric we show that it has the practical advantages of speed, power, and a low false-positive rate.

Power and false positives: We compared the power and false-positive rates of our Δ -method to the 14 methods

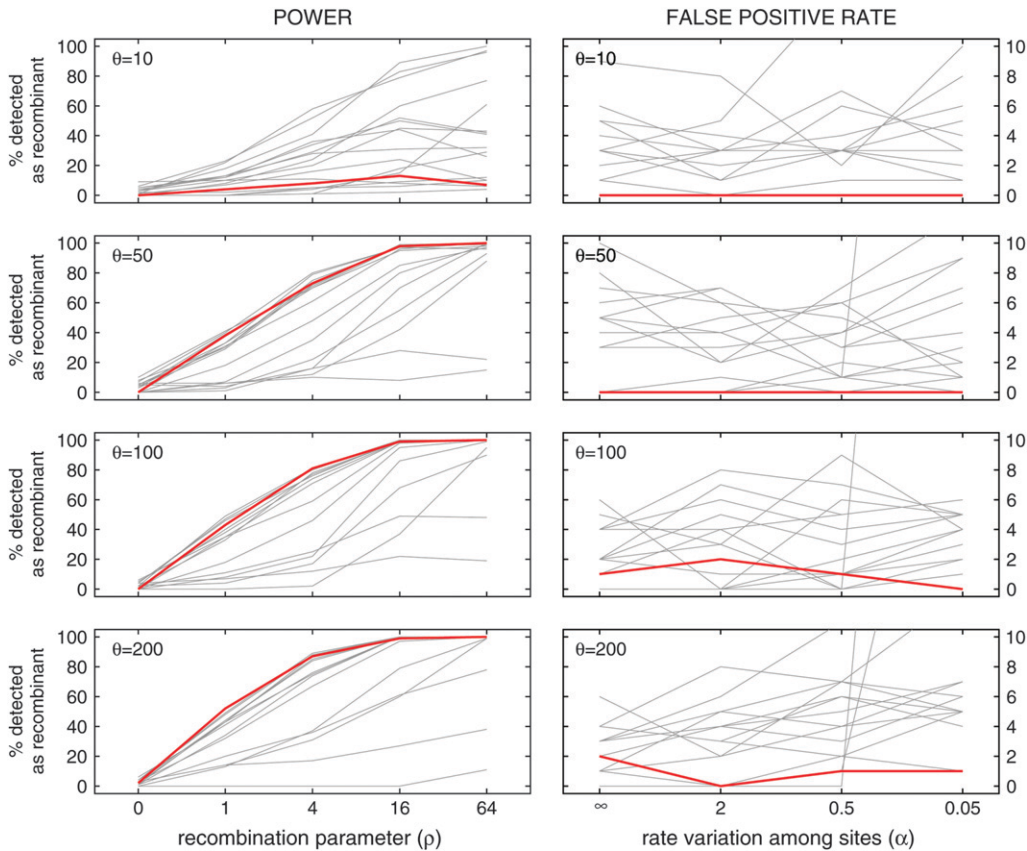


FIGURE 2.—Power and false-positive comparisons to the 14 methods tested in POSADA and CRANDALL (2001). The top four graphs include two additional LPT methods described in CARVAJAL-RODRÍGUEZ *et al.* (2006). The graphs in the left column plot power under different recombination rates, while the right-hand column shows false-positive rates when there is variation in mutation rates but recombination is not present; $\alpha = \infty$ means that there is no rate variation, while lower values of α indicate higher rate variation. The red line shows the power and false-positive rate of $\Delta_{m,n,2}$ in detecting recombination. The gray lines show the power and false-positive rates of 14 (or 16) other methods. $\alpha = \infty$ in the left column; $\rho = 0$ in the right column.

evaluated in POSADA and CRANDALL (2001). Figure 2 duplicates the conditions of Figure 1 in POSADA and CRANDALL (2001); in addition, two of the methods described by CARVAJAL-RODRÍGUEZ *et al.* (2006) are included in the top two rows of comparisons in Figure 2. Power and false-positive rates are tested for different values of the population-genetic parameter $\theta = 4N_e\mu L$, where N_e is the effective population size, μ is the per site per generation mutation rate, and L is the sequence length. Power is tested across different values of the recombination parameter $\rho = 4N_e r L$, where r is the per site per generation recombination rate. False-positive rates are tested for different levels α of rate variation (α is the shape parameter of a fixed-mean Γ -distribution of evolutionary rates as in YANG 1996) since, as noted in the *Neisseria* and influenza examples, statistical tests for recombination can confound recombination and variation in mutation/fixation rates.

The left column of Figure 2 shows the power of 14 (or 16) other methods as well as the power of our Δ -method, which was determined as follows. Each data point corresponds to 100 simulated sequence sets with 10 sequences in each set (details in POSADA and CRANDALL 2001). In a set of 10 sequences, there are 720 unique parent–parent–child arrangements; the quantity $\Delta_{m,n,2}$ was calculated for each of these 720 triplets and the P -value associated with that quantity was computed with recursions (9)–(12). The minimum of these 720 P -values was corrected with a Dunn–Šidák correction and then

reported as the P -value for rejecting clonal evolution in that 10-sequence set. This procedure was implemented in C++ as a command-line Linux program called 3SEQ; source code is available from the authors. The number of sets in which clonal evolution could be rejected at the 0.05 level was reported as the power of our Δ -method. The false-positive rates in the right-hand column of Figure 2 were computed in the same way.

Figure 2 shows that for a high enough mutation rate, our method is among the most powerful available for detecting recombination. For the sequence sets where $\theta = 10$, the mean pairwise distance within each set of 10 sequences ranges from 1 to 30 nt. Using $\Delta_{m,n,2}$ to test for recombination requires a minimum of nine informative sites to reject clonality at the 0.05 level; when correcting with a Dunn–Šidák correction for 720 comparisons, a minimum of 20 informative sites is needed. For this reason, our method has low power for data sets with little polymorphism. For the tested parameter combinations, our false-positive rate is at most 2% and among the lowest of all methods tested. It is important to note that some of the more powerful methods in the left-hand column had high false-positive rates in the right column. The plots in supplemental Figure S1 (<http://www.genetics.org/supplemental/>) show the ratios of power to false-positive rate for the 16 methods from Figure 2.

Supplemental Figure S2 at <http://www.genetics.org/supplemental/> shows an additional false-positive

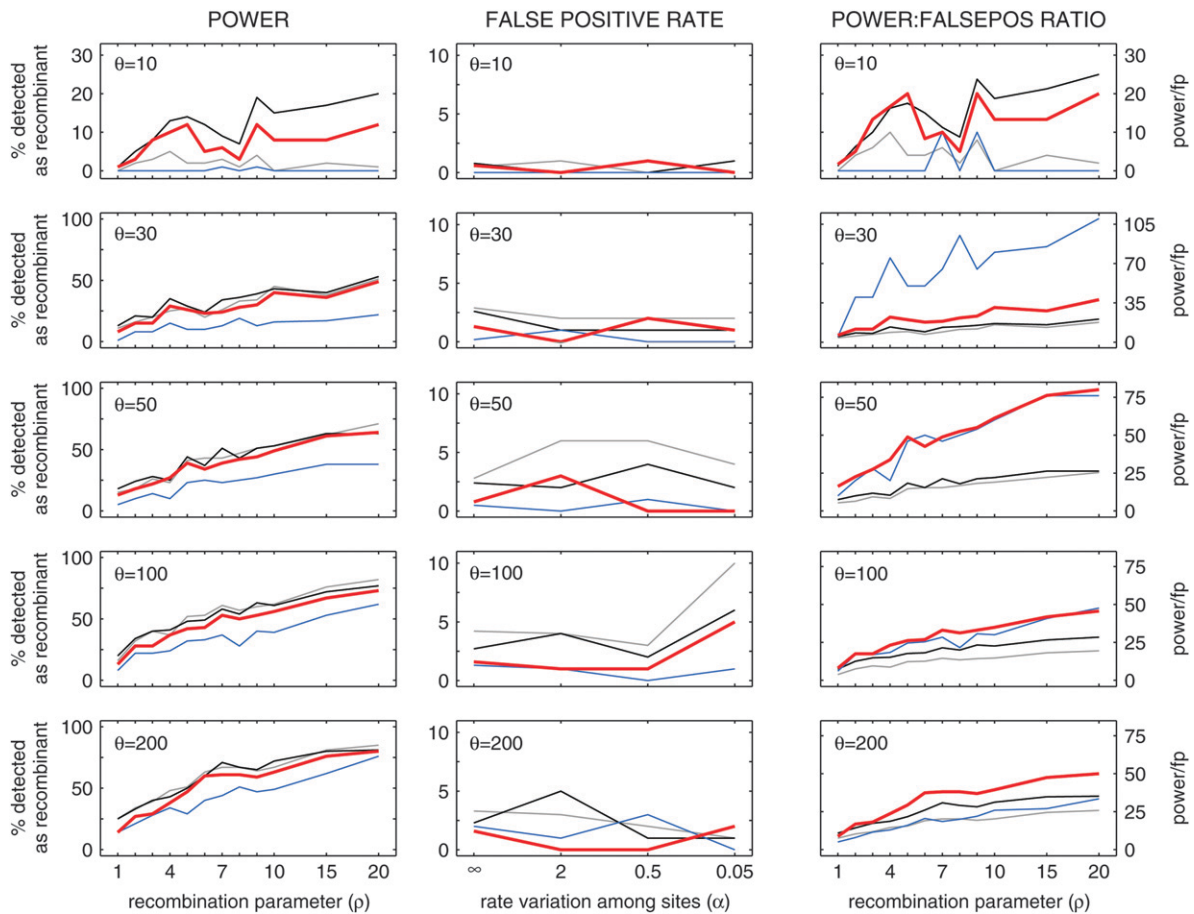


FIGURE 3.—Power and false-positive comparisons with MR and Chimaera on sequence triplets. The red line shows power and false-positive rates for $\Delta_{m,n,2}$. The black line shows the power and false-positive rates for Chim-Sp, a single-breakpoint no-window Chimaera implementation (described on p. 14 of the supplemental materials of POSADA and CRANDALL 2001) whose P -values were calculated using the method of SPENCER (2003). The gray line shows the power and false-positive rates of Chim-2006, a new Chimaera implementation with a sliding-window and sliding-breakpoint scheme; P -values were computed by permuting alignment columns 1000 times. The blue line shows the power and false-positive rates for MR-30,1 (Martin–Rybicki method with window size 30 nt and step size 1 nt). The third column shows ratio of power to false-positive rate at $\alpha = \infty$. False-positive rates at $\alpha = \infty$ were calculated with 1000 simulated triplets; all other data points were calculated with 100 simulated triplets. $\alpha = \infty$ in the left column; $\rho = 0$ in the middle column.

analysis in data sets generated with autocorrelated mutation rates (from Figure 5c of BRUEN *et al.* 2006); our false-positive rate was never $>3.2\%$ for these data sets. Supplemental Figure S3 at <http://www.genetics.org/supplemental/> shows a power analysis under conditions with population growth, using the simulated data from Figure 4 of BRUEN *et al.* (2006). $\Delta_{m,n,2}$ is quite powerful under a scenario of population growth (as long as sequence diversity is high enough), and it retains very high power even when the recombination parameter ρ is small.

Since our statistical test is designed for sequence triplets we perform an additional power analysis that focuses exclusively on detecting recombination in sets of three sequences. We compare $\Delta_{m,n,2}$ to three other common statistical tests designed to identify recombination in sequence triplets (a total of eight methods were tested of which the three most powerful are shown in Figure 3; details of and results for all eight methods are in

the supplemental materials at <http://www.genetics.org/supplemental/>). For each data point in Figure 3, the program TREEVOLVE (GRASSLY *et al.* 1999) was used to generate 100 replicates of three sequences with the given population-genetic parameters, using the F84 model of nucleotide substitution (FELSENSTEIN and CHURCHILL 1996) with $\pi_A = 0.4$, $\pi_C = 0.2$, $\pi_G = 0.1$, $\pi_T = 0.3$, and a transition/transversion ratio of two. The black line in Figure 3 denotes the power and false-positive rate of a single-breakpoint version of Chimaera with exact P -value computations (POSADA and CRANDALL 2001; SPENCER 2003), the gray line corresponds to the most recent version of Chimaera (Chim-2006), and the blue line corresponds to the Martin–Rybicki method with window size 30 nt and step size 1 nt.

For statistical identification of mosaic structure in sequence triplets, our Δ -method is as powerful as the most powerful methods available. All four methods in Figure 3 have similar power and false-positive rates, with

TABLE 3

Computation times (last four columns) for computing recombination statistics and P -values in large data sets

| Data set | Segregating sites | No. sequences | P -value | $\Delta_{m,n,2}$ (min) | MR-30,1 | Chim-Sp | Chim-2006 |
|--------------|-------------------|---------------|----------------------|------------------------|---------|---------|-----------|
| Dengue E | 618 | 69 | 3.3×10^{-5} | 2 | 86 min | 24 min | ~100 hr |
| Human mtDNA | 1079 | 262 | 4.6×10^{-3} | 6 | ~180 hr | ~48 hr | ~550 days |
| Influenza HA | 316 | 308 | 1 | 4 | ~43 hr | 9 hr | ~105 days |

All times and estimates are for a single 3.2-GHz processor. Dengue data are serotype 2 from HOLMES *et al.* (1999); human mitochondrial DNA sequences are a subset of distinct strains from KIVISILD *et al.* (2006); influenza sequences are New Zealand H3N2 isolates from 2000–2005 analyzed in BONI (2007). The P -value reported in this table is the minimum P -value (testing with $\Delta_{m,n,2}$) from all comparisons in a data set, corrected with a Dunn–Šidák correction.

the distinguishing feature that Chimaera is the least conservative method, MR is the most conservative, and $\Delta_{m,n,2}$ is somewhere in between. For $\theta \geq 50$, $\Delta_{m,n,2}$ has the best combination of power and false-positive rate.

Speed: Table 3 shows the computation times of our method compared to MR and Chimaera. Our method has a clear advantage, especially in large data sets, since P -values are simply read from memory once a table of $y_{m,n,k,j}$ -values is built. For example, analysis of the influenza data (BONI 2007) requires reading ~29 million P -values from memory, which is not a time-consuming task for a 3.2-GHz processor. Likewise, computing exact P -values using the method described by SPENCER (2003) is quite fast; this is slightly slower than our Δ -method since a new table needs to be built for each P -value computation. On the other hand, performing 14.5 million sliding-window χ^2 -computations on each of 1000 randomized data sets (Chim-2006) or computing 9.6 million P -values from a binomial distribution for each of 287 possible windows (MR-30,1) can be quite computationally expensive.

Note that nontriplet methods can be much faster than triplet methods. For example, analyzing the data in Table 3 with Φ_w (BRUEN *et al.* 2006) takes seconds, but the recombinant sequences cannot be isolated.

DISCUSSION

Comparison: Many statistical methods have already been developed for detecting recombination from sequence data. The usual recombination signals that these methods attempt to identify are (i) varying patterns of sequence identity, (ii) phylogenetic incongruencies, (iii) excess homoplasies, (iv) clustered polymorphism, and (v) low linkage disequilibrium; our method is of the first type. Here, we summarize the main similarities/differences between and advantages/disadvantages of our method and previous ones.

Most importantly, our method considers three sequences at a time using the appropriate mechanistic framework in which to view mosaic structure: the existence of one sequence that is a mosaic of a second and a third. MAYNARD SMITH (1992) also acknowledged this

as the appropriate framework, although the test he developed is designed for two sequences. Maynard Smith's maximum χ^2 -method was later reformulated as a proper three-sequence problem and is now called maximum-match χ^2 or Chimaera (POSADA and CRANDALL 2001; POSADA 2002). TAKAHATA (1994) recognized that one needed to look at a minimum of three sequences by focusing on sites that support a particular sister-group status where exactly two of three nucleotides agree. The BOOTSCAN search method (SALMINEM *et al.* 1995) examines candidate recombinants to see how different regions cluster with either of two parental sequences; bootstrap support, rather than a significance test, provides a measure of reliability of the proposed clustering. Recently, MARTIN *et al.* (2005) modified the BOOTSCAN method to search only sequence triples and to find recombinants statistically using the binomial test in MARTIN and RYBICKI (2000). Finally, HOLMES *et al.* (1999) describe a phylogenetic method called LARD that considers three sequences at a time and tests the hypothesis of completely clonal evolution *vs.* the hypothesis of clonal evolution for segments on either side of a breakpoint; their problem is formulated similarly to ours, the main difference being that their method focuses on phylogeny. It should be noted that some methods (ROBERTSON *et al.* 1995; GIBBS *et al.* 2000) require four sequences: three involved in a recombination event and a fourth used as an outgroup.

The mechanistic three-sequence approach contrasts with approaches that attempt to identify indirect signals from sequence data, such as an excess of homoplasies (HUDSON and KAPLAN 1985; JAKOBSEN and EASTEAL 1996; MAYNARD SMITH and SMITH 1998; MAYNARD SMITH 1999; BRUEN *et al.* 2006) or a clustering of polymorphisms (STEPHENS 1985; MAYNARD SMITH 1992; MARTIN and RYBICKI 2000) that would be indicative of a recent recombination or gene conversion. While these methods can be quite effective, one must keep in mind that polymorphism clustering can be caused by selection or mutational hotspots and that an excess of homoplasies can be quite difficult to detect in rapidly mutating organisms such as RNA viruses.

Our method has several technical advantages. First, we do not use Monte Carlo methods to generate

P -values, which makes our P -value computations very fast. Moreover, once a table is built in memory to calculate a particular $\mathbf{x}_{m,n,k}$, successive P -values can simply be extracted from the table; this means that repeated application of our Δ -tests is limited only by how quickly the computer's memory can be accessed. Monte Carlo methods have the additional disadvantage that the precision of computed P -values is limited by the number of permutations that can be done; this could be problematic in large data sets where precise P -values may be needed to survive multiple-comparisons corrections. Second, we avoid the widely used sliding-window approaches (SALMINEM *et al.* 1995; SIEPEL *et al.* 1995; GRASSLY and HOLMES 1997; LOLE *et al.* 1999; MARTIN and RYBICKI 2000; STRIMMER *et al.* 2003; MARTIN *et al.* 2005) that require the user to define a window size at the scale at which recombination is believed to have occurred. By considering all possible breakpoints in expression (4), we find the optimal "window size" that should be used for inferring recombination in a particular sequence triplet. This allows for the detection of recombinant segments at any scale.

By removing uninformative sites, our Δ -method should not confound variation in mutation/fixation rates with recombination; indeed, the middle column of Figure 3 and supplemental Figure S2 at <http://www.genetics.org/supplemental/> show that even under high rate variation our false-positive rate is at most 5% (and usually <3%). However, lineage-specific or heterotachous rate variation can, in the absence of recombination, produce the pattern that is meant to be rejected by our Δ -distributions. Consider the tree in Figure 4. Branch 1 connects the root to sequence **p** while branch 2 connects the **q**-**c** common ancestor to sequence **q**. Differential environmental pressures on branches 1 and 2 can create the impression of mosaic structure. Suppose that the organism, during its evolution along branch 1, experiences an environment where the right-hand side of the sequence evolves rapidly and accumulates many substitutions while the left-hand side is either conserved or mutates neutrally. Suppose further that the organism, during evolution along branch 2, experiences an environment where the left-hand side of the sequence evolves rapidly and accumulates substitutions while the right-hand side is conserved or mutates neutrally. Under this scenario of clonal evolution, where environmental pressure increases substitution rates in the right part of the sequence on branch 1 and in the left part of the sequence on branch 2, the resulting sequence triple (**p**, **q**, **c**) will give the appearance that a recombination event occurred. In this case, the right part of sequence **c** will be very similar to sequence **q** while the left part will be very similar to sequence **p**. This type of sequence identity in different sequence regions is exactly what our Δ -statistics are designed to reveal.

While this combination of events may seem unlikely, the influenza sequences described here may have under-

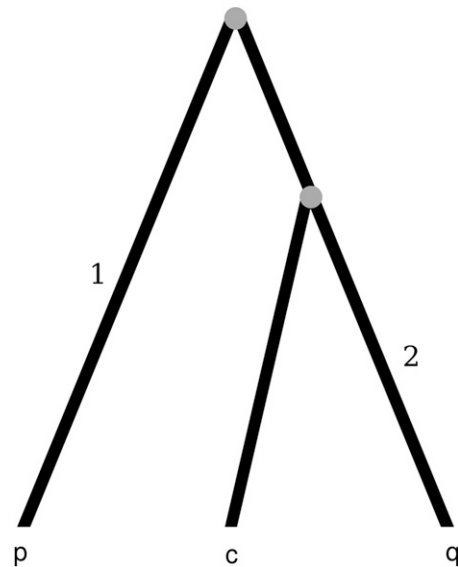


FIGURE 4.—Phylogenetic tree that shows a possible clonal evolutionary history for the sequences **p**, **q**, and **c**. Mutations occurring in branch 1 will result in an informative site of type **Q**, while mutations occurring in branch 2 will result in an informative site of type **P**. The distributions describing the probability that the mutations in branch 1 or 2 cluster on either side of a breakpoint or between some pair of breakpoints are those of $\Delta_{m,n,1}$ and $\Delta_{m,n,2}$.

gone just such evolutionary pressures. A key component in this scenario where mosaic structure is generated without recombination is that the organism experiences different selective environments on different branches of its phylogeny.

General conclusions: We have introduced exact, non-parametric statistical tests for identifying nucleotide sequence mosaic structure with one or two breakpoints. Our test statistic is a function of a given sequence triple where one sequence is hypothesized to be a recombinant of the other two. Given a sequence triple, we calculate the difference in proximity (to the child sequence) between the closer parent sequence and the closest candidate recombinant sequence. This difference is denoted $\Delta_{m,n,b}$ —where m and n describe the numbers of informative sites at which the child sequence clusters with one or the other parent, and b denotes the number of breakpoints allowed in a candidate recombinant—and it is studied as a random variable under the null hypothesis of clonal evolution. The distribution of $\Delta_{m,n,1}$ has been described in the probability literature on ballot problems, while the distribution of $\Delta_{m,n,2}$ has been approximated but not described exactly. With brute-force methods, exact probabilities of the distribution of $\Delta_{m,n,2}$ would require exponentially growing computation times that would become unmanageable once $m + n > 35$. To remedy this problem, we derive a set of recursive equations to calculate the probability mass function of $\Delta_{m,n,2}$ in $\mathcal{O}(mn^3)$ -time. These calculations can be performed in seconds on a single-processor personal

computer (3 GHz, 2 GB RAM) as long as $m + n < 250$. When $250 < m + n < 400$, most computations are equally quick although some may require additional memory or the use of virtual memory.

Our method relies on deducing parent-child sequence identity for different parents in different sequence regions. If a recombination occurred between sequences \mathbf{p} and \mathbf{q} to create the sequence \mathbf{c} , then one segment of sequence \mathbf{c} should be more similar to parent \mathbf{p} while the remaining segment(s) of sequence \mathbf{c} should be more similar to parent \mathbf{q} . If this pattern is statistically significant—*i.e.*, if it appears in the far right-hand tail of the distribution of $\Delta_{m,n,b}$ —we deduce that a recombination occurred.

Our Δ -method is among the most powerful available for detecting recombination in sequence data, even in highly recombinant data sets (generating data sets as in Figure 2 with $\rho = 128$, our method had 100% power for $\theta \geq 50$) or in data sets generated under conditions of population growth (see supplemental Figure S3 at <http://www.genetics.org/supplemental/>). For many of the simulated data sets in this article, $\Delta_{m,n,2}$ appears to have the best combination of power and low false-positive rate. With comparable power to the best available methods, the most immediate practical advantage of using $\Delta_{m,n,2}$ over other methods is its speed in large data sets. As can be seen in Table 3, computing P -values from $\Delta_{m,n,2}$ can be many orders of magnitude faster than other triplet methods, depending on the number of sequences and the amount of polymorphism in the data set. For N sequences, triplet methods will make on the order of N^3 comparisons, which for $N > 1000$ can be quite a large number for a personal computer. For example, 1000 influenza sequences with a similar level of polymorphism as in Table 3 would take 137 min to analyze with $\Delta_{m,n,2}$, while 2000 sequences would take 18 hr. Fortunately, our method (along with most triplet methods) is completely parallelizable, which means that as sequence databases grow we can take advantage of parallel computing to search for recombinants in very large data sets. Note that if we have a particular query sequence that we would like to test for recombination, the number of comparisons is of order N^2 .

Our choice of applications here represents only a small sample of the clonal or nearly clonal sequences we could analyze with our Δ -statistics. They would also be quite useful in finding recombinants in human immunodeficiency virus databases and in larger dengue virus data sets and in analyzing the recently suggested recombinants in measles (SCHIERUP *et al.* 2005). Human mitochondrial DNA is generally believed to evolve clonally, although the data set in Table 3 has quite strong mosaic signals; a reanalysis of other mtDNA data sets (PIGANEAU and EYRE-WALKER 2004; PIGANEAU *et al.* 2004) would help determine whether recombination occurred during the evolution of the mitochondrion. For the influenza virus, our test could be used on whole

(concatenated) influenza genomes, as in HOLMES *et al.* (2005), to detect possible reassortment; hundreds of sequenced whole influenza genomes have already been analyzed (NELSON *et al.* 2006) and thousands more have been deposited in GenBank. As sequence databases expand in the genomic era, the Δ -method presented here could become one of the most efficient methods for detecting recombination and finding recombinants in large data sets.

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