

DETECTING SELECTION ON NUCLEOTIDE POLYMORPHISMS

Introduction

At this point, we've refined the neutral theory quite a bit. Our understanding of how molecules evolve now recognizes that some substitutions are more likely than others, but we're still proceeding under the assumption that most nucleotide substitutions are neutral or detrimental. So far we've argued that variation like what Hubby and Lewontin [5, 9] found is not likely to be maintained by natural selection. But we have strong evidence that heterozygotes for the sickle-cell allele are more fit than either homozygote in human populations where malaria is prevalent. That's an example where selection is acting to maintain a polymorphism, not to eliminate it. Are there other examples? How could we detect them?

In the 1970s a variety of studies suggested that a polymorphism in the locus coding for alcohol dehydrogenase in *Drosophila melanogaster* might not only be subject to selection but that selection may be acting to maintain the polymorphism. As DNA sequencing became more practical at about the same time,¹ population geneticists began to realize that comparative analyses of DNA sequences at protein-coding loci could provide a powerful tool for unraveling the action of natural selection. Synonymous sites within a protein-coding sequence provide a powerful standard of comparison. Regardless of

- the demographic history of the population from which the sequences were collected,
- the length of time that populations have been evolving under the sample conditions and whether it has been long enough for the population to have reached a drift-migration-mutation-selection equilibrium, or
- the actual magnitude of the mutation rate, the migration rate, or the selection coefficients

¹It was still *vastly* more laborious than it is now.

the synonymous positions within the sequence provide an internal control on the amount and pattern of differentiation that should be expected when substitutions are neutral.² Thus, if we see different patterns of nucleotide substitution at synonymous and non-synonymous sites, we can infer that selection is having an effect on amino acid substitutions.

Nucleotide sequence variation at the *Adh* locus in *Drosophila melanogaster*

Kreitman [6] took advantage of these ideas to provide additional insight into whether natural selection was likely to be involved in maintaining the polymorphism at *Adh* in *Drosophila melanogaster*. He cloned and sequenced 11 alleles at this locus, each a little less than 2.4kb in length.³ If we restrict our attention to the coding region, a total of 765bp, there were 6 distinct sequences that differed from one another at between 1 and 13 sites. Given the observed level of polymorphism within the gene, there should be 9 or 10 amino acid differences observed as well, but only one of the nucleotide differences results in an amino acid difference, the amino acid difference associated with the already recognized electrophoretic polymorphism. Thus, there is significantly less amino acid diversity than expected if nucleotide substitutions were neutral, consistent with my assertion that most mutations are deleterious and that natural selection will tend to eliminate them. In other words, another example of the “sledgehammer principle.”

Does this settle the question? Is the *Adh* polymorphism another example of allelic variants being neutral or selected against? Would I be asking these questions if the answer were “Yes”?

Kreitman and Aguadé

A few years after Kreitman [6] appeared, Kreitman and Aguadé [7] published an analysis in which they looked at levels of nucleotide diversity in the *Adh* region, as revealed through analysis of RFLPs, in *D. melanogaster* and the closely related *D. simulans*. Why the comparative approach? Well, Kreitman and Aguadé remembered that the neutral theory of molecular evolution makes two predictions that are related to the underlying mutation rate:

- If mutations are neutral, the substitution rate is equal to the mutation rate.

²Ignoring, for the moment, the possibility that there may be selection on codon usage.

³Think about how the technology has changed since then. This work represented a major part of his Ph.D. dissertation, and the results were published as an article in *Nature*. Now an undergraduate would do substantially more for an independent study project.

- If mutations are neutral, the diversity within populations should be about $4N_e\mu/(4N_e\mu + 1)$.

Thus, if variation at the *Adh* locus in *D. melanogaster* is selectively neutral, the amount of divergence between *D. melanogaster* and *D. simulans* should be related to the amount of diversity within each. What they found instead is summarized in Table 1.

The expected level of diversity in each part of the *Adh* locus is calculated assuming that the probability of polymorphism is independent of what position in the locus we are examining.⁴ Specifically, Kreitman and Aguadé calculated the expected polymorphism as follows:

- They calculated the number of “site equivalents” in each region of the locus. A site equivalent is the actual length of the region (in number of nucleotides) times the fraction of changes within that sequence that would lead to gain or loss of a restriction site.⁵ There were 414 site equivalents in the 5’ flanking region, 411 site equivalents in the *Adh* locus, and 129 site equivalents in the 3’ flanking region.
- They calculated the fraction of site equivalents that were polymorphic across the entire locus:

$$\frac{25}{414 + 411 + 129} \approx 0.026 \quad .$$

- They calculated the expected number of polymorphic sites within a region as the product of the number of site equivalents and the fraction of polymorphic site equivalents.

They used the same approach to calculate the expected divergence between *D. melanogaster* and *D. simulans* with one important exception. They directly compared the nucleotide sequence of one *Adh* allele from *D. melanogaster* with one *Adh* allele from *D. simulans*.⁶ As a result, they didn’t have to use the site equivalent correction. They could directly use the number of nucleotides in each region of the gene.

Notice that there is substantially less divergence between *D. melanogaster* and *D. simulans* at the *Adh* locus than would be expected, based on the average level of divergence

⁴It’s important to note that what I’ve labeled as the *Adh* locus in Table 1 is the region that contains the protein coding part of the locus. The 5’ and 3’ flanking regions are physically adjacent, but none of the nucleotides in these parts of the gene are translated into the *Adh* enzyme.

⁵Because sequencing was extremely time-consuming in the mid-1980s, it was impractical to sequence the *Adh* locus in all of the 81 lines they used in the analysis. Instead they used restriction enzymes to reveal some of the nucleotide sequence variation in the locus.

⁶Can you explain why it’s reasonable to estimate divergence between alleles in these species using only one allele from each of them?

	5' flanking	<i>Adh</i> locus	3' flanking
Diversity ¹			
Observed	9	14	2
Expected	10.8	10.8	3.4
Divergence ²			
Observed	86	48	31
Expected	55	76.9	33.1

¹Number of polymorphic sites within *D. melanogaster*

²Number of nucleotide differences between *D. melanogaster* and *D. simulans*

Table 1: Diversity and divergence in the *Adh* region of *Drosophila* (from [7]).

across the entire region. That's consistent with the earlier observation that most amino acid substitutions are selected against. On the other hand, there is *more* nucleotide diversity within *D. melanogaster* than would be expected based on the levels of diversity seen in across the entire region. What gives?

Time for a trip down memory lane. Remember something called “coalescent theory?” It told us that for a sample of neutral genes from a population, the expected time back to a common ancestor for all of them is about $4N_e$ for a nuclear gene in a diploid population. That means there's been about $4N_e$ generations for mutations to occur. Suppose, however, that the electrophoretic polymorphism were being maintained by natural selection. Then we might well expect that it would be maintained for a lot longer than $4N_e$ generations. If so, there would be a lot more time for diversity to accumulate. Thus, the excess diversity could be accounted for if there is balancing selection at ADH.

Kreitman and Hudson

Kreitman and Hudson [8] extended this approach by looking more carefully within the region to see where they could find differences between observed and expected levels of nucleotide sequence diversity. They used a “sliding window” of 100 silent base pairs in their calculations. By “sliding window” what they mean is that first they calculate statistics for bases 1-100, then for bases 2-101, then for bases 3-102, and so on until they hit the end of the sequence (Figure 1).

To me there are two particularly striking things about this figure. First, the position of the single nucleotide substitution responsible for the electrophoretic polymorphism is clearly evident. Second, the excess of polymorphism extends for only a 200-300 nucleotides in each direction. That means that the rate of recombination *within* the gene is high enough to

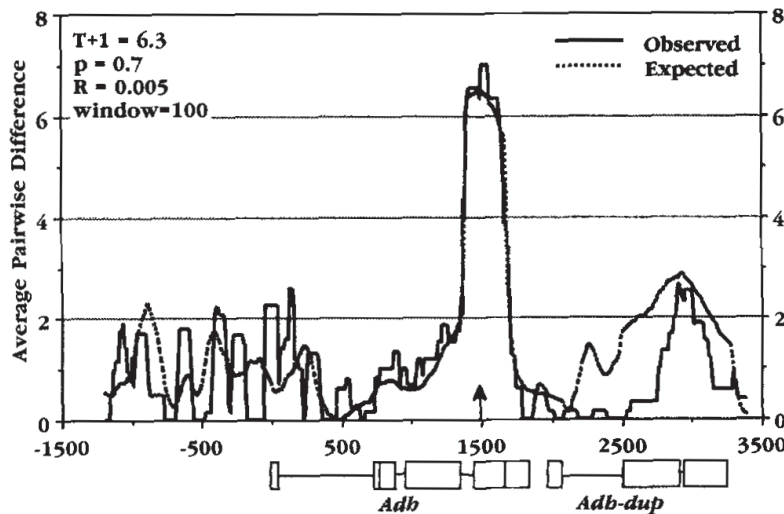


Figure 1: Sliding window analysis of nucleotide diversity in the *Adh-Adh-dup* region of *Drosophila melanogaster*. The arrow marks the position of the single nucleotide substitution that distinguishes *Adh-F* from *Adh-S* (from [8])

randomize the nucleotide sequence variation farther away.⁷

Detecting selection in the human genome

I've already mentioned the HapMap project [3], a collection of genotype data at roughly 3.2M SNPs in the human genome. The data in phase II of the project were collected from four populations:

- Yoruba (Ibadan, Nigeria)
- Japanese (Tokyo, Japan)
- Han Chinese (Beijing, China)
- ancestry from northern and western Europe (Utah, USA)

⁷Remember this observation when we get to association mapping at the end of the course. In organisms with a large effective population size, associations due to physical linkage may fall off *very* rapidly, meaning that you would have to have a *very* dense map to have a hope of finding associations.

We expect genetic drift to result in allele frequency differences among populations, and we can summarize the extent of that differentiation at each locus with F_{ST} . If all HapMap SNPs are selectively neutral,⁸ then all loci should have the same F_{ST} within the bounds of statistical sampling error and the evolutionary sampling due to genetic drift. A scan of human chromosome 7 reveals both a lot of variation in individual-locus estimates of F_{ST} and a number of loci where there is substantially more differentiation among populations than is expected by chance (Figure 2). At very fine genomic scales we can detect even more outliers (Figure 3), suggesting that human populations have been subject to divergent selection pressures at many different loci [4].

Tajima's D

So far we've been comparing rates of synonymous and non-synonymous substitution to detect the effects of natural selection on molecular polymorphisms. Tajima [10] proposed a method that builds on the foundation of the neutral theory of molecular evolution in a different way. I've already mentioned the infinite alleles model of mutation several times. When thinking about DNA sequences a closely related approximation is to imagine that every time a mutation occurs, it occurs at a different site.⁹ If we do that, we have an *infinite sites* model of mutation.

When dealing with nucleotide sequences in a population context there are two statistics of potential interest:

- The *number* of nucleotide positions at which a polymorphism is found or, equivalently, the number of segregating sites, k .
- The average number of nucleotide differences between two sequences, π , where π is estimated as

$$\pi = \sum x_i x_j \delta_{ij} \quad .$$

In this expression, x_i is the frequency of the i th haplotype and δ_{ij} is the number of nucleotide sequence differences between haplotypes i and j .¹⁰

⁸And unlinked to sites that are under selection.

⁹Of course, we know this isn't true. Multiple substitutions *can* occur at any site. That's why the percent difference between two sequences isn't equal to the number of substitutions that have happened at any particular site. We're simply assuming that the sequences we're comparing are closely enough related that nearly all mutations have occurred at different positions.

¹⁰I lied, but you must be getting used to that by now. This isn't quite the way you estimate it. To get an unbiased estimate of π , you have to multiply this equation by $n/(n-1)$, where n is the number of haplotypes in your sample. And, of course, if you're Bayesian you'll be even a little more careful. You'll estimate x_i

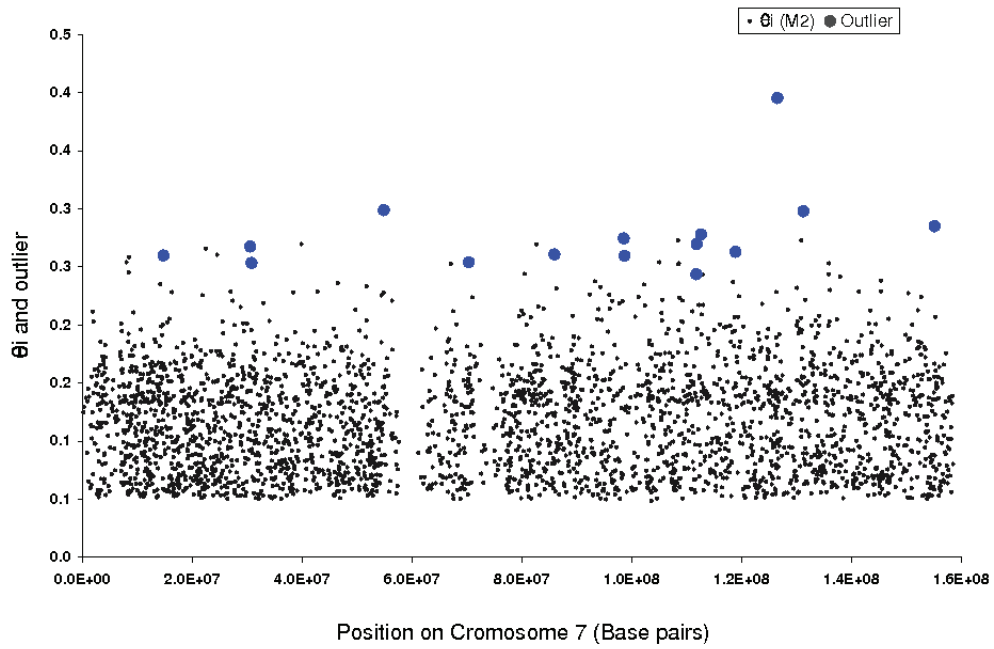


Figure 2: Single-locus estimates of F_{ST} along chromosome 7 in the HapMap data set. Blue dots denote outliers. Adjacent SNPs in this sample are separated, on average, by about 52kb. (from [4])

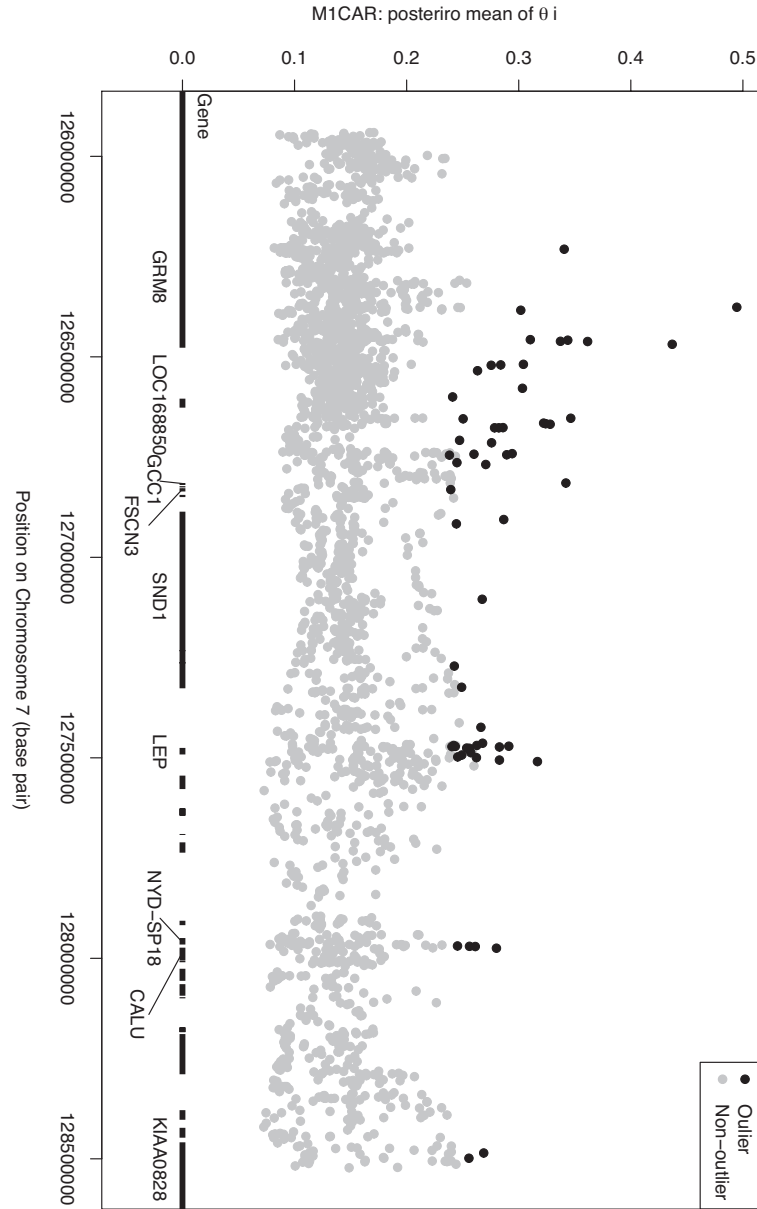


Figure 3: Single-locus estimates of F_{ST} along a portion of chromosome 7 in the HapMap data set. Black dots denote outliers. Solid bars refer to previously identified genes. Adjacent SNPs in this sample are separated, on average, by about 1kb. (from [4])

The quantity $4N_e\mu$ comes up a lot in mathematical analyses of molecular evolution. Population geneticists, being a lazy bunch, get tired of writing that down all the time, so they invented the parameter $\theta = 4N_e\mu$ to save themselves a little time.¹¹ Under the infinite-sites model of DNA sequence evolution, it can be shown that

$$\begin{aligned} E(\pi) &= \theta \\ E(k) &= \theta \sum_i^{n-1} \frac{1}{i} \quad , \end{aligned}$$

where n is the number of haplotypes in your sample.¹² This suggests that there are two ways to estimate θ , namely

$$\begin{aligned} \hat{\theta}_\pi &= \hat{\pi} \\ \hat{\theta}_k &= \frac{k}{\sum_i^{n-1} \frac{1}{i}} \quad , \end{aligned}$$

where $\hat{\pi}$ is the average heterozygosity at nucleotide sites in our sample and k is the observed number of segregating sites in our sample.¹³ If the nucleotide sequence variation among our haplotypes is neutral and the population from which we sampled is in equilibrium with respect to drift and mutation, then $\hat{\theta}_\pi$ and $\hat{\theta}_k$ should be statistically indistinguishable from one another. In other words,

$$\hat{D} = \frac{\hat{\theta}_\pi - \hat{\theta}_k}{\text{Var}(\hat{\theta}_\pi - \hat{\theta}_k)}$$

should be indistinguishable from zero.¹⁴ If it is either negative or positive, we can infer that there's some departure from the assumptions of neutrality and/or equilibrium. Thus, \hat{D} can

using an appropriate prior on haplotype frequencies and you'll estimate the probability that haplotypes i and j are different at a randomly chosen position given the observed number of differences and the sequence length and multiply that probability by the sequence length giving you the expected number of differences between those two haplotypes. The expected number of differences will be close δ_{ij} , but it won't be identical and it won't be a single number.

¹¹This is *not* the same θ we encountered when discussing F -statistics. Weir and Cockerham's θ is a different beast. I know it's confusing, but that's the way it is. When reading a paper, the context should make it clear which conception of θ is being used. Another thing to be careful of is that sometimes authors think of θ in terms of a haploid population. When they do, it's $2N_e\mu$. Usually the context makes it clear which definition is being used, but you have to remember to pay attention to be sure. If you follow population geneticists on X/Twitter, you'll often see them complaining about "off by two" errors.

¹²The "E" refers to expectation. It is the average value of a random variable. $E(\pi)$ is read as "the expectation of π ."

¹³If your memory is really good, you may recognize that those estimates are method of moments estimates, i.e., parameter estimates obtained by equating sample statistics with their expected values.

¹⁴Dividing the difference between $\hat{\theta}_\pi$ and $\hat{\theta}_k$ by its variance makes the expectation of \hat{D} zero and gives it

be used as a test statistic to assess whether the data are consistent with the population being at a neutral mutation-drift equilibrium. Consider the value of D under following scenarios:

Neutral variation If the variation is neutral and the population is at a drift-mutation equilibrium, then \hat{D} will be statistically indistinguishable from zero.

Overdominant selection Overdominance will allow alleles belonging to the different classes to become quite divergent from one another. δ_{ij} within each class will be small, but δ_{ij} between classes will be large and both classes will be in intermediate frequency, leading to large values of θ_π . There won't be a similar tendency for the *number* of segregating sites to increase, so θ_k will be relatively unaffected. As a result, \hat{D} will be positive.

Population bottleneck If the population has recently undergone a bottleneck, then π will be little affected unless the bottleneck was prolonged and severe.¹⁵ k , however, may be substantially reduced. Thus, \hat{D} should be positive.

Purifying selection If there is purifying selection, mutations will occur and accumulate at silent sites, but they aren't likely ever to become very common. Thus, there are likely to be lots of segregating sites, but not much heterozygosity, meaning that $\hat{\theta}_k$ will be large, $\hat{\theta}_\pi$ will be small, and \hat{D} will be negative.

Population expansion Similarly, if the population has recently begun to expand, mutations that occur are unlikely to be lost, increasing $\hat{\theta}_k$, but it will take a long time before they contribute to heterozygosity, $\hat{\theta}_\pi$. Thus, \hat{D} will be negative.

In short, \hat{D} provides a different avenue for insight into the evolutionary history of a particular nucleotide sequence. But interpreting it can be a little tricky.

$\hat{D} = 0$: We have no evidence for changes in population size or for any particular pattern of selection at the locus.¹⁶

a variance of one. This allows us to construct a statistical test of the difference between the observed \hat{D} and the expectation if sequences are evolving neutrally and if the population is at a drift-mutation equilibrium. See [10] for details.

¹⁵Why? Because most of the heterozygosity is due to alleles of moderate to high frequency, and those are not the ones likely to be lost in a bottleneck.

¹⁶Please remember that the failure to detect a difference from 0 could mean that your sample size is too small to detect an important effect. If you can't detect a difference, you should try to assess what values of D are consistent with your data and be appropriately circumspect in your conclusions.

$\hat{D} < 0$: The population size may be increasing or we may have evidence for purifying selection at this locus.

$\hat{D} > 0$: The population may have suffered a recent bottleneck (or be decreasing) or we may have evidence for overdominant selection at this locus.

If we have data available for more than one locus, we may be able to distinguish changes in population size from selection at any particular locus. After all, all loci will experience the same demographic effects, but we might expect selection to act differently at different loci, especially if we choose to analyze loci with different physiological function.

A quick search in Google Scholar reveals that the paper in which Tajima described this approach [10] has been cited over 15,000 times.¹⁷ Clearly it has been widely used for interpreting patterns of nucleotide sequence variation. Although it is a very useful statistic, Zeng et al. [11] point out that there are important aspects of the data that Tajima’s D does not consider. As a result, it may be less powerful, i.e., less able to detect departures from neutrality, than some alternatives.

How much genetic change is due to selection?

We’ve seen that both drift and natural selection can lead to allele frequency changes in a population. Is there any way to tell how much of the allele frequency change in a population is a result of natural selection?¹⁸ Well, to do so we need a set of allele frequencies measured at many loci at several different time steps. With that we can define

$$\Delta p_t = p_{t+1} - p_t \quad ,$$

where $p_{i,t}$ is the frequency of one allele at time t ¹⁹ and

$$\text{Var}(\Delta p_t)$$

is the variance of Δp_t across loci. Buffalo and Coop [1] point out that

$$\text{Var}(\Delta p_t) = \sum_{i=0}^{t-1} \text{Var}(p_i) + \sum_{i \neq j} \text{Cov}(p_i, p_j) \quad .$$

¹⁷Search on 8 October 2023.

¹⁸Do I even need to say it anymore? Would I be asking this question if the answer were “No”?

¹⁹Notice that I am implicitly assuming that we have only two alleles at each locus. This method will be useful with SNP data, but may not be useful for other data.

If allele frequency changes are entirely neutral, then there won't be any correlation between them at different time steps.²⁰ If we have a way to estimate $\text{Cov}(p_i, p_j)$ and it turns out to be different from zero, then we have evidence of selection.²¹ In a later paper Buffalo and Coop estimate that between 17 and 37 percent of the allele frequency changes seen in a 10-generation, high-temperature selection experiment with ten replication populations is due to natural selection [2]

References

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²⁰Remember that I told you drift has no memory. The probability of moving from p_t to p_{t+1} depends only on what p_t is and how big the effective population size is. Not on the allele frequency trajectory leading to p_t .

²¹It's actually a bit more complicated than that, because things other than selection can lead to a non-zero covariance. Read [1] if you want all of the gory details.

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