tion. One would be the use of model materials of unit density. This would give the models neutral buoyancy in water and they could be suspended unsupported, so that their "spontaneous" three-space configurations would have greater fidelity. This could be of particular value in coiling-uncoiling and replication problems. Other useful inventions for an ideal model would be a way to represent strong ionic and electrostatic attractions, or the weak charge-transfer forces. In fact, it would be desirable, although it is probably not feasible, to represent all the major chemical force-fields with strengths more or less according to scale.

Some day it would also be most valuable to have molecular models that can represent a chemical reaction, by snapping from some ground-state configuration into some transition-state configuration and on over into the new configuration after the reaction. I tend to believe that certain DNA, enzyme, and other configuration problems may not be solvable by considering merely the static configurations in the dry state, and that we will have to think in terms of the dynamic transition-state configurations of the whole coiled system at the moment of attachment or reaction and in the presence of water.

However this may be, it would appear that it should be feasible to incorporate in molecular models at least some of the features I have mentioned. But I have listed them mainly to exemplify my main point, which is that molecular models could be made which would be cheaper, more widely available, more convenient, and yet more accurate in representing the essential features of macromolecular structures than any models we now have. The production of such models would be of the greatest importance to both research and teaching in the biophysical and biochemical sciences.

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Blood Types in Fur Seals

Abstract. Individual variations exist in the erythrocyte antigens of fur seals (*Callorbinus ursinus*).

Studies of blood type are being conducted on several species of whales and fishes (*1*). They have the common aim of obtaining information useful in the characterization of intraspecific interbreeding populations similar to those that have been demonstrated in human beings and cattle (*2*). Our research shows that such studies have a potential for similar usefulness in the fur seal species (*Callorbinus ursinus*).

Table 1. Summary of fur seal blood types so far differentiated by the absorption of rabbit anti-fur seal serum.

Type	Distinguishing antigens	Individuals collected and date (1958)
1	I, II, III	No. 636, 23 Mar.
2	I, III	No. 132, 24 Mar.; No. 637 and 639, 23 Mar.
3	III	All except those noted here
4	Negative	No. 329, 27 May

Table 2. Reactions of the serums of winter (1959) fur seals with fur seal erythrocytes.

Reaction	Asiatic coast	American coast
A. Number of cell samples reacting positively with serum No. 408 (American coast)		
Positive	2	0
Negative	142	27
Total	144	27
B. Number of serum samples reacting positively with cells of individual No. 113 (Asiatic coast)		
Positive	5	12
Negative	5	8
Total	10	20

The fur seals of the North Pacific Ocean are noted for their interesting migratory and breeding habits. These seals winter in two separate groups off the northern coast of Asia and North America, respectively. These groups move north in the spring to reproduce on the Robben, Komandorski, and Pribilof islands. An international commission representing Canada, Japan, the United States, and the U.S.S.R. was established in 1957 to coordinate the management of this species (*3*). Present biological studies under this commission include efforts to determine the degree to which the total species population may be subdivided into separate breeding stocks, and the extent to which these stocks intermingle in winter. Starting in 1958 these efforts have included some exploratory work in blood typing and serology, carried on independently by Fujino in Japan (*4*) and by Ridgway in the United States (*5*). This paper reports on blood type variations discovered for the first time in this species by Fujino. These variations occurred among seals wintering off northern Honshu, Japan.

Table 1 summarizes the results of observations that demonstrated the individuality of these variations. At least four different blood types occur that distinguish certain individuals from the majority of seals sampled. While these individuals occur in low frequency, additional antigenic variations exist that have not yet been sufficiently characterized. These include one within an antigen that resembles the species-specific human B-like antigen recently described in fin whales (*6*). Isoimmunization, although not yet attempted, would seem to offer a practical possibility for revealing further blood types in this species.

No natural antibodies have yet been found in serums of the horse, cow, pig, goat, and sheep that distinguish individual blood types. However, the normal serums of four rabbits all agglutinated type 1 cells (No. 636), and three of these also agglutinated type 2 cells (No. 639). Titers averaged one in eight.

Isoagglutinins also occur at high frequency. A series of 12 serums contained seven that agglutinated type 1 cells (No. 636), plus one that agglutinated both type 1 cells (No. 636) and type 2 cells (No. 639). Titers averaged one in two. Table 2 outlines a simple method of obtaining data on the frequency of isoagglutinin positive types. (In developing this method recognition must be given to the fact that the isoantibodies in some serums are lost after several freezings and thawings, and that therefore isoserums should be divided into aliquots while they are still fresh.)

While the 234 samples studied in 1958 were collected rather evenly over a range of 4 months (March through June), all individuals of types 1 and 2 were taken on 23 and 24 March. Similarly, out of 144 samples tested in 1959, both isoagglutinin positive individuals were collected on 2 April. These samples were collected during March, April, and May. This nonrandom distribution of types in the early part of the season is suggestive that some localization of breeding stocks is maintained within the winter population from year to year.

The glycerol-freezing technique, as applied in the blood typing of whales (*7*), has been successfully used to preserve intact erythrocytes of fur seals for several months. This observation, together with those on antigenic variations summarized above, leads to the conclusion that there is a good probability that blood type antigens could be used to advantage in research on fur seal populations (*8*).

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Gene Flow and Divergence under Disruptive Selection

Abstract. Two halves of a population exposed to selection in opposing directions can diverge despite gene flow of the same amount as is given by random mating. Divergence was as great as it is with complete isolation. Isolation, therefore, is not a prerequisite of divergence under divergent selection pressures.

Thoday and Boam (*1, 2*) have demonstrated that two halves of a population of *Drosophila melanogaster* can diverge when selected for opposite extreme values of a metric character (sternopleural chaeta number) even though all the individuals of every generation are the progeny of hybridization between the two halves. They have pointed out that their results throw doubt on the assumption that isolation is a necessary prerequisite of such divergence in natural populations.

The population maintained by Thoday and Boam involved forced gene flow such that the two halves of the population exchanged 50 percent of their genes in each generation. This is twice as much gene flow as the maximum usually considered in relation to natural populations, for random mating involves only 25 percent gene flow. We have accordingly run two selection lines under disruptive selection with positive assortative mating, using a system that gives 25 percent gene flow by male migration (Table 1). For comparative purposes, two lines with 50 percent gene flow (which differed from that of Thoday and Boam in that males were used for migration), and two with no gene flow (complete isolation) were maintained. All originated from the wild stock that was used by Thoday and Boam (*1–3*). Culture conditions and the proportion of flies selected were also the same.

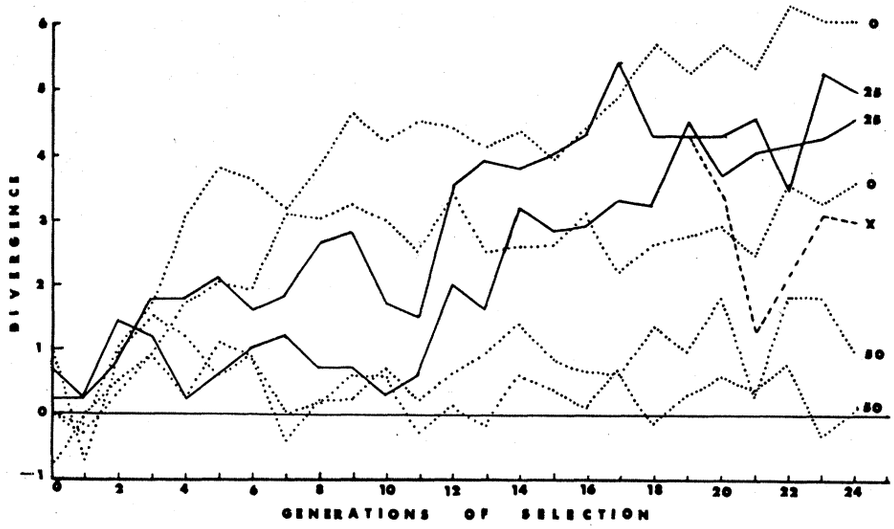

Fig. 1. Differences, in chaetae per fly, between the mean for the high half and that for the low half of each line in each generation. Dotted curves, the 0 and 50 percent gene-flow lines. Solid curves, the 25 percent gene-flow lines. Broken curve (*X*), the 25 percent gene-flow negative-assortative-mating subline.

The results are presented in Fig. 1, in which the differences between the mean chaeta number of the high and that of the low halves of each line are plotted for each generation.

Fifty percent gene flow permitted some divergence, though it is clearly a great restriction. The divergences of the 25 percent gene flow populations are very much greater. Though slower to develop than those permitted by complete isolation (no gene flow), their magnitude is of the same order. This might not be so if the population sizes were larger, but it provides a striking demonstration that very considerable divergence is possible without isolation. The mean chaeta numbers of these populations are of the order of 19, and the differences between the high and low halves of the 25 percent gene flow populations must be considered very large in relation to this mean.

The relevance of these results to theories related to natural populations is somewhat limited by the fact that the flies which convey genes from one half of a population to the other are selected for chaeta numbers deviating in the direction appropriate to the half population *to* which they are made to migrate. We have therefore taken a subsidiary line from one of the 25 percent gene flow populations and maintained it under 25 percent gene flow, disruptive selection with negative assortative mating. That is to say, the flies that are to carry genes from the low- to the high-chaeta-number half of the population are selected for low chaeta number, and those that migrate from high to low halves are selected for high

Table 1. Mating and selection system used for disruptive selection with 25 percent gene flow. The entries designate the flies chosen to perpetuate each of four female lines in each generation. H indicates the highest, and L the lowest chaeta number fly found in the appropriate culture. The letters A, B, C, and D indicate the culture from which the fly was selected.

Female line	Female parent	Male parent, Generation 1	Male parent, Generation 2	Male parent, Generation 3	Male parent, Generation 4
		High half population			
A	AH	BH	DH	BH	DH
B	BH	CH	AH	CH	AH
		Low half population			
C	CL	DL	BL	DL	BL
D	DL	AL	CL	AL	CL