only conditions of performance and nonperformance but also the long-term effects of training.

Our observations indicate a clear dependence of cortical cell activity on the behavioral state of the animal (*10*). On the basis of these results we argue that the interpretation of electrophysiological data in sensory systems must take into consideration not only the physiological state of the preparation but also the training and current behavioral state of the awake animal. We suggest that interpretation of cellular activity in sensory behavior requires, beyond the traditional analysis of neuronal response to stimulus manipulation, the specification of rigidly defined behavioral contexts within which stimuli are presented. The effects on cell activity of systematic changes in the animal's behavior can then be assessed. A number of conditioning procedures, such as the RT method, are available for the precise measurement of sensory function in animals (*11*). Coupled with available chronic electrophysiological procedures and adequate control of the sensory stimuli, these procedures satisfy the requirements of such an approach. They permit the systematic independent control of both the peripheral input to the animal and the behavioral context within which it is presented. It is proposed that such an approach is necessary if we are to evaluate the role of central structures in behavior (*12*).

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References and Notes

1. An "acute" electrophysiological procedure is a short-term experiment beyond which no further data are required. Ordinarily, the animal is under local or general anesthesia, may be paralyzed, and is usually killed immediately at the termination of the experimental session. In a "chronic" procedure the study involves prolonged, repetitive observations, and the animal is usually not anesthetized during recording sessions.
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8. Subsequently, we have observed some cells in the behaviorally trained animal which were not influenced by ongoing performance in the behavioral task.
9. We have also noted a decrease in amplitude in auditory evoked primary potentials when monkeys are switched from a performing to a nonperforming condition in this simple RT task.
10. This conclusion is supported by others [R. Galambos and D. F. Brogdanski, in *Neural Mechanisms in the Auditory and the Vestibular Systems*, G. L. Rasmussen and W. F. Windle, Eds. (Thomas, Springfield, Ill., 1960), p. 143; E. F. Evans and I. C. Whitfield, *J. Physiol. London* **171**, 476 (1964)]. Alternative interpretations are possible [E. F. Evans, in *Hearing Mechanisms in Vertebrates*, A. V. S. DeReuck and J. Knight, Eds. (Churchill, London, 1968), p. 272].
11. W. C. Stebbins, Ed., *Animal Psychophysics: The Design and Conduct of Sensory Experiments* (Appleton-Century-Crofts, New York, 1970).
12. This material was presented in part at a workshop sponsored by the Information Center for Hearing, Speech, and Disorders of Human Communication, Baltimore, Maryland, 26–27 June 1971, and will be published in *The Physiology of the Auditory System*, M. Sachs, Ed. (National Educational Consultants, Baltimore, in press).
13. We are indebted to R. Smith for invaluable technical assistance. Supported by PHS grants RR 00166 and NS 08181.

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Nucleotide Conformations

Rubin *et al.* (*1*) in comparing the conformations of uridylyl-(3′,5′)-adenosine phosphate (UpA) (*2*) and A-RNA (*3*) have perpetuated errors in Sundaralingam's earlier dihedral angle calculations (*4*) from A-RNA coordinates. The correct values of the conformations are shown in the first column of Table 1. In any case, these RNA coordinates, from a manual model-building study, have for some time been superseded by the more accurate results of linked-atom least-squares refinements (*5*, *6*), the second of which utilized high quality data from a synthetic, complementary double-helical RNA that provided almost twice as many x-ray reflections as the original (isostructural) viral RNA. Rubin *et al.* (*1*) were concerned also to emphasize the conformational differences between UpA and A-RNA. Use of the erroneous angles or even the corresponding correct, but inaccurate, values obscures some striking similarities in conformation.

Rather than compare the UpA conformations with a single polymer structure determination (however accurate), we show in Table 1 the mean values (and estimated standard deviations from the mean) of conformation angles (Fig. 1) found in eight appropriate (*7*), helical, polynucleotide structure determinations. We also show corresponding data derived from x-ray analyses of monomer crystals (*8*).

Twenty values for conformation angles in two structurally distinct UpA molecules are available (Table 1). Except in three instances (ϕ of one molecule and ψ, ϕ of the second) the values, or average values where appropriate, differ by less than two standard deviations from the corresponding average values observed for polynucleotides to date. The three exceptional values are equally similar to conformational alternatives noted in monomers (*9*). In the great majority of its conformation-angles, therefore, UpA has values no more different from any particular

Table 1. A comparison of the backbone conformations in UpA, double-helical polynucleotides and monomers. The angles are defined in Fig. 1. No estimated standard deviation (E.S.D.) from the mean is shown for σ in the case of the polymer structures (*) since the sugar ring was kept fixed in the linked-atom, least-squares refinements.

Conformation angles	Early A-RNA results (deg)	(UpA) I (deg)		(UpA) II (deg)		UpA mean (deg)	Mean values (and E.S.D.)	
		A	U	A	U		Linear polymers (deg)	Monomers (deg)
χ	62	108	80	98	69	89	89(9)	79(10)
σ	75	94	81	83	87	86	83(*)	77(13)
ξ	69	52	54	57	49	53	53(3)	52(8), −179(9), −67(2)
θ	165	−167		−159		−163	−169(17)	176(13)
ψ	−78	−88		84			−69(17)	60(15), −179(9), −60(14)
ϕ	−83	164		84				
ω	−136	−138		−159		−149	−166(19)	−108(16)

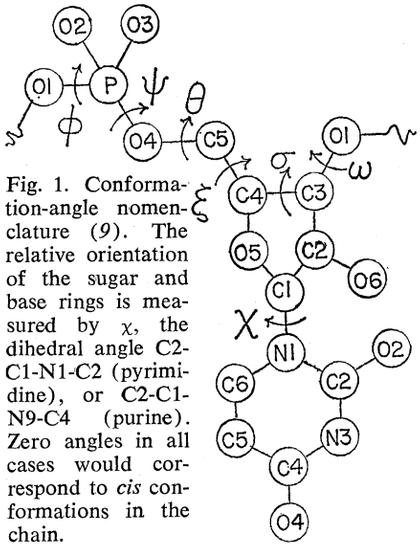

Fig. 1. Conformation-angle nomenclature (*9*). The relative orientation of the sugar and base rings is measured by χ, the dihedral angle C2-C1-N1-C2 (pyrimidine), or C2-C1-N9-C4 (purine). Zero angles in all cases would correspond to *cis* conformations in the chain.

polynucleotide result than is commonly observed. The three exceptions, while noteworthy, should not be allowed to obscure this interesting result.

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7. The polymer structure determinations considered appropriate all involve nucleotides with (C3′-*endo*, C2′-*exo*)furanose conformations as in UpA. Further, only structure determinations where linked-atom, least-squares refinement (*5*) has produced optimized conformation angle values are included.
8. The monomer survey presented here includes only values of χ corresponding to the *anti* conformation of J. Donohue and K. N. Trueblood [*J. Mol. Biol.* **2**, 363 (1960)] since this is the only type observed at the four bases of the two different UpA molecules.
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10. This research was supported by NIH grant GM17371 and an Eli Lilly grant.

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Arnott and Hukins' comment consists of essentially two parts. First, they point out that we have made some errors in reporting the torsion angles of A-RNA (RNA-11). Second, they claim that our emphasizing the conformational differences between UpA and A-RNA has obscured the similarities in their conformation. Regarding the first point, we acknowledge that errors were made in citing some of the torsion angles of A-RNA. Four of the values were in error by 2°, 4°, 5°, and 8°. It should be remarked that these errors are comparable to the estimated standard errors (E.S.D.'s in the torsion angles generally obtained in fiber diffraction studies of polynucleotides [It may be noted that Arnott and Hukins in their comment have made errors of 6°, 8°, and 11° in reporting the values of the torsion angles C2-C1-N1-C2 (pyrimidine) and C2-C1-N9-C4 (purine) of UpA1 and UpA2 which they deduced from our published values of the glycosyl tension angles X_{CN}. These errors are highly significant in comparison to the E.S.D.'s in the torsion angles in the UpA structure.] The errors in the A-RNA torsion angles neither invalidate our conclusion that the major differences in the overall conformations of UpA1 and UpA2 and the corresponding unit in A-RNA occur in the conformation angles about the P-O3′ and P-O5′ ester bonds, nor do they obscure the similarities in the remaining conformation angles of the sugar-phosphate bonds (*1*, table 1). We naturally emphasized these striking conformational differences because the conformation about the P-O3′ bond in UpA1 differs by 113° from the corresponding value in A-RNA while the conformations about P-O3′ and P-O5′ in UpA2 differ by 167° and 162°, respectively, from the corresponding values in A-RNA. Furthermore, the emphasis of P-O bond rotations was made because it has important bearing on the folding of polynucleotide chains into hairpin loops.

With respect to their second point of having obscured the conformational similarities in UpA and A-RNA, we completely disagree. It is clear from our comparison of the torsion angles given in Table 1 that the conformational angles of the sugar-phosphate backbone other than those about the P-O ester bonds are similar. In addition, we did emphasize (*1*) that all four nucleoside moieties of the two UpA molecules exhibit the preferred *anti* conformation about the glycosyl bond and C3′-*endo*, C2′-*exo* sugar puckering similar to that of A-RNA.

We have given further details of the comparison between UpA, mononucleotides and nucleosides, and polynucleotides elsewhere (*2*).

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Stability in Zoological Nomenclature

Mayr *et al.* (*1*) discussed the procedure of protecting well-established names of animals by means of Article 23(b) of the International Code of Zoological Nomenclature but they did not present the complete history of Declaration 43 (*2*) in their article. They quote Declaration 43, but omit the first two items of the Declaration, which read:

1. Article 23(b) is hereby repealed.
2. For the period from 6 November 1961 to the date of publication of this present Declaration [December 1970], Article 23(b) is to be read as follows:

The only reference to these statements by Mayr *et al.* is in their note 2:

The so-called "Declaration 43" . . . purporting to repeal Art. 23(b), does not represent the vote of the Commission . . . Furthermore, the Commission has the authority to classify and interpret the Rules, but only the International Congress of Zoology can repeal any provision of the Rules.

Repeal of Art. 23(b) certainly does represent the vote of a majority of the Commission as shown in the 27-page history of the case that follows the Declaration. The members of the Commission voted on four proposals:

1) Accepting the draft Declaration as a satisfactory new text of Art. 23(b) —passed 16 to 7.

2) Requesting the XVII International Congress of Zoology to replace the text of Art. 23(b) with the present Declaration—passed 14 to 8.

3) Making the Declaration come into force as of January 1961—passed 16 to 6.

4) Requesting the XVII International Congress to delete Art. 23(b) from the Code—passed 13 to 10.

Item 4 seems to us clear and unambiguous, and there can be no question of the opinion of the majority of the Commission. This vote was taken only for the record (*2*), and was not