of pure polyvalent metals[5]. The application to InBi of the nearly free electron model[6,7], which has met with some success in understanding pure metals, will be attempted when more data are available. de Haas–van Alphen measurements should be possible on a wide variety of metallic compounds, thus providing insight into the nature of electronic binding and structure in such materials.

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A Method of Calibrating Two-Sphere Non-directional Radiometers

When two heated spheres, one black and one bright, but otherwise identical, are kept at the same temperature, they lose an equal amount of heat by conduction and convection[1]. Any difference in heat input is due to the difference in radiational exchange. Neither air temperature nor air velocity enters the calculations for determining the mean radiant temperature of the surroundings. The quantities needed are: the heat input of the two spheres; the temperatures of the two spheres (which should be equal); the surface area; the emissivities of the bright and the black sphere. Nickel[1] or gold[2] is used for plating the bright sphere.

Attempts have been made to predict the accuracy of the two-sphere radiometer from the above quantities. Roose[1] reasoned that, as the heat input can be measured with an accuracy of ± 0·5 per cent, the error in mean radiant temperature would be ± 0·36° F. Sutton and McNall[2] anticipated errors not exceeding ± 2° F.

The method now proposed avoids the need to measure surface areas and emissivities. Advantage is taken of times and circumstances when the readings of a globe thermometer[3] and of air temperature happen to be equal. This is so, for example, out of doors in the evening during the transition from solar heat gain to radiational loss; or it may be so indoors under certain conditions. In such circumstances, it is clear that there is then, for the time being, a state of thermal equilibrium in which globe temperature and air temperature are both equal also to the mean ambient radiant temperature, so that the latter is known. Thus, if the two-sphere radiometer is operated at such a time, the answer which it should give is known, and only the heat inputs to the spheres need be measured, in addition, in order to enable its calibration constant to be found.

Using the above method it was found that the average error when measuring mean radiant temperatures with the Sutton–McNall[2] instrument was 0·4 deg. F.; the highest deviation encountered was 1 deg. F.

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BIOPHYSICS

Montmorillonite as a Caliper for the Size of Protein Molecules

It is known that proteins may be adsorbed from solution by the clay montmorillonite, leading to an increase in $d(001)$ crystallographic spacings[1]. In order to compare these increases with the size of protein molecules one must be certain that a complete mono-molecular layer of protein has been adsorbed, and this can be calculated to require 1·3–2·0 gm. of protein per gm. of clay. As the clay becomes saturated the adsorption isotherm levels off, but the isotherms are initially steeper than curves of the Langmuir type[2]. Assuming that protein molecules are spherical, we have calculated the expected $d(001)$ spacings and compared them with the experimental values found (Table 1). The agreement is moderately good for all but pepsin. Hæmoglobin appears to be adsorbed as a monomer, whereas lactoglobulin enters the clay particles as a dimer.

Table 1. Adsorption of Proteins by Montmorillonite

Protein	Mol. wt.	Adsorption (gm./gm.) Theoretical	Adsorption (gm./gm.) Experimental	Calculated mol. diam., Å	$d(001)$, Å. Theoretical	$d(001)$, Å. Experimental
Lysozyme (native)	14,700	1·3	1·3	32·6	42·2	44
(denatured)	14,700	—	1·3	—	—	46
Chymotrypsinogen	22,500	1·5	1·4	37·2	46·8	40
Lactoglobulin	35,000 (17,500)*	1·7	1·5	43·8 (34·8)	53·4 (44·4)	54 —
Pepsin	35,000	1·7	1·0	43·8	53	18
Hæmoglobin (human)	63,000 (40,000)*	2·0	1·9	53·2 (45·6)	62·8 (55·2)	58 —

* These proteins dissociate under extreme conditions of dilution and/or salt concentration to give the values in parentheses (ref. 3).

Our result with native pepsin agrees with that of Talibudeen[4], namely, that the $d(001)$ spacing is about 18 Å. for a wide range of amounts of protein adsorbed; it indicates an unfolding of pepsin molecules into extended polypeptide chains within the clay particles.

It has often been suggested that during heat denaturation of proteins there is a tendency for protein molecules to undergo unfolding or expansion. We have found that the $d(001)$ spacings of montmorillonite–lysozyme complexes are the same for adsorbed, heat-inactivated lysozyme as for native lysozyme, from which it may be concluded that lysozyme does not change drastically in shape on undergoing denaturation in solution.

Tobacco mosaic virus (isoelectric point 3·5) was allowed to react with sodium (Wyoming) bentonite at *p*H 3·2 (citrate buffer, ionic strength 0·0375). According to spectrophotometric analysis, 1,830 mgm. of virus was adsorbed per gm. of clay. At this value, about 15 per cent of the internal surface area