

for it to be possible for the transition to a polymer to occur spontaneously within the solid. Thus, it seems more likely that the polymerization is a surface phenomenon, involving free radicals, and that it slowly affects the entire crystal.

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A Barbiturate Without Hydrogen Bonding: The Crystal Structure of Sodium 1-Methyl-5,5-diethylbarbiturate (Sodium Metharbital)

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The crystal structure of sodium 1-methyl-5,5-diethylbarbiturate $\text{Na}_2\text{C}_9\text{N}_2\text{O}_3\text{H}_{13}$ (also called sodium metharbital or sodium gemonil) has been determined from X-ray data measured on an automatic diffractometer. The crystal data are: space group $Pna2_1$, $a = 12.670$ (3), $b = 10.796$ (2), $c = 7.802$ (2) Å, $Z = 4$, $D_m = 1.369$ g.cm⁻³. The final R is 0.023. The conformation of the metharbital ion is similar to the conformations of the barbital ion and the barbital molecule. Methylation of the pyrimidine ring at N(1) and deprotonation at N(3) decrease the internal bond angles at N(1) and N(3) by approximately 4–5° each. In the absence of hydrogen bonding, the dominant role in crystal packing is played by ionic coordination interactions. The sodium ion is fivefold coordinated by four oxygen atoms and the deprotonated nitrogen atom. The extremely short Na–N distance of 2.42 Å suggests that this nitrogen atom carries a great part of the formal negative charge of the metharbital anion.

Introduction

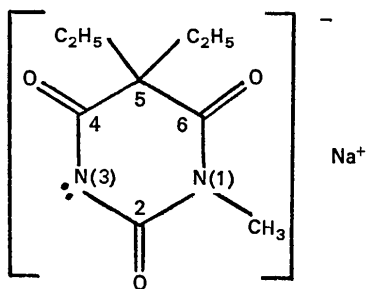
In the crystal structures of barbiturates determined so far, hydrogen bonding seems to play the dominant role in packing the barbiturate molecules or ions. Depending on the type of compound (free barbituric acid, salt, or complex), other intermolecular interactions may also be important: the requirements of effective packing of the alkyl groups (Gartland & Craven, 1971), C=O...C=O dipole-dipole interactions (Prout & Wallwork, 1966), and coordination of cations (Berking & Craven, 1971; Berking, 1971*a,b*).

In those barbiturates in which the hydrogen atoms at C(5) are substituted, the imino nitrogen atoms N(1) and N(3) in the pyrimidine ring serve as donors (or if deprotonated, as acceptors), and the exocyclic oxygen atoms serve as acceptors for hydrogen-bonding in a variety of ways.

The crystal structure of sodium 1-methyl-5,5-diethylbarbiturate (also called sodium metharbital or sodium gemonil) was determined because here, N(1) being methylated and N(3) being deprotonated, hydrogen-bonding is *a priori* impossible. Therefore the other binding types mentioned above are dominant. The re-

sults have already been reported briefly (Berking, 1971c).

sity was measured by flotation in a mixture of chloroform and *n*-hexane. The crystal data are:



Space group: *Pna*2₁ (from systematic absences)
M.W. 220.20

a = 12.670(3), *b* = 10.796(2), *c* = 7.802(2) Å

V = 1067.97 Å³, *Z* = 4

D_m = 1.369, *D_x* = 1.370 g.cm⁻³.

Experimental

The lattice parameters and X-ray intensities were measured on a Picker FACS I automatic diffractometer, using Cu *K*α radiation and a graphite monochromator. The crystal, with dimensions 0.2 × 0.1 × 0.1 mm, was mounted with *c* along the diffractometer ϕ axis. Intensities for 962 independent reflections (each intensity being measured at least twice) were measured in the θ -2 θ scanning mode up to 2 θ = 130°. Of these, 73 reflections were considered to be 'unobserved', because their net intensities did not exceed three times the standard deviation estimated from counting statistics. Absorption corrections were not applied.

Sodium metharbital was prepared by adding sodium hydroxide and metharbital in ethanol solution. Crystals were transparent and prismatic, the longest dimension being along the *c* axis. X-ray reflections were absent for *Ok**l* (*k* + *l* = 2*n* + 1) and *h*0*l* (*h* = 2*n* + 1). The den-

Table 1. |*F*_o| and |*F*_c| multiplied by 10

Unobserved reflections are indicated by *; reflections affected by extinction and not included in the final refinement are indicated by +.

Table with 12 columns of numerical data representing |F_o| and |F_c| values for various reflections. The table is organized in a grid-like structure with 12 columns. The first column contains reflection indices (hkl) and the following 11 columns contain intensity values. Unobserved reflections are marked with an asterisk (*) and reflections affected by extinction are marked with a plus sign (+).

Structure determination and refinement

The phase problem was easily solved using direct methods. The assignment of origin- and enantiomorph-determining phases in space group $Pna2_1$ (type $1P220$ in the notation of Hauptman & Karle, 1955) is similar to that in space group $P2_1$ (type $1P202$). A tangent refinement with the starting phases:

No.	h	k	l	$ E $	α
1	2	3	0	2.90	π
2	5	7	0	2.56	π
13	5	3	1	2.10	0
15	10	1	5	2.03	0.6π

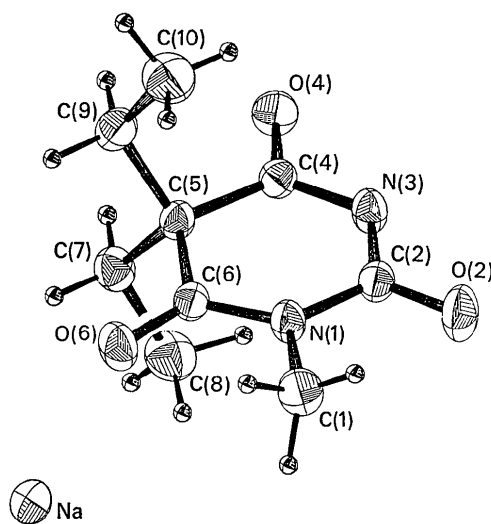


Fig. 1. The structure of sodium metharbutal in the 50% probability ellipsoidal representation of the atomic thermal parameters (Johnson, 1965).

converged with $R_E = \sum ||E_o| - |E_c|| / \sum |E_o| = 0.20$ and yielded the phases for 146 reflections with $|E| > 1.36$. An E map, based on these phases, showed all 15 non-hydrogen atoms.

The atomic parameters were refined by full-matrix least-squares program *ORFLS* in the IBM 7090 version of Shiono (1966). The X-ray atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1962) for the heavy atoms and from Stewart, Davidson & Simpson (1965) for the hydrogen atoms. The sodium ion was treated as an atom with $Z=11$. Anomalous dispersion was applied for the sodium ($\Delta f' = 0.1$, $\Delta f'' = 0.2$) and for the oxygen atoms ($\Delta f' = 0.0$; $\Delta f'' = 0.1$). The function minimized was $\sum w\Delta^2$, using the empirical weighting scheme, $1/w = \sigma^2(F) = 1.25 - 0.075F + 0.0015F^2$. The refinement reduced $R = \sum |\Delta F_{\text{meas}}| / \sum |F_{\text{meas}}|$ to 0.076 and 0.050, using individual isotropic and anisotropic thermal parameters respectively. At this stage, the hydrogen atoms were located from a difference electron density map.

Refinement with anisotropic thermal parameters for the heavy atoms and isotropic ones for the hydrogen atoms, and removing nine reflections which appeared to be affected by extinction, reduced the R value to 0.023 (0.027) for the observed (all) reflections, and R_w to 0.030 (0.030) with $[\sum w(\Delta F)^2 / (m-n)]^{1/2} = 1.28$. The observed and calculated structure amplitudes are given in Table 1. The final atomic positional and thermal parameters are given in Table 2. The thermal parameters (Fig. 1) are represented as 50% probability ellipsoids (*ORTEP*, Johnson, 1965). The best least-squares fit of anisotropic thermal parameters to a rigid-body motion (Schomaker & Trueblood, 1968) was calculated and found to be satisfactory when the atoms of the two ethyl groups are omitted. Bond length corrections, assuming rigid-body motion, are about 0.005 Å (Table 3).

Table 2. Atomic parameters with *e.s.d.*'s

Positional parameters are given as fractions of the lattice translations. Thermal parameters are given according to the expression:

$$T = \exp [- (\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)].$$

The *e.s.d.*'s given in parentheses refer to the least significant figures in the parameter values. The z coordinate of the sodium atom has been set at zero and fixed.

(a) Heavy atoms

All values are $\times 10^4$.

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
Na	4511.7 (5)	81.3 (7)	0	33.7 (4)	59.1 (6)	96.9 (12)	-4.8 (4)	0.6 (7)	1.0 (7)
N(1)	2837 (1)	3146 (2)	-1491 (2)	37 (1)	60 (1)	73 (3)	13 (1)	1 (1)	3 (2)
C(1)	3497 (2)	2730 (3)	-2923 (4)	57 (2)	79 (2)	88 (3)	22 (2)	15 (2)	-6 (2)
C(2)	1914 (2)	3842 (2)	-1844 (3)	36 (1)	53 (2)	82 (3)	3 (1)	-5 (2)	2 (2)
O(2)	1699 (1)	4004 (2)	-3380 (2)	61 (1)	106 (2)	80 (3)	27 (1)	-7 (1)	12 (2)
N(3)	1314 (1)	4302 (2)	-581 (2)	32 (1)	61 (2)	88 (3)	12 (1)	-1 (1)	4 (2)
C(4)	1553 (1)	4098 (2)	1071 (3)	31 (1)	48 (2)	86 (3)	-1 (1)	-1 (2)	-1 (2)
O(4)	989 (1)	4552 (1)	2196 (2)	42 (1)	74 (1)	101 (2)	14 (1)	13 (1)	-14 (2)
C(5)	2495 (2)	3312 (2)	1617 (3)	33 (1)	51 (2)	67 (3)	5 (3)	0 (2)	-1 (2)
C(6)	3108 (1)	2789 (2)	125 (3)	32 (1)	48 (1)	79 (4)	3 (1)	-4 (2)	-2 (2)
O(6)	3852 (1)	2080 (1)	343 (2)	46 (1)	79 (1)	116 (3)	29 (1)	-4 (1)	0 (2)
C(7)	3262 (2)	4127 (2)	2678 (3)	37 (1)	67 (2)	98 (4)	3 (1)	-6 (2)	-13 (2)
C(8)	3732 (2)	5208 (2)	1691 (4)	52 (2)	74 (2)	195 (6)	-9 (2)	-8 (3)	1 (3)
C(9)	2100 (2)	2223 (2)	2730 (3)	46 (1)	57 (2)	94 (4)	4 (1)	3 (2)	9 (2)
C(10)	1309 (2)	1397 (2)	1810 (4)	57 (2)	65 (2)	171 (5)	-10 (2)	1 (2)	12 (3)

Table 2 (cont.)

(b) Hydrogen atoms

Positional parameters are $\times 10^3$.				
	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i>
H(11)	342 (3)	185 (4)	-322 (7)	7.9 (1.0)
H(12)	425 (4)	273 (4)	-265 (7)	6.7 (0.9)
H(13)	347 (4)	329 (4)	-372 (7)	8.2 (1.2)
H(71)	285 (2)	442 (2)	365 (4)	2.9 (0.5)
H(72)	390 (2)	361 (3)	296 (4)	3.5 (0.6)
H(81)	419 (3)	566 (3)	248 (5)	5.3 (0.8)
H(82)	430 (3)	497 (3)	84 (6)	5.8 (0.8)
H(83)	323 (3)	572 (4)	133 (6)	6.1 (0.9)
H(91)	177 (2)	261 (2)	361 (4)	3.2 (0.5)
H(92)	273 (2)	175 (2)	298 (4)	2.8 (0.5)
H(101)	110 (2)	77 (3)	250 (5)	3.8 (0.6)
H(102)	65 (2)	188 (3)	132 (4)	4.1 (0.6)
H(103)	168 (3)	102 (3)	78 (7)	6.7 (1.0)

Table 3. Intra- and intermolecular distances and angles

The standard deviations are estimated as follows:

C-N, C-O, C-C bonds within the pyrimidine ring, Na-O and Na-N distances	0.002 Å
C-C bonds in the aliphatic chains	0.003-4
C-H bonds	0.04
C-N-O angles and angles between atoms at the ring	0.3°
C-C-C angles in the diethyl chains	0.5

(a) Bond lengths

The values for bond lengths between nonhydrogen atoms are corrected for rigid-body thermal motion. The uncorrected values are given in Fig. 3.

N(1)-C(2)	1.423 Å
C(2)-N(3)	1.344
N(3)-C(4)	1.348
C(4)-C(5)	1.530
C(5)-C(6)	1.514
C(6)-N(1)	1.368
N(1)-C(1)	1.470
C(2)-O(2)	1.246
C(4)-O(4)	1.238
C(6)-O(6)	1.230
C(7)-H(71)	0.97
C(7)-H(72)	1.01
C(8)-H(81)	0.97
C(8)-H(82)	1.02
C(8)-H(83)	0.89
C(9)-H(91)	0.90
C(9)-H(92)	0.96
C(10)-H(101)	0.91
C(10)-H(102)	1.05
C(10)-H(103)	1.01
C(1)-H(11)	0.98
C(1)-H(12)	0.97
C(1)-H(13)	0.87

(b) Bond angles (see also Fig. 3).

C(7)-C(5)-C(4)	108.9°
C(9)-C(5)-C(6)	108.4

(c) Sodium coordination tetrahedra

O(6)-Na-O(2) <i>g</i>	100°
O(6)-Na-O(4) <i>a</i>	92
O(6)-Na-N(3) <i>a</i>	96
O(6)-Na-C(4) <i>a</i>	90
O(6)-Na-O(4') <i>i</i>	104

Table 3 (cont.)

(d) Close intermolecular approaches

Na—C(4) <i>a</i>	2.86 Å
O(2)—H(71) <i>b</i>	2.78
O(2)—H(91) <i>b</i>	2.79
O(4)—H(11) <i>d</i>	2.61
O(6)—H(102) <i>a</i>	2.65
N(3)—H(92) <i>e</i>	3.1
H(71)—H(103) <i>d</i>	2.47
H(71)—H(13) <i>c</i>	2.51
H(72)—H(102) <i>a</i>	2.61
H(81)—H(12) <i>f</i>	2.65
H(82)—H(102) <i>a</i>	2.65
H(83)—H(11) <i>d</i>	2.45
H(91)—O(2) <i>c</i>	2.79
H(92)—H(83) <i>g</i>	3.09
H(101)—H(82) <i>h</i>	2.74

Symmetry code

	<i>x</i>	<i>y</i>	<i>z</i>
<i>a</i>	$\frac{1}{2} + x$	$\frac{1}{2} - y$	<i>z</i>
<i>b</i>	<i>x</i>	<i>y</i>	<i>z</i> - 1
<i>c</i>	<i>x</i>	<i>y</i>	<i>z</i> + 1
<i>d</i>	$\frac{1}{2} - x$	$\frac{1}{2} + y$	$\frac{1}{2} + z$
<i>e</i>	$\frac{1}{2} - x$	$\frac{1}{2} + y$	$-\frac{1}{2} + z$
<i>f</i>	1 - <i>x</i>	1 - <i>y</i>	$\frac{1}{2} + z$
<i>g</i>	$\frac{1}{2} - x$	$-\frac{1}{2} + y$	$\frac{1}{2} + z$
<i>h</i>	$-\frac{1}{2} + x$	$\frac{1}{2} - y$	<i>z</i>
<i>i</i>	$\frac{1}{2} - x$	$-\frac{1}{2} + y$	$-\frac{1}{2} + z$

Discussion

The metharbital ion

The conformation of the metharbital anion (Fig. 1) is similar to that of the barbital anions in sodium barbital (Berking & Craven, 1971) and calcium barbital trihydrate (Berking, 1971*a*), as well as the barbital molecule (Craven, Vizzini & Rodrigues, 1969; Craven & Gartland, 1970). The trioxypyrimidine ring including C(1) is nearly planar and the ethyl groups together with C(5) form a hydrocarbon chain which is nearly in the all *trans* configuration. Deviations from this idealized geometry are given in Table 4(b) as atomic displacements from the best least-squares planes and in Table 4(c) as torsion angles.

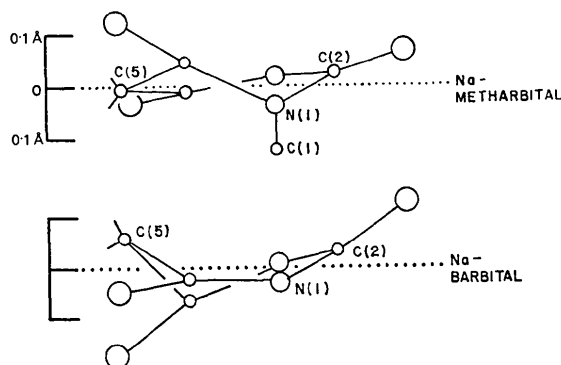


Fig. 2. Conformations of the trioxypyrimidine rings in sodium barbital and sodium metharbital. The dotted lines are the traces of the best least-squares plane through the six ring atoms. The scale in the vertical direction is about six times that in the horizontal.

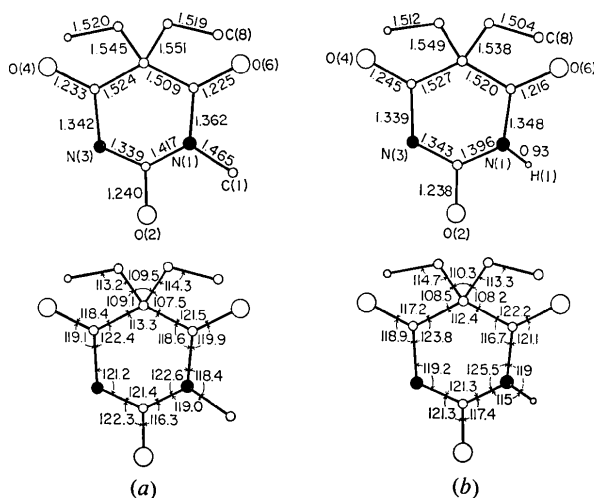


Fig. 3. Bond lengths (Å, top) and bond angles (°, bottom) for (a) the metharbital anion and (b) the barbital anion in their sodium salts. The e.s.d.'s are given in Table 3.

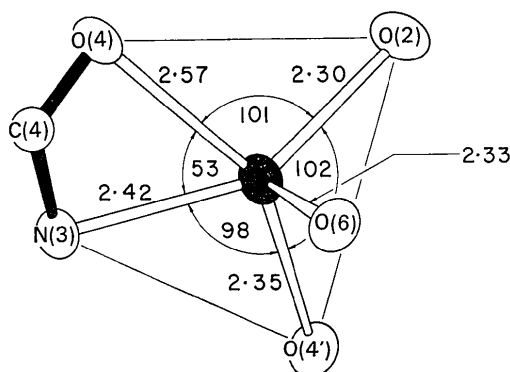


Fig. 4. The coordination of the sodium ion. The atoms N(3)–C(4)=O(4) belong to the same metharbital anion.

The slight puckering of the pyrimidine ring is shown in Fig. 2. It is evident that atoms N(1) and C(6) are farthest out of the plane, with a twist of 9.2° along N(1)–C(6), whereas in the barbital anion of sodium barbital and in three of four independent ions in calcium barbital trihydrate (the fourth one being flat) the tetrahedrally surrounded atom C(5) is farthest out of the plane, probably in order to relieve angular strain induced by the ring closure. All torsion angles including hydrogen atoms within the ethyl groups show *anti* conformation.

Bond lengths and bond angles for the metharbital ion are shown in Fig. 3 and Table 3 and if relevant are compared with those of the barbital anion in sodium barbital. As expected, these are very similar for the C–C bonds in the aliphatic chains and differ from the expected value (1.526 Å, Lide, 1962) in the same way: C(5)–C(7) and C(5)–C(9) are elongated, probably because of steric hindrance around C(5), whereas the terminal bonds C(7)–C(8) and C(9)–C(10) are shortened,

probably because of high thermal motion. Within the trioxypyrimidine ring, the C–N and C–O bonds show the characteristic features of deprotonation (Singh, 1965): the internal angle at N(3) is reduced by 5° . The C–N bonds on the deprotonation site N(3) are shorter (1.339 and 1.342 Å) than those at the nondeprotona-

Table 4. Least-squares planes and torsion angles

Plane 1: Through the six pyrimidine ring atoms.
 Plane 2: Through C(2), N(3), C(4), C(5).
 Plane 3: Through the atoms of the chain C(5), C(7), C(8), C(9), C(10).
 Plane 4: Through the atoms of the base of the coordination pyramid.

(a) Equations of the planes

$$\begin{aligned} \text{Plane 1: } & 0.571x + 0.820y + 0.028z = 4.762 \\ \text{Plane 2: } & 0.571x + 0.821y + 0.016z = 4.762 \\ \text{Plane 3: } & 0.760x - 0.570y - 0.312z = -0.029 \\ \text{Plane 4: } & -0.417x + 0.908y + 0.043z = -2.658 \end{aligned}$$

(b) Distances (Å) of atoms from the least-squares planes. The underlined values belong to atoms forming the planes. The e.s.d.'s are 0.002 Å for planes (1), (2), and (4) and 0.003–0.004 Å for plane (3).

	Plane 2	Plane 2	Plane 3
N(1)	<u>0.044</u>	0.058	—
C(2)	<u>-0.015</u>	<u>0.003</u>	—
N(3)	<u>-0.014</u>	<u>-0.007</u>	—
C(4)	<u>0.015</u>	<u>0.006</u>	-1.256
C(5)	<u>0.011</u>	<u>-0.003</u>	<u>0.001</u>
C(6)	<u>-0.040</u>	-0.041	1.277
C(1)	0.121	0.148	—
O(2)	-0.061	-0.028	—
O(4)	0.033	0.014	—
O(6)	-0.126	-0.129	—
C(7)	1.312	1.288	-0.020
C(8)	2.587	2.573	<u>0.009</u>
C(9)	-1.214	-1.239	<u>0.019</u>
C(10)	-2.537	-2.554	<u>-0.010</u>

Plane 4: O(2)*g* O(4')*i* N(3)*a* O(4)*a* Na O(6) C(4)*a*
 -0.006 0.007 -0.011 0.010 0.356 2.676 0.119

(c) Torsion angles within the pyrimidine ring (e.s.d.'s, 0.2°)

Bond vector	Torsion angle
N(1)–C(2)	7.23°
C(2)–N(3)	-1.43
N(3)–C(4)	-1.59
C(4)–C(5)	-0.55
C(5)–C(6)	5.79
C(6)–N(1)	-9.24

Torsion angles, including atoms of the methyl and the ethyl groups (e.s.d.'s, 0.3 – 0.4°)

C(1)–N(1)–C(2)–N(3)	-176.32°
C(1)–N(1)–C(2)–O(2)	3.35
C(1)–N(1)–C(6)–C(5)	174.29
C(1)–N(1)–C(6)–O(6)	-4.14
C(9)–C(5)–C(7)–C(8)	178.02
C(7)–C(5)–C(9)–C(10)	177.90
N(3)–C(4)–C(5)–C(7)	119.03
N(3)–C(4)–C(5)–C(9)	-121.46
N(1)–C(6)–C(5)–C(7)	-114.57
N(1)–C(6)–C(5)–C(9)	127.07

Table 4 (cont.)

Torsion angles including hydrogen atoms:			
H(71)–C(7)–C(8)–H(81)	60°	H(92)–C(9)–C(10)–H(101)	64°
	H(82) 167		H(102) –171
	H(83) –58		H(103) –54
H(72)–C(7)–C(8)–H(81)	–64	C(2)–N(1)–C(1)–H(11)	–104
	H(82) 42		H(12) 145
	H(83) 178		H(13) 34
H(91)–C(9)–C(10)–H(101)	–67	C(6)–N(1)–C(1)–H(11)	73
	H(102) 58		H(12) –38
	H(103) 176		H(13) –150

* Symmetry code: see Table 3.

tion site (1.362 and 1.417 Å); the two C–O bonds adjacent to N(3) are longer (1.240, 1.233 Å) than the remote C–O bond (1.225 Å) in this compound and the corresponding values in the crystal structure of the free acid metharbital (1.205, 1.209, 1.221 Å, Wunderlich, 1971). This indicates that part of the formal negative charge of the anion is equally distributed between the O(2) and O(4) oxygen atoms.

Methylation of the trioxypyrimidine ring at N(1) has the effect of decreasing the internal angle at N(1) (122.6 *vs.* 125.5° in sodium barbital) and lengthening the two adjacent C–N bonds (1.417 and 1.362 Å *vs.* 1.396 and 1.348 Å); other parts of the ring do not seem to be affected if the compensation for the decrease in the angle C(6)–N(1)–C(2) is neglected. The C–O bonds are shorter (Fig. 3) than most of the corresponding ones in the barbital anions of the sodium and calcium salt and longer than those in the metharbital acid. Obviously, these results cannot be attributed to the decreasing degree of participation in hydrogen-bonding within these groups. Rather, they suggest that *N*-methylation and differences in interactions with the sodium ion may also be important. All C–H distances (average 0.97 Å) are in expected ranges.

The coordination of the sodium ion and the crystal packing

The crystal packing is dominated by ionic interactions. The sodium ion is fivefold coordinated (Fig. 4): three metharbital oxygen atoms and the deprotonated nitrogen atom form the base, and another oxygen atom, O(6), forms the apex of a pyramid surrounding the sodium ion. The coordination polyhedron may also be pictured as a tetrahedron, in which one corner is replaced by the intramolecular grouping N(3)–C(4)=O(4). Of particular interest is the coordination of the sodium ion by a nitrogen atom, the Na–N distance 2.42 Å being the shortest one so far reported. While three Na–O distances are in the expected range (2.30–2.35 Å), the fourth involving atom O(4), which is part of the same metharbital ion as N(3), is extremely long (2.57 Å). O(4) is the only oxygen atom that simultaneously coordinates two Na atoms.

The alkaline and alkaline-earth metal ions are known to prefer coordination by oxygen rather than by nitrogen. In the few reported cases of coordination of

the sodium ion by nitrogen, the Na–N distances are at least 2.50 Å, even in the structures of sodium azide NaN₃ (Pringle & Noakes, 1968; Hendricks & Pauling, 1925) and NaCl·5½NH₃ (Olovsson, 1965) where there are no competing oxygen atoms. Only in different modifications at low temperatures do these structures show Na–N distances of 2.44 and 2.47 Å, which are comparably short.

In the crystal structures of salts of barbiturates where cation coordination by deprotonated nitrogen atoms *a priori* could be possible, three different degrees of involvement of the N atom in the coordination have been found: in sodium barbital (Berkling & Craven, 1971), and in the isomorphous potassium barbital (Berthou, Rérat & Rérat, 1965), the cation is surrounded by an almost regular tetrahedron consisting of barbital oxygen atoms. In sodium barbital, all four Na–O distances are within 2.31–2.35 Å, whereas the deprotonated nitrogen atom N(3) with Na–N = 2.80 Å is not involved in intermolecular interactions at all.

In the crystal structure of calcium barbital trihydrate (Berkling, 1971*a,b*), the coordination may be pictured as an octahedron in which one corner is replaced by the same intramolecular grouping, namely N(3)–

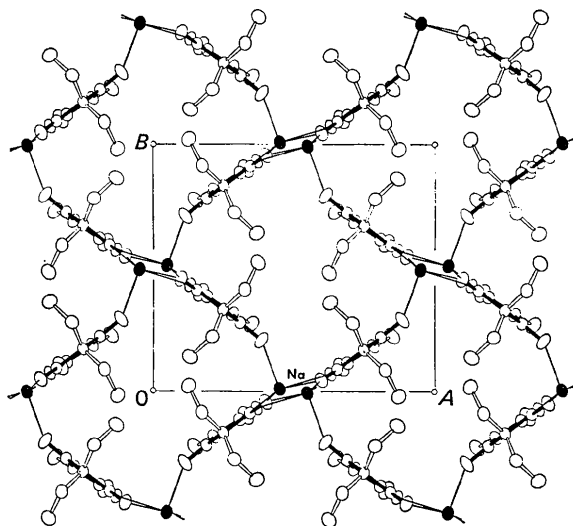


Fig. 5. The crystal structure of sodium metharbital as a projection down the *c* axis.

C(2)=O(2). Here, the Ca–N distances (2.52 and 2.55 Å for two independent Ca ions) are only 0.08 and 0.04 Å shorter than the Ca–O(2) distances (2.60 and 2.59 Å). This may not give sufficient evidence that the Ca–N interaction is primarily due to the coordination need of the Ca ion and the electronegativity of the deprotonated nitrogen, but it still allows the assumption that it is a consequence of the rigid N–C=O grouping, where the coordination itself is by the O atoms.

Finally, in the structure of sodium metharbital reported here, the relatively large difference of 0.15 Å between the short Na–N distance and the long Na–O(4) distance clearly indicates that N(3) does coordinate the Na ion, and that it is, at least, not much less electronegative than the competing oxygen atoms at the pyrimidine ring. There is no evidence that the involvement of N(3) in the cation coordination affects the intramolecular N(3)–C bonds (1.339 and 1.342 Å in sodium metharbital *vs.* 1.339 and 1.343 Å in sodium barbital).

Intermolecular interactions other than ionic are less important. Van der Waals interactions are weak, the shortest H···H intermolecular distance is 2.45 Å and there are seven additional distances less than 2.70 Å [Table 3(d)]. For an H···H approach, $d=2.4$ Å could be expected (Pauling, 1960). The shortest intermolecular C–O distance is 3.70 Å, indicating that there are no C=O···C=O dipole–dipole interactions.

The packing of the molecules in the unit cell (Figs. 5 and 6) is similar to that in the crystal structure of sodium barbital (Fig. 3 in Berking & Craven, 1971), with respect to the hydrophobic and hydrophilic channels along the shortest axis and the orientation of the trioxo-

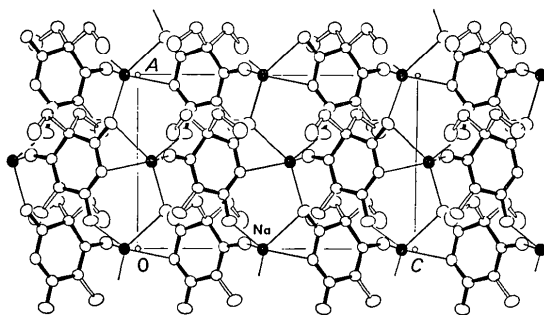


Fig. 6. The crystal structure of sodium metharbital as a projection along the *b* axis.

pyrimidine ring. This is consistent with a certain similarity in lattice dimensions. Despite these agreements, hydrogen-bonding in sodium barbital seems to be a dominant factor.

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