

## Sensible mathematics

SIR—Dirac<sup>1</sup>, after describing the electron self-energy problem and mass renormalization, states, "Most physicists say that QED is a good theory. I must say I am very dissatisfied with the situation because this so-called 'good theory' does involve neglecting infinities which appear in its equations, neglecting them in an arbitrary way. This is just not sensible mathematics. Sensible mathematics involves neglecting a quantity when it is small. . . not just because it is infinite and you do not want it."

In agreement with Dirac, we believe that perturbation theory must be altered or reconstructed into such a form (without spoiling relativistic invariance) that the self-energy integral (in momentum space) taken over the momenta of all virtual photons converges. Feynman, in his paper on QED, multiplied the photon propagator,  $k^{-2}$ , by the *ad hoc* factor  $-f^2/(k^2 - f^2)$ , where  $k$  is the momentum of the virtual photon (essentially its frequency) and  $f$  is an arbitrarily large parameter. Although this convergence factor, which is essentially equivalent to a high-frequency cutoff, preserves relativistic invariance, it is objectionable because of its *ad hoc* character and the presence of  $f$  without any theoretical justification. We show below, however, that the Feynman convergence factor appears in the self-energy integral naturally if general relativity is taken into account.

Isham *et al.*<sup>2</sup> have shown that in a 'gravity-modified' QED the "inverse of the gravitational constant appears as an effective cut-off mass" in the calculation of the electron self-energy, but their calculation is so encumbered by formalism that it is difficult to see the physics that is involved. For that reason, our calculation below, which leads essentially to the same result and to a general relativistic Feynman convergence factor, is important. Our calculation takes into account the gravitational reddening suffered by a virtual photon owing to the increased mass of the emitting particle produced by its recoil momentum.

Because momentum, unlike energy, is conserved in each single virtual process (each integral for a single virtual photon is taken over all configuration space, so that there is no uncertainty in momentum, as emphasized by Dirac<sup>1</sup>) the frequency  $\nu_0$  of the virtual photon, just when it is emitted, is given by the equation  $2\pi\hbar\nu_0/c = m_0\nu/[1 - (\nu/c)^2]^{1/2}$ ; here  $m_0$  is the resting mass of the emitting particle,  $\nu$  is its recoil velocity, and  $m = m_0/[1 - (\nu/c)^2]^{1/2}$  is its effective mass, which redshifts the frequency of the virtual photon in accordance with the Einstein formula  $\nu = \nu_0[1 - (2Gm/c^2r)]^{1/2}$ , where  $r$  is the Compton wavelength  $\hbar/mc$

of the emitting particle. From our first equation (the conservation of momentum), we have for the recoil velocity

$$\nu = (h\nu_0/m_0c)[1 + (h\nu_0/m_0c^2)^2]^{1/2}$$

and

$$m = m_0[1 + (2\pi\hbar\nu_0/m_0c^2)^2]^{1/2}$$

On substituting this into the equation for the effective frequency of the virtual photon, we obtain

$$\nu = \nu_0[1 - \frac{2Gm_0^2}{\hbar c} - 8\pi^2G\hbar\nu_0^2/c^5]^{1/2}$$

Because the second term  $2Gm_0^2/\hbar c$  in the parenthesis is negligible for the electron, we can exclude it and write  $\nu = (f^2)^{-1/2}(f^2 - \nu_0^2)^{1/2}\nu_0$ , where  $f^2 = c^5/8\pi^2G\hbar$ , a universal constant (the square of a frequency), is of

the order of  $10^{95}$  and therefore extremely large, as required by Feynman. Multiplying  $f$  by  $h$  and dividing by  $c^2$ , we obtain the universal mass  $m = (\hbar c/G)^{1/2}$  as the cut-off mass. This is just the Planck mass, which indicates that gravity is important in perturbation theory.

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## Short alpha-helix stability

SIR—Because C-peptides, the 13-residue peptides simulating an  $\alpha$ -helix of RNase, are significantly helical in aqueous solution near 0 °C<sup>1,2</sup>, the helicity has been attributed to specific side-chain interaction. The helicity is 30 times more than that predicted by Zimm-Bragg theory with host-guest stability parameters<sup>3</sup>.

Yet the observed helicity of C-peptides (between 15 per cent and 45 per cent depending on amino-acid composition and pH) is close to that expected for uncharged polylysine fragments of the same length, where specific side-chain interactions (salt bridges, hydrogen-bonding, aromatic interactions) are absent.

By direct measurement<sup>4</sup>, the helix-stability parameters for uncharged polylysine have been found to be  $s_a = 1.3$  (at

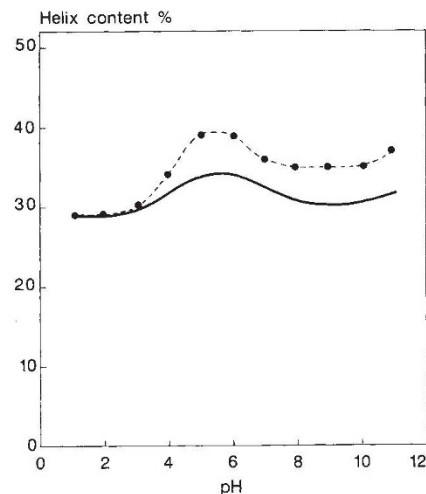
about 0 °C) and  $\sigma_a = 0.0025$ . Using these values, the Zimm-Bragg theory<sup>5</sup> gives 30 per cent helicity for 13-residue polylysine with -CONH groups at either end (as in C-peptides). Thus the 'general level' of the observed helicity of C-peptides is normal (at about 0 °C) for a short peptide consisting of helix-forming residues without the intervention of specific side-chain interactions.

At room temperature, the helicity of polylysine fragments must be half as much;  $s_a$  falls<sup>1</sup> to 1.14 at 25 °C, similar to the decrease of helicity found for the C-peptides<sup>1</sup>. It is relevant that helicity of about 5 per cent has been predicted<sup>6</sup> for the corresponding fragment of unfolded RNase.

The helicity of a peptide differs from the 'general level' because of a multitude of specific side-chain interactions, (usually rather weak), many of which (usually very weak) have been taken account of theoretically<sup>6,7</sup>. Thus the 1.2-fold increase of helicity of C-peptides on ionization (see figure) is explained by the electrostatic attraction of Glu<sup>-</sup> and His<sup>+</sup> to the partial charges at the nearest termini of a fluctuating  $\alpha$ -helix. Present theory<sup>6,7</sup> may thus serve as a guide for singling out the more specific effects observed in experiments with short peptides<sup>2</sup>.

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pH dependence of  $\alpha$ -helical content for the C-peptide (acetyl-AETAAAKALRAHA-amide) at 3 °C in 0.1 M NaCl. Solid line, experiment<sup>2</sup>; dotted line, theory<sup>7</sup>. The temperature change of  $s_a$  was calculated using the helix-coil transition enthalpy  $\Delta H = -1.1$  kcal mol<sup>-1</sup> (see ref. 4) for all amino acids. All other parameters are independent of temperature<sup>6,7</sup>.

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