

## Figure 9-13 Gating currents directly measure the changes in charge distribution associated with Na+ channel activation.

**A.** When the membrane is depolarized the Na<sup>+</sup> current ( $I_{Na}$ ) first activates and then inactivates. The activation of the Na<sup>+</sup> current is preceded by a brief outward gating current ( $I_g$ ), reflecting the outward movement of positive charge within the Na<sup>+</sup> channel protein associated with the opening of the activation gate. To detect the small gating current it is necessary to block the flow of lonic current through the Na<sup>+</sup> and K<sup>+</sup> channels and mathematically subtract the capacitive current due to charging of the lipid bilayer.

**B.** Illustration of the position of the activation and inactivation gates when the channel is at rest (1), when the Na<sup>+</sup> channels have been opened (2), and when the channels have been inactivated (3). It is the movement of the positive charge on the activation gate through the membrane electric field that generates the gating current.

## 2

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1 11 111 11	I I RR GA I - RVFVINSAENFFIM FTÎFSNC I FMT ÎS NPPAWSKÎVEYÎFTGIYTFEVI VKVL SR GFCI GHFTFL RD PW NW LD F L KKWVH - FVMMDPFTDLFI[LCIIILNTLFMSIEHHPMNESFQSLLSAGNLVFTTIFAAEMVLKIIA-LD PYYFQQTWNFFDS L RRTCYTIVEHDYF-ETFIIFMILLSSGVLAFEDIYIWRRRVIKVILEYADKVFTYVFIVENLLKWVAYGFKR-YFTDAWCWLD F VQGVYYDIV-TQPFTDIFIMALICINMVAMMVESEDQSQVKKDILSQÎNVLFVILFTVECLLKLA-LRQY-FFTVGWNVFDF SI	111- 189 555- 635 989-1071 1311-1390
1 11 111 VI	SVVTMTYTTIEFIDURNVSALRTFRVLRALKTIITIFPGUKTIVRALIESMKQMGDVVIUTVFSUAVFTAGMQL IIVSLSLLEUGLSNM	190- 262 636- 709 1072-1150 1391-1472
1 11 111 VI	FMGNLRH-KCIRWPISNU-TU-DYE	263- 383 710- 771 1151-1242 1473-1548
1 11 111 111 V1	MVIFLGSFYLINLILAVVAMAYEEQNOATLAEAQEK 384-419 MVIIIGNLVMLNLFLALLLSSFSSDNLSSIEEDDEV 772-807 YFVLFIVFGAFFTLNLFIGVIIDNFNRQKQKLGGEDLFM 1243-1281 SYIILSFLVVVNMYIAIILENFGVAQEESSDLLCEDDFV 1549-1587	

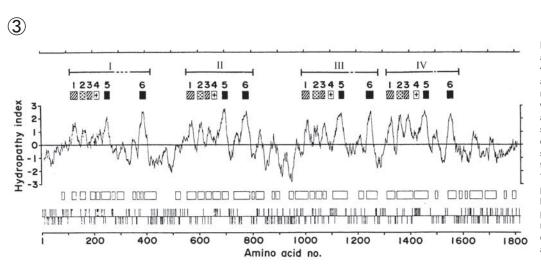


Figure 6.8. Hydropathy profile of the amino acid sequence of the Electrophorus sodium channel. The averaged hydropathic index of amino acid residues i - 9 to i + 9 is plotted against i, where *i* is the position number of the amino acid residue in the sequence. The bars show the positions of the homologous domains I to IV, and the boxes below them show the positions of the sections S1 to S6 that are thought to cross the membrane. The line of open boxes shows all sections of predicted  $\alpha$ -helix or  $\beta$ -strand structure. The bottom line shows the positions of the positively charged lysine and arginine residues as upward lines and the negatively charged aspartate and glutamate residues as downward lines. (From Noda et al., 1984.)

Fig. 6.7 Parts of the amino acid sequence of the Electrophorus sodium channel, to show the four homologous domains. The four domains are aligned, with gaps introduced to maximize homology. The oneletter amino acid code is used. Boxes enclose identical or similar amino acids. The segments S 1 to S6 are thought to be regions where the chain forms  $\alpha$ -helices which traverse the membrane. (From Noda et al. 1984.)