

CLAIMS

1. A method of nucleic acid sequencing, comprising:
 - (a) providing a polymerase attached to a solid support charge sensor;
 - (b) contacting the polymerase with a mixture of nucleotide triphosphates, wherein the mixture comprises different types of nucleotide triphosphates, wherein a first two types of the nucleotide triphosphates are in a first distinguishable state compared to a second two types of the nucleotide triphosphates in the mixture, and wherein the polymerase incorporates nucleotides from the mixture into a nascent strand against a template nucleic acid strand;
 - (c) detecting the incorporation of the nucleotides via the charge sensor, wherein the first two types of the nucleotide triphosphates produce a signal that distinguished from signals produced by second two types of the nucleotide triphosphates in the mixture, thereby acquiring a first signal pattern;
 - (d) repeating steps (b) and (c) using the polymerase, the template nucleic acid, and a second mixture of nucleotide triphosphates, wherein one of the first two types of the nucleotide triphosphates is in a distinguishable state compared to the other of the first two types of the nucleotide triphosphates in the second mixture, thereby acquiring a second signal pattern; and
 - (e) comparing the first and second signal patterns to determine the sequence of the template nucleic acid, wherein the template nucleic acid strand is circular.