CLAIMS

[Claim 1]. A method for performing incremental secondary analysis of nucleic acid sequence reads, the method comprising:

(i) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval, wherein each of the first reads represents a first ordered sequence of nucleotides

(ii) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval that is performed after the first read interval, wherein each of the second reads represents a second ordered sequence of nucleotides, wherein while the second data is being obtained:

(a) providing, by the nucleic acid sequencing device, the first data as an input to a mapping and alignment unit;

(b) receiving, from the mapping and alignment unit, alignment results; and

(c) storing the received alignment results;

and, thereafter

(iii) instructing the mapping and alignment unit to begin alignment of the second data representing the second plurality of reads to the reference sequence.

[Claim 2]. The method of claim 1, wherein at least a portion of the mapping and alignment unit is implemented using (i) a programmable logic device or (ii) an application specific integrated circuit (ASIC).

[Claim 3]. The method of claim 1, wherein the mapping and alignment unit is included within the nucleic acid sequencing device.

[Claim 4]. The method of claim 1,

wherein one or more of the first reads includes data representing a first sample identifier, and

wherein one or more of the second reads includes data representing a second sample identifier.

[Claim 5]. The method of claim 4, further comprising:

while the second data is being obtained:

organizing the one or more first reads into respective groups based on at least a first sample identifier or a second sample identifier; and

generating organization statistics, the organization statistics indicating a number of first reads corresponding to each sample identifier.

[Claim 6]. The method of claim 1, the method further comprising:

providing output data that represents the stored alignment results corresponding to the plurality of first reads before or while aligning the second portion of the cluster of reads.

[Claim 7]. The method of claim 1, the method further comprising:

instructing the mapping and alignment module to begin a subsequent alignment of the data representing the first plurality of reads to the reference sequence.

[Claim 8]. The method of claim 1, the method further comprising:

while obtaining the second data, determining a set of likely variants for the first data representing the first plurality of reads that was aligned to the reference sequence.

[Claim 9]. The method of claim 1, wherein the at least a portion of the second data representing the second plurality of reads is aligned while at least a different portion of second data representing the second plurality of reads is being obtained.

[Claim 10]. The method of claim 1, wherein the mapping and alignment unit is instructed to begin alignment of the second data representing the second plurality of reads a predetermined number of sequencing cycles before the second data is completely obtained.

[Claim 11]. A system for performing incremental secondary analysis of nucleic acid sequence reads, the system comprising:

a nucleic acid sequencing device; and

one or more memory devices storing instructions that, when executed by one or more processors of the nucleic acid sequencing device, cause the nucleic acid sequencing device to perform operations, the operations comprising:

(i) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval, wherein each of the first reads represents a first ordered sequence of nucleotides;

(ii) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval that is performed after the first read interval, wherein each of the second reads represents a second ordered sequence of nucleotides, wherein while the second data is being obtained:

(a) providing, by the nucleic acid sequencing device, the first data as an input to a mapping and alignment unit;

(b) receiving, from the mapping and alignment unit, alignment results; and

(c) storing the received alignment results;

and, thereafter

(iii) instructing the mapping and alignment unit to begin alignment of the second data representing the second plurality of reads to the reference sequence.

[Claim 12]. The system of claim 11, wherein at least a portion of the mapping and alignment unit is implemented using (i) a programmable logic device or (ii) an application specific integrated circuit (ASIC).

[Claim 13]. The system of claim 11, wherein the mapping and alignment unit is included within the nucleic acid sequencing device.

[Claim 14]. The system of claim 11,

wherein one or more of the first reads includes data representing a first sample identifier, and

wherein one or more of the second reads includes data representing a second sample identifier.

[Claim 15]. The system of claim 14, the operations further comprising:

while the second data is being obtained:

organizing the one or more first reads into respective groups based on at least a first sample identifier or a second sample identifier; and

generating organization statistics, the organization statistics indicating a number of first reads corresponding to each sample identifier.

[Claim 16]. The system of claim 11, the operations further comprising:

providing output data that represents the stored alignment results corresponding to the plurality of first reads before or while aligning the second portion of the cluster of reads.

[Claim 17]. The system of claim 11, the operations further comprising:

instructing the mapping and alignment module to begin a subsequent alignment of the data representing the first plurality of reads to the reference sequence.

[Claim 18]. The system of claim 11, the operations further comprising:

while obtaining the second data, determining a set of likely variants for the first data representing the first plurality of reads that was aligned to the reference sequence.

[Claim 19]. The system of claim 11, wherein the at least a portion of the second data representing the second plurality of reads is aligned while at least a different portion of second data representing the second plurality of reads is being obtained.

[Claim 20]. The system of claim 11, wherein the mapping and alignment unit is instructed to begin alignment of the second data representing the second plurality of reads a predetermined number of sequencing cycles before the second data is completely obtained.

[Claim 21]. A computer-readable storage medium storing instructions that, when executed by one or more computers, causes the one or more computers to perform operations, the operations comprising:

(i) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval, wherein each of the first reads represents a first ordered sequence of nucleotides

(ii) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval that is performed after the first

read interval, wherein each of the second reads represents a second ordered sequence of nucleotides, wherein while the second data is being obtained:

(a) providing, by the nucleic acid sequencing device, the first data as an input to a mapping and alignment unit;

(b) receiving, from the mapping and alignment unit, alignment results; and

(c) storing the received alignment results;

and, thereafter

(iii) instructing the mapping and alignment unit to begin alignment of the second data representing the second plurality of reads to the reference sequence.

[Claim 22]. The computer-readable storage medium of claim 21,

wherein one or more of the first reads includes data representing a first sample identifier, and

wherein one or more of the second reads includes data representing a second sample identifier.

[Claim 23]. The computer-readable storage medium of claim 22, the operations comprising:

while the second data is being obtained:

organizing the one or more first reads into respective groups based on at least a first sample identifier or a second sample identifier; and

generating organization statistics, the organization statistics indicating a number of first reads corresponding to each sample identifier.

[Claim 24]. The computer-readable storage medium of claim 21, the operations further comprising:

providing output data that represents the stored alignment results corresponding to the plurality of first reads before or while aligning the second portion of the cluster of reads.

[Claim 25]. The computer-readable storage medium of claim 21, the operations further comprising:

instructing the mapping and alignment module to begin a subsequent alignment of the data representing the first plurality of reads to the reference sequence.

[Claim 26]. The computer-readable storage medium of claim 21, the operations further comprising:

while obtaining the second data, determining a set of likely variants for the first data representing the first plurality of reads that was aligned to the reference sequence.

[Claim 27]. The computer-readable storage medium of claim 21, wherein the at least a portion of the second data representing the second plurality of reads is aligned while at least a different portion of second data representing the second plurality of reads is being obtained.

[Claim 28]. The computer-readable storage medium of claim 21, wherein the mapping and alignment unit is instructed to begin alignment of the second data representing the second plurality of reads a predetermined number of sequencing cycles before the second data is completely obtained.

[Claim 29]. A method for performing incremental secondary analysis of nucleic acid sequence reads, the method comprising:

(i) generating a plurality of first entity identifiers, where each entity first identifier corresponds to a particular read that will be generated during a first read interval;

(ii) generating a plurality of second entity identifiers, where each second entity identifier corresponds to a particular read that will be generated during a second read interval;

(iii) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device, based on multiple different samples, during the first read interval, wherein each of the plurality of first reads corresponds to at least the first or second entity identifiers, wherein while the first data is being obtained, the method further comprises:

organizing the plurality of first reads into organized groups based on a first or second entity identifier associated with each of the first reads;

providing, by the nucleic acid sequencing device, the organized plurality of reads to a mapping and alignment unit configured to align the base calls to a reference sequence;

receiving, from the mapping and alignment unit, alignment results; and

storing the received alignment results;

(iv) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device, based on multiple different samples, during the second read interval that is performed after the first read interval, where each of the plurality of second reads corresponds to at least the first or second entity identifiers; and,

(v) providing, by the nucleic acid sequencing device, the second data to a mapping and alignment unit configured to align the second data to a reference sequence.

[Claim 30]. The method of claim 29, wherein at least a portion of the mapping and alignment unit is implemented using (i) a programmable logic device or (ii) an application specific integrated circuit (ASIC).

[Claim 31]. The method of claim 29, wherein the mapping and alignment unit is included within the nucleic acid sequencing device.

[Claim 32]. The method of claim 29, wherein the organizing of the plurality of first reads includes generating data indicating the number of reads corresponding to each entity identifier.

[Claim 33]. The method of claim 29, the method further comprising:

while obtaining the second data, determining, for each organized set of first reads, a set of likely variants for the organized set of first reads that were aligned to the reference sequence.

[Claim 34]. A system for performing incremental secondary analysis of nucleic acid sequence reads, the system comprising:

a nucleic acid sequencing device; and

one or more memory devices storing instructions that, when executed by one or more processors of the nucleic acid sequencing device, cause the nucleic acid sequencing device to perform operations, the operations comprising:

(i) generating a plurality of first entity identifiers, where each entity first identifier corresponds to a particular read that will be generated during a first read interval;

(ii) generating a plurality of second entity identifiers, where each second entity identifier corresponds to a particular read that will be generated during a second read interval;

(iii) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device, based on multiple different samples, during the first read interval, wherein each of the plurality of first reads corresponds to at least the first or second entity identifiers, wherein while the first data is being obtained, the method further comprises:

organizing the plurality of first reads into organized groups based on a first or second entity identifier associated with each of the first reads;

providing, by the nucleic acid sequencing device, the organized plurality of reads to a mapping and alignment unit configured to align the base calls to a reference sequence;

receiving, from the mapping and alignment unit, alignment results; and storing the received alignment results;

(iv) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device, based on multiple different samples, during the second read interval that is performed after the first read interval, where each of the plurality of second reads corresponds to at least the first or second entity identifiers; and,

(v) providing, by the nucleic acid sequencing device, the second data to a mapping and alignment unit configured to align the second data to a reference sequence.

[Claim 35]. The system of claim 34, wherein at least a portion of the mapping and alignment unit is implemented using (i) a programmable logic device or (ii) an application specific integrated circuit (ASIC).

[Claim 36]. The system of claim 34, wherein the mapping and alignment unit is included within the nucleic acid sequencing device.

[Claim 37]. The system of claim 34, wherein the organizing of the plurality of first reads includes generating data indicating the number of reads corresponding to each entity identifier.

[Claim 38]. The system of claim 34, the operations further comprising:

while obtaining the second data, determining, for each organized set of first reads, a set of likely variants for the organized set of first reads that were aligned to the reference sequence.

[Claim 39]. A computer-readable storage medium storing instructions that, when executed by one or more computers, causes the one or more computers to perform operations, the operations comprising:

(i) generating a plurality of first entity identifiers, where each entity first identifier corresponds to a particular read that will be generated during a first read interval;

(ii) generating a plurality of second entity identifiers, where each second entity identifier corresponds to a particular read that will be generated during a second read interval;

(iii) obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device, based on multiple different samples, during the first read interval, wherein each of the plurality of first reads corresponds to at least the first or second entity identifiers, wherein while the first data is being obtained, the method further comprises:

organizing the plurality of first reads into organized groups based on a first or second entity identifier associated with each of the first reads;

providing, by the nucleic acid sequencing device, the organized plurality of reads to a mapping and alignment unit configured to align the base calls to a reference sequence;

receiving, from the mapping and alignment unit, alignment results; and

storing the received alignment results;

(iv) obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device, based on multiple different samples, during the second read interval that is performed after the first read interval, where each of the plurality of second reads corresponds to at least the first or second entity identifiers; and,

(v) providing, by the nucleic acid sequencing device, the second data to a mapping and alignment unit configured to align the second data to a reference sequence.

[Claim 40]. The computer-readable storage medium of claim 39, wherein at least a portion of the mapping and alignment unit is implemented using (i) a programmable logic device or (ii) an application specific integrated circuit (ASIC).

[Claim 41]. The computer-readable storage medium of claim 39, wherein the mapping and alignment unit is included within the nucleic acid sequencing device.

[Claim 42]. The computer-readable storage medium of claim 39, wherein the organizing of the plurality of first reads includes generating data indicating the number of reads corresponding to each entity identifier.

[Claim 43]. The computer-readable storage medium of claim 39, the operations further comprising:

while obtaining the second data, determining, for each organized set of first reads, a set of likely variants for the organized set of first reads that were aligned to the reference sequence.

[Claim 44]. A method for performing incremental secondary analysis of nucleic acid sequence reads, the method comprising:

obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval of a first sequencing run;

obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval of a first sequencing run that is performed after the first read interval, wherein while obtaining at least a portion of the second data:

initiating performance of one or more secondary analysis operations on the first data or second data;

using the nucleic acid sequencing device to perform a second sequencing run, wherein while using the nucleic acid sequencing device to perform the second sequencing run:

continuing performance of the one or more secondary analysis operations on at least the first data or the second data, and

storing results data representing the results of the secondary analysis operations.

[Claim 45]. A system for performing incremental secondary analysis of nucleic acid sequence reads, the system comprising:

a nucleic acid sequencing device; and

one or more memory devices storing instructions that, when executed by one or more processors of the nucleic acid sequencing device, cause the nucleic acid sequencing device to perform operations, the operations comprising:

obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval of a first sequencing run;

obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval of a first sequencing run that is performed after the first read interval, wherein while obtaining at least a portion of the second data:

initiating performance of one or more secondary analysis operations on the first data or second data;

using the nucleic acid sequencing device to perform a second sequencing run, wherein while using the nucleic acid sequencing device to perform the second sequencing run:

continuing performance of the one or more secondary analysis operations on at least the first data or the second data, and

storing results data representing the results of the secondary analysis operations.

[Claim 46]. A computer-readable storage medium storing instructions that, when executed by one or more computers, causes the one or more computers to perform operations, the operations comprising:

obtaining first data describing a plurality of first reads generated by a nucleic acid sequencing device during a first read interval of a first sequencing run;

obtaining second data describing a plurality of second reads generated by the nucleic acid sequencing device during a second read interval of a first sequencing run that is

performed after the first read interval, wherein while obtaining at least a portion of the second data:

initiating performance of one or more secondary analysis operations on the first data or second data;

using the nucleic acid sequencing device to perform a second sequencing run, wherein while using the nucleic acid sequencing device to perform the second sequencing run:

continuing performance of the one or more secondary analysis operations on at least the first data or the second data, and

storing results data representing the results of the secondary analysis operations.

[Claim 47]. A method for performing secondary analysis of nucleic acid sequence reads, the method comprising:

obtaining one or more genomic workflow attributes;

determining, based on the one or more genomic workflow attributes, a workflow context-switching type for a programmable circuit, wherein the workflow context-switching type defines reconfiguration cycles for the programmable circuit; and

instructing the programmable circuit controller to perform secondary analysis using the determined context-switching type.

[Claim 48]. A system for performing secondary analysis of nucleic acid sequence reads, the system comprising:

one or more computers; and

one or more memory devices storing instructions that, when executed by one or more processors, cause the one or more computers to perform operations, the operations comprising:

obtaining one or more genomic workflow attributes;

determining, based on the one or more genomic workflow attributes, a workflow context-switching type for a programmable circuit, wherein the workflow context-switching type defines reconfiguration cycles for the programmable circuit; and

instructing the programmable circuit controller to perform secondary analysis using the determined context-switching type.

[Claim 49]. A computer-readable storage medium storing instructions that, when executed by one or more computers, causes the one or more computers to perform operations, the operations comprising:

obtaining one or more genomic workflow attributes;

determining, based on the one or more genomic workflow attributes, a workflow context-switching type for a programmable circuit, wherein the workflow context-switching type defines reconfiguration cycles for the programmable circuit; and

instructing the programmable circuit controller to perform secondary analysis using the determined context-switching type.