



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

Table with 5 columns: APPLICATION NO., FILING DATE, FIRST NAMED INVENTOR, ATTORNEY DOCKET NO., CONFIRMATION NO.
12/770,089 04/29/2010 Paolo Carnevali 92171-002110US-798099 9005

16167 7590 06/04/2018
Kilpatrick Townsend & Stockton LLP/ Complete
Genomics, Inc.
1100 Peachtree Street, Suite 2800
Mailstop: IP Docketing - 22
Atlanta, GA 30309

Table with 1 column: EXAMINER

SKIBINSKY, ANNA

Table with 2 columns: ART UNIT, PAPER NUMBER

1631

Table with 2 columns: NOTIFICATION DATE, DELIVERY MODE

06/04/2018

ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

ipefiling@kilpatricktownsend.com
KTSDocketing2@kilpatrick.foundationip.com

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte PAULO CARNEVALI, JONATHAN M. BACCASH,
IGOR NAZARENKO, AARON L. HALPERN, GEOFFERY NILSEN,
BRUCE MARTIN, and RADJOE DRMANIC.¹

Appeal 2017-007405
Application 12/770,089
Technology Center 1600

Before DONALD E. ADAMS, JOHN E. SCHNEIDER, and
TIMOTHY G. MAJORS, *Administrative Patent Judges*.

SCHNEIDER, *Administrative Patent Judge*.

DECISION ON APPEAL

This is an appeal under 35 U.S.C. § 134(a) involving claims to a method for analyzing polynucleotide sequences, which have been rejected as directed to non-statutory subject matter. We have jurisdiction under 35 U.S.C. § 6(b).

We AFFIRM.

¹ Appellants identify the Real Party in Interest as Complete Genomics, Inc. Appeal Br. 3.

STATEMENT OF THE CASE

“In genetic research, genetic testing, personalized medicine, and many other applications, it is often useful to obtain a sample of genetic material, determine a sequence of that sample, and to analyze that sequence with respect to one or more existing references to identify sequence variations or obtain other useful information for the sample.” Spec. ¶ 2. “[S]ome techniques used for obtaining sample sequences yield a polynucleotide sequence comprising multiple shorter sequences (sometimes referred to as oligomers) with predicted spatial relationships, and in some cases with spatial relationships of variable distances.” Spec ¶ 3. These techniques “are not adequate to provide high speed, low cost de novo assembly or reassembly of short sequences comprising continuous reads that are variably gapped.” Spec. ¶ 4.

The Specification describes “methods and systems for calling variations in a sample polynucleotide sequence compared to a reference polynucleotide sequence.” Spec. ¶ 6.

Claims 2, 4, 7–29, 38–61² are on appeal. Claim 8 is representative of the rejected claims and reads as follows:

8. A computer-implemented method for calling variations in a sample polynucleotide sequence with respect to a reference polynucleotide sequence, the method comprising:
locating, by at least one computer, local areas in the reference polynucleotide sequence where a likelihood that one or more bases of the sample polynucleotide sequence are changed from corresponding bases in the reference polynucleotide sequence exceeds a likelihood threshold, wherein the at least one computer determines the likelihood at

² Claim 3 is also pending in the application but has been withdrawn from consideration as directed to a non-elected species. Non-Final Act. 3.

least in part based on mapped mated reads of the sample polynucleotide sequence, wherein locating the local areas likely to have changed from the reference polynucleotide sequence comprises:

computing reference scores using a Bayesian formulation process, comprising:

for each of a plurality of base positions in the reference polynucleotide sequence:

generating a set of initial hypotheses for the base position by modifying a base value at that position in p alleles by all possible I-base variations;

determining a set of mapped mated reads that are near the base position; and

computing a reference score by computing, for each of the initial hypotheses in the set, a probability ratio P_v/P_{ref} , where P_v is a probability of a 1-base variation hypothesis, and P_{ref} is a probability of the base value in the reference polynucleotide sequence, and where the set of mapped mated reads near the base position are used during calculation of the probability ratio at the base position; and

comparing the reference scores to the likelihood threshold;

generating, by the at least one computer, a plurality of sequence hypotheses for each of the local areas, each of the plurality of sequence hypotheses including a plurality of bases at positions in the corresponding local area, the plurality of sequence hypotheses for a respective local area being generated by changing bases relative to the initial hypotheses at positions of the respective local area;

identifying, by the at least one computer, one or more optimized sequence hypotheses of maximum probability from the plurality of sequence hypotheses for each of the local areas by calculating a probability estimate for each of the plurality of sequence hypotheses, wherein the mapped mated reads are generated independently of each other, and wherein the probability estimates take into account all of the mapped mated reads are calculated by

$$\frac{P(G|MtdRds)}{P(G_0|MtdRds)} = \left(\frac{N_{G_0}}{N_G}\right)^{N_D} \prod_{MtdRds} \frac{\sum_M P(g)P(MtdRd|G, M)}{\sum_M P(g)P(MtdRd|G_0, M)}$$

where M is a number of mappings for each mapped mated read, N_{G0} represent a number of bases in the reference genome, N_G represents a number of bases in the sample genome, and N_D represents a number of mated reads; and

analyzing, by the at least one computer, the optimized sequence hypotheses to identify a series of variation calls in the sample polynucleotide sequence.

Claims 2, 4, 7–29, 38–61 have been rejected under 35 U.S.C. § 101 as directed to non-statutory subject matter.

DISCUSSION

The issue with respect to this rejection is whether a preponderance of the evidence supports the Examiner's conclusion that claims 2, 4, 7–29, 38–61 are directed to non-statutory subject matter.

The Examiner finds that the claimed method relies on “the abstract ideas of performing algorithmic analysis of sequence data, comparing sequence data, and using mathematical concepts including mathematical algorithms and formulas. The claims are entirely drawn to a computational algorithmic method and do not include additional steps outside of [] the abstract idea.” Non-Final Act. 4. The Examiner finds that although some of the claims contain additional elements, “[v]iewed as a whole, these additional claim element(s) do not provide meaningful limitation(s) to transform the abstract idea into a patent eligible application of the abstract idea such that the claim(s) amounts to significantly more than the abstract idea itself.” *Id.*

Appellants argue that the claims are not directed to a mere transformation of data but to determination of a physical property of a sample. Appeal Br. 14. Appellants argue that the claims are not directed to a mathematical formula and that the cases cited by the Examiner are limited

Appeal 2017-007405
Application 12/770,089

to claims involving a mathematical formula. Appeal Br. 16–19. Appellants contend that the claims are directed to solving a technical problem namely how to identify variations in sample nucleotide sequences from measurements of polynucleotide fragments from a sample organism. Appeal Br. 19–21. Appellants also contend that the claims are directed to an improvement of a technology or technical field. Appeal Br. 21–25. Appellants also contend that the claims recite limitations that represent something significantly more than abstract concepts.

Analysis

“Laws of nature, natural phenomena, and abstract ideas are not patentable.” *Mayo Collaborative Services v. Prometheus Labs., Inc.*, 132 S. Ct. 1289, 1293 (2012) (citation omitted). “Groundbreaking, innovative, or even brilliant discovery does not by itself satisfy the § 101 inquiry.” *Ass’n for Molecular Pathology v. Myriad Genetics, Inc.*, 133 S. Ct. 2107, 2117 (2013).

The Supreme Court articulated a two-step test for patent eligibility under § 101 that “distinguish[es] patents that claim laws of nature, natural phenomena, and abstract ideas from those that claim patent-eligible applications of those concepts.” *Alice Corp. Pty. Ltd. v. CLS Bank Int’l*, 134 S. Ct. 2347, 2355 (2014) (citing *Mayo*, 132 S. Ct. at 1296-97) (“the *Alice/Mayo* test”). “First, we determine whether the claims at issue are directed to one of those patent-ineligible concepts. If so, we then ask, ‘[w]hat else is there in the claims before us?’” *Id.* (citation and quotations omitted). Second, we “search for an inventive concept—i.e., an element or combination of elements that is sufficient to ensure that the patent in practice amounts to significantly more than a patent upon the ineligible concept itself.” *Id.* (quotations and alterations omitted).

We agree with the Examiner that the claims are directed to ineligible subject matter. Each of the recited steps, locating, computing, generating, determining, comparing, identifying, and analyzing involve abstract ideas and are not patent eligible. *See SAP America, Inc. v. Investpic, LLC*, No 2017-2081, 2018 WL 2207254, at *4 (Fed. Cir, May 15, 2018). That the claims are directed to a certain type of data content and call for the use of a computer does not render the claims patent eligible. *Id.* at *5–6.

Appellants contend that the claims are directed to a determination of a physical property of a sample involving accurately identifying variations in a sample polynucleotide sequence from measurements of polynucleotide fragments from a sample organism. Appeal Br. 15. We are not persuaded. Although claim 8 refers to comparing a sample polynucleotide sequence to a reference sequence, nowhere does the claim require the sample sequence be a fragment from a sample organism. The claim calls for comparing one sequence with another. This is abstract data analytics and we are unpersuaded that the type of data (sequence information) saves the claim from abstraction.

Moreover, even if the sample sequence was from a sample organism, this is merely limiting the data to a particular content or source. This is insufficient to render the claimed method patentable. *SAP* at *5.

Appellants next argue that the claims are not directed to a mathematical formula and that the cases where abstract ideas were found unpatentable all relate to mathematical formulas. Appeal Br. 19. We remain unpersuaded. As discussed above, the claimed method relates to collecting information and analyzing it. The Federal Circuit has made it clear that claims focused on collecting and analyzing information, without significantly more, are not patent eligible. *SAP* at *4.

“Information as such is an intangible,” hence abstract, and “collecting information, including when limited to particular content (which does not change its character as information), [i]s within the realm of abstract ideas.” *Id.* (citing cases). So, too, is “analyzing information . . . by mathematical algorithms, without more.” *Id.* at 1354 (citing cases, including *Parker v. Flook*, 437 U.S. 584 (1978), and *Gottschalk v. Benson*, 409 U.S. 63 (1972)). And “merely presenting the results of abstract processes of collecting and analyzing information, without more (such as identifying a particular tool for presentation), is abstract as an ancillary part of such collection and analysis.” *Id.* (citing cases). The claims here are directed at abstract ideas under those principles.

Id.

Appellants argue that the claims are patent eligible because they are directed to a specific technology, identification of variations in polynucleotide sequences and show an improvement over other techniques. Appeal Br. 20–25. Once again, we are unpersuaded. Even assuming the claimed method may be innovative, it is an innovation in ineligible subject matter. *SAP* at *1. No matter how much of an advance may be represented by the method of the claims, “the advance lies entirely within the realm of abstract ideas. . . . An advance of that nature is ineligible for patenting.” *Id.*

Appellants cite to *McRO, Inc. v. Bandai Namco Games America Inc.*, 837 F.3d 1299 (Fed. Cir. 2016) for the proposition that data processing rules, such as those reflected in the present claims are patent eligible. Appeal Br. 18 and 26. We remain unpersuaded.

As the Federal Circuit has pointed out, the claims in *McRO*, “were directed to the creation of something physical – namely the display of ‘lip synchronization and facial expressions.’” *SAP* at *4. For this reason the claims in *McRO*, were deemed patent eligible. *Id.* In the present

Appeal 2017-007405
Application 12/770,089

application, the claims do not produce a tangible result. All that is claimed are the rules for data handling.

Appellants also rely on *In re Abele*, 684 F.2d 902 (CCPA 1982) to support the patentability of the present claims. Appeal Br. 20. Appellants contend that like claim 6 in *Abele*, the present claims are directed to solving a physical problem and are therefore patent eligible. Appeal Br. 20.

We have considered Appellants' argument and find it unpersuasive. *In re Abele*, was decided before the Supreme Court's decision in *Alice* and its progeny. Subsequent decisions by the Federal Circuit make it clear that merely limiting the particular data being analyzed is insufficient to render the claims patent eligible. *SAP* at *5.

Finally, Appellants contend that the present claims recited unconventional steps, which represent something substantially more than an abstract idea. Appeal Br. 28. Appellants point to the fact that several of the steps are not found in the prior art and cannot be deemed conventional. *Id.*

Here again, even if the claims may be novel and non-obvious, that alone is insufficient to show that the claims are patent eligible. *SAP* at *1. As discussed above the claims, as a whole, are directed to a series of abstract steps, and are not patent eligible. *Id.* This is true even for the steps which Appellants contend are unconventional and not found in the prior art. *See*, Appeal Br. 28.

We conclude that a preponderance of the evidence supports the Examiner's conclusion that the claims are directed to non-statutory subject matter.

SUMMARY

We affirm the rejection under 35 U.S.C. § 101.

Appeal 2017-007405
Application 12/770,089

TIME PERIOD FOR RESPONSE

No time period for taking any subsequent action in connection with this appeal may be extended under 37 C.F.R. § 1.136(a).

AFFIRMED