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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte IGNAT V. SHILOV

Appeal 2017-011343
Application 13/697,707¹
Technology Center 1600

Before ERIC B. GRIMES, FRANCISCO C. PRATS, and
RACHEL H. TOWNSEND, *Administrative Patent Judges*.

Opinion for the Board filed by Administrative Patent Judge TOWNSEND.

Opinion Concurring filed by Administrative Patent Judge PRATS.

TOWNSEND, Administrative Patent Judge.

DECISION ON APPEAL

This is an appeal under 35 U.S.C. § 134 involving claims to a system for calculating and recalculating protein confidence values, which have been rejected as directed to patent ineligible subject matter. Oral argument was heard May 1, 2019. We have jurisdiction under 35 U.S.C. § 6(b).

We reverse.

¹ Appellant identifies the real party in interest as DH TECHNOLOGIES DEVELOPMENT PTE. LTD. (Appeal Br. 1.)

STATEMENT OF THE CASE

“In proteomics analysis, a sample is proteolytically digested into surrogate peptide analytes that are identified by tandem mass spectrometry coupled with a database search.” (Spec. ¶ 2.) “The identifications of these surrogate peptide analytes are then used to infer the detection of their parent proteins” by assigning peptide confidence values “based on a heuristic or a database search,” to the surrogate peptide, which values are then used to calculate protein confidence values. (*Id.*)

The present invention is directed to a system that uses a method of calculating protein confidence values in a proteomic analysis from a comparison of data measured by the mass spectrometer with data from a protein database for distinguishing or identifying proteins in a sample analyzed by a mass spectrometer. (Supplemental Appeal Br. 1, Apr. 29, 2017.)

Claims 1, 3, and 4 are on appeal.² Claim 1 is representative and reads as follows:

1. A system for calculating and recalculating protein confidence values by recalculating peptide confidence values in proteomic analysis in order to distinguish proteins found in a sample from random or false positive results, comprising:
 - a protein database;
 - one or more mass spectrometers that perform a plurality of scans of a sample that is proteolytically digested into surrogate peptide analytes producing a plurality of spectra; and
 - a processor in communication with the protein database and the one or more mass spectrometers that

² Claims 10–20 are pending but have been withdrawn from consideration. (Advisory Action 1.)

- a. obtains the plurality of spectra from the mass spectrometer,
- b. identifies a plurality of peptides from the plurality of spectra,
- c. searches the protein database for proteins matching peptides from the plurality of peptides producing a set of proteins and a corresponding set of peptides,
- d. determines peptide confidence values for the set of peptides, wherein a peptide confidence, C_i , of an i th peptide of the set of peptides is a probability that the i th peptide is identified from the plurality of spectra,
- e. calculates a protein confidence value for each protein in the set of proteins based on one or more peptide confidence values of one or more corresponding peptides from the set of peptides, wherein a protein confidence value P_p is a probability calculated according to

$$P_p = 1 - \prod(1 - C_i),$$

where $\prod(1 - C_i)$ is the product of one or more peptide confidence values,

- f. selects a protein from the set of proteins with a largest protein confidence value, saves the largest protein confidence value for the protein, removes the protein from the set of proteins, and removes one or more peptides corresponding to the protein from the set of peptides,
- g. recalculates the protein confidence value, P_p , for each protein in the set of proteins based on one or more peptide posterior probability values of one or more corresponding peptides from the set of peptides according to

$$P_p = 1 - \prod(1 - P(+ | B)_i),$$

wherein a posterior probability of the i^{th} peptide, $P(+ | B)$, of the set of peptides is calculated using

$$P(+ | B) = \frac{P(B | +) \cdot P(+)}{P(B)}$$

$$P(B)$$

where $P(B | +)$ is the peptide confidence value of the i^{th} peptide, C_i , $P(B)$ is the marginal probability of observing the peptide with a given confidence, and $P(+)$ is the prior probability of randomly selecting a true positive and $P(+)$ is calculated from all confidence values of peptides currently in the set of peptides and all confidence values of peptides removed from the set of peptides to account for the effect of removing the one or more peptides corresponding to the removed protein from the set of peptides, and

h. repeats steps (f)-(g) until all proteins are removed from the set of proteins or until a protein confidence value of the selected protein with a largest protein confidence value is below a threshold of interest and identifies proteins found in the sample as the proteins with the saved largest protein confidence values.

(Appendix A filed with Supp. Appeal Br. on April 29, 2017 at i–iii.)

The following ground of rejection by the Examiner is before us on review:

Claims 1, 3, and 4³ under 35 U.S.C. § 101 as being directed to non-statutory subject matter.

DISCUSSION

The Appeal

The Examiner finds that the claims are directed to a system that comprises a processor with instructions to execute a computational method that includes “using mathematical formulas to compute peptide probabilities

³ The Final Action indicates claims 1, 4, and 21. However, Appellant indicates that the claims subject to this rejection are claims 1, 3, and 4, which are the only claims on Appeal. (Appeal Br. 9)

and to recalculate them into protein probabilities.” (Final Action 3; Ans. 2.) The Examiner explains that the method “describes the concept of gathering and combining data” and employing “mathematical relationships to manipulate existing information to generate additional information.” (*Id.*) The Examiner points out that the “additional element of the claimed system other than the abstract idea *per se* is a mass-spectrometer and processor, i.e., a known analytical device with processor addressed at high level of generality.” (Ans. 2; Final Action 3.) The Examiner explains that “[t]he claims do not recite inventive steps outside of data manipulation, or improvements to the function of the computer itself” and that “[t]here are no meaningful limitations in the claims . . . that transform the judicial exception into a patent-eligible application such that the claim amounts to significantly more than the exception itself.” (Final Action 3–4; Ans. 3.)

Regarding preemption, the Examiner, among other things, notes that the absence of preemption does not demonstrate patent eligibility and thus that showing alternative uses of the judicial exception outside of the scope of the claims does not establish patent eligibility where the claims are deemed only to disclose patent ineligible subject matter. (Ans. 4.)

Appellant argues that the Examiner’s rejection fails on technical grounds as well as substantive ones. In particular, Appellant argues that the Examiner did not point with specificity to the limitation as claimed that is the abstract idea and explain why courts have identified such a limitation as abstract, that the Examiner did not address the limitations as a combination in determining whether the claim as a whole recited eligible subject matter, and did not explain why the inclusion of specific structural components of the system did not render the claims patent eligible as a particular useful

application. (Appeal Br. 12–14.) Appellant contends that the claim is directed to a technological improvement over protein identification techniques and is so specific that it does not preempt all uses and as such is directed to patent eligible subject matter. (Appeal Br. 14–30; Reply Br. 10–14.)

After briefing was completed, in response to the changed landscape of analyzing patent eligibility at the PTO, Appellant presented two additional briefs. The first supplemental Appeal Brief was filed on October 30, 2018 (“Supp. Appeal Br. I”), and the second supplemental Appeal Brief was filed January 17, 2019 (“Supp. Appeal Br. II”).⁴ In the first of these briefs, Appellant argued that the technological improvement is tied to the steps f-h of claim 1 and that those steps are not well-understood, routine, conventional activity, even if they are drawn to the judicial exception. (Supp. Appeal Br. I.) In the second of these briefs, Appellant assumes *arguendo* that the Examiner properly articulated that claim 1 recites a judicial exception because it includes mathematical concepts. (Supp. Appeal Br. II at 5.) However, Appellant argues, similarly to the original Appeal Brief, that claim 1 integrates the mathematical probability formulas into a practical application of identifying proteins in a sample using a mass spectrometer and a protein database. (Supp. Appeal Br. II at 5–8.)

⁴ Appellant’s first supplemental Appeal Brief was filed in response to the April 19, 2018 memorandum to the Patent Examining Corps regarding *Berkheimer v. HP, Inc.* The second supplemental Appeal Brief was filed shortly after the PTO issued the *2019 Revised Patent Subject Matter Eligibility Guidance* (“Guidance”), 84 Fed. Reg. 50–57 (January 7, 2019).

We address the Examiner’s patent ineligibility rejection below, not against the prior guidance extant at the time Appellant filed its Appeal Brief, Reply Brief and First Supplemental Appeal Brief, but in accordance with the current Guidance.

Analysis

35 U.S.C. § 101 defines patent eligible subject matter. The Supreme Court has carved out exceptions to what would otherwise appear to be within the literal scope of § 101. *Alice Corp. Pty. Ltd. v. CLS Bank Int’l*, 573 U.S. 208, 216 (2014). One of these exceptions are claims “directed to” an abstract idea. *Id.* at 217. This appeal involves the abstract idea exception to patent eligibility under section 101.

The Supreme Court has established a two-step framework for “distinguishing patents that claim laws of nature, natural phenomena, and abstract ideas from those that claim patent-eligible applications of those concepts.” *Id.* “First, we determine whether the claims at issue are directed to” a patent-ineligible concept. *Id.* If so, “we consider the elements of each claim both individually and ‘as an ordered combination’ to determine whether the additional elements ‘transform the nature of the claim’ into a patent-eligible application.” *Id.* (quoting *Mayo Collaborative Servs. v. Prometheus Labs., Inc.*, 566 U.S. 66, 78–79 (2012)).

STEP 2A, Prong One:

Under the Guidance, in determining what concept a claim is “directed to” in step one of the Supreme Court’s two-step framework, we first look to whether the claim recites any judicial exceptions, such as a mathematical concept. Guidance at 52, 54 (Step 2A, Prong One). As conceded by Appellant, claim 1 recites the use of mathematical probability formulas for

determining peptide confidence values and protein confidence values.
(Supp. Appeal Br. II at 5.) These are steps d, e, and g of claim 1.

There is no dispute that claim 1, in reciting these formulae, recites mathematical concepts that are considered an abstract idea. *See* Guidance at 52 (citing, e.g., *SAP America, Inc. v. InvestPic, LLC*, 898 F.3d 1161, 1163 (Fed. Cir. 2018) (holding that claims to a “series of mathematical calculations based on selected information” are directed to abstract ideas); *Digitech Image Techs., LLC v. Elecs. for Imaging, Inc.*, 758 F.3d 1344, 1350 (Fed. Cir. 2014) (holding that claims to a “process of organizing information through mathematical correlations” are directed to an abstract idea); *Bancorp Servs., LLC v. Sun Life Assurance Co. of Can.(U.S.)*, 687 F.3d 1266, 1280 (Fed. Cir. 2012) (identifying the concept of “managing a stable value protected life insurance policy by performing calculations and manipulating the results” as an abstract idea).)

STEP 2A, Prong Two:

Having made that determination, under the Guidance, we next examine whether there are additional elements *beyond* the recited mathematical formulae that integrate them into a practical application. Under the Guidance, this is referred to as the “Prong Two” inquiry under “Step 2A.” Guidance at 54–55. That is, under the Prong Two analysis we look to whether the claim as a whole “appl[ies], rel[ies] on, or use[s] the judicial exception in a manner that imposes a meaningful limit on the judicial exception.” *Id.*

In performing this analysis, we are mindful that “a claim is not patent eligible merely because it applies an abstract idea in a narrow way.” *BSG Tech LLC v. BuySeasons, Inc.*, 899 F.3d 1281, 1287 (Fed. Cir. 2018). Thus,

for example, the Supreme Court in *Parker v. Flook*, 437 U.S. 584 (1978), found the use of a novel mathematical algorithm in a process for adjusting alarm limits, which limits signal inefficiency or danger when exceeded, in catalytic conversion of hydrocarbons patent ineligible. *Mayo*, 566 U.S. at 80 (discussing *Flook*, 437 U.S. at 585–87). The process included “the steps of: (1) measuring the current level of the variable, e.g., the temperature; (2) using an apparently novel mathematical algorithm to calculate the current alarm limits; and (3) adjusting the system to reflect the new alarm-limit values.” *Id.* Moreover, the Supreme Court has stated that “simply implementing a mathematical principle on a physical machine, namely a computer, was not a patentable application of that principle.” *Id.* at 84 (citing *Gottschalk v. Benson*, 409 U.S. 63, 71 (1972).)

On the other hand, the Supreme Court in *Diamond v. Diehr*, 450 U.S. 175 (1981), found the overall physical and chemical process for molding precision synthetic rubber “patent eligible because of the way the additional steps of the process integrated the equation into the process as a whole.” *See e.g., Mayo*, 566 U.S. at 80 (discussing *Diehr*, 450 U.S. at 177–79); *Recognicorp, LLC v. Nintendo Co. Ltd.*, 855 F.3d 1322, 1326 (Fed. Cir. 2017) (“In confirming patentability, the Supreme Court focused not on the presence of a mathematical formula but on the subject matter of the claims as a whole. [*Diehr*, 450 U.S.] at 192”). The process included “installing rubber in a press, closing the mold, constantly determining the temperature of the mold, constantly recalculating the appropriate cure time through the use of the formula and a digital computer, and automatically opening the press at the proper time.” *Mayo*, 566 U.S. at 80–81. The Court stated: “[A] claim containing a mathematical formula” satisfies § 101 when it

“implements or applies that formula in a structure or process which, when considered as a whole, is performing a function which the patent laws were designed to protect, (e.g., transforming or reducing an article to a different state or thing).” *Diehr*, 450 U.S. at 192. Outside of the math, *Diehr* was directed to a process that was directed to otherwise eligible subject matter, an industrial process for the molding of rubber products. *Id.* at 192–93; see *Thales Visionix Inc. v. United States*, 850 F.3d 1343, 1348 (Fed. Cir. 2017) (“In terms of the modern day *Alice* test, the *Diehr* claims were directed to an improvement in the rubber curing process, not a mathematical formula.”).

We first note that unlike *Diehr*, the claims are not directed to a process. They are system claims. But as the Supreme Court indicated in *Alice*, whether a device is “a tangible system (in § 101 terms, a ‘machine’)” is not dispositive. See 573 U.S. at 224. Resolving the § 101 inquiry based on such an argument “would make the determination of patent eligibility ‘depend simply on the draftsman’s art.’” *Id.* (quoting *Flook*, 437 U.S. at 593). Here, the system is directed at carrying out a process of distinguishing proteins in a sample.

However, unlike the process performed in *Diehr*, the process carried out by the claimed system does not involve additional elements *beyond* the recited mathematical formulae that use the formulae to transform or reduce an article into a different state or thing. It is true that proteins are required to be digested to peptides for the processor to be able to distinguish the proteins in the sample, but that is not a part of the system or a processor step. The process that is recited to be carried out by the processor is one that starts after the proteins have been digested. The processor “obtains the plurality of spectra” and “identifies a plurality of peptides from the plurality of spectra.”

Thus, any transformation occurs prior to the process carried out by the processor of the system; the processor just employs the mathematical formulae.

The Examiner found that the claims do not recite inventive steps outside of data manipulation, or improvements to the function of the computer itself. (Final Action 3–4; Ans. 3.) We agree.

We examine the additional elements of the claim beyond the recited mathematical calculations to determine whether they integrate the exception into a practical application. The claims require the system to include a protein database, at least one mass spectrometer, and a processor in communication with both the protein database and the mass spectrometer(s). In Appellant’s view, a claim is not directed to an abstract idea at step one of *Alice* so long as it recites limitations that render it narrower than the abstract idea, e.g. the data collected here and acted upon is mass spectra of proteolytically digested peptides of a protein sample. (Supp. Appeal Br. II at 6.) That a mass spectrometer and a protein database are required by the claims, which are not generic computers, certainly limits the use of the abstract idea to a particular technological environment. However, our reviewing court has held “consistently. . . that claims are not saved from abstraction merely because they recite components more specific than a generic computer.” *BSG Tech*, 899 F.3d at 1286–87 (“the recitation of a database structure slightly more detailed than a generic database does not save the asserted claims at step one.”).

The mass spectrometer, here, is used in its conventional manner to obtain spectra of a sample of digested proteins by which the peptides are then identified. (*See, e.g.*, Spec. ¶ 2; Appeal Br. 5–6 (noting that steps a-e of

the claim is conventional activity in calculating protein confidence values); Supp. Appeal Br. II at 6; accord Supp. Appeal Br. I (arguing only that steps f-h of the claims are not well-understood, routine or conventional activity); US2006/0030053⁵ ¶¶3–5.) In addition, the protein database is used in its conventional manner in proteomic analysis, that is, it is consulted to determine a set of sample proteins to which the identified peptides belong. (*Id.*) These physical components are directed to pre-solution activity that generates data used in the calculation of peptide confidence values, protein confidence values, and recalculated protein confidence values. Even though they may be “integral” to the ultimate ability to identify the proteins in the sample “because they provide the inputs to the confidence calculations made with the mathematical probability formulas” (Supp. Appeal Br. II at 6–7; Appeal Br. 6–7), this pre-solution activity simply limits the technological environment in which the mathematical formulae are used. (*Accord* Amendment filed Apr. 4, 2016 at 33–34 (explaining that the calculation that takes place at step g does not require the use of the mass spectrometer or the use of a protein database and that these instruments are used to provide the inputs for the calculation of confidence values and the recalculations that take place using Bayes law in step g.)) They are not improved by the calculations, i.e., the calculations do not provide a technological improvement of the mass spectrometer or the protein database.

“*Flook* stands for the proposition that the prohibition against patenting abstract ideas cannot be circumvented by attempting to limit the use of [the

⁵ Seymour et al., US2006/0030053 A1, published Feb. 9, 2006. This reference was cited by the Examiner during prosecution of this application. See Non-Final Action, Dec. 7, 2015, at 6–7.

idea] to a particular technological environment.” *Alice*, 573 U.S. at 222–23 (quoting *Bilski v. Kappos*, 561 U.S. 593, 610–611 (2010) (internal quotation marks omitted); see also *In re Grams*, 888 F.2d 835, 840 (“[t]he presence of a physical step in the claim to derive data for the algorithm will not render the claim statutory.”). Unlike the case in *Diehr*, Appellant’s claimed mass spectrometer and protein database do not integrate the equation into a process; they limit the technological environment in which the abstract idea is used. (See Supp. Appeal Br. II at 5 (“In other words, claim 1 is directed to a system for identifying proteins in a sample analyzed by a mass spectrometer using a specific method of calculating protein and peptide confidence values from a comparison of data measured by the mass spectrometer with data from a protein database.”).) That is, even though proteins are transformed into peptides, that transformation takes place prior to implementation of the abstract idea. The abstract idea is then simply used to analyze the data without any effects on the process itself. Thus, the fact that the claim requires a mass spectrometer and a protein database is not sufficient to support finding a “practical application.” These additional elements do not use a judicial exception in conjunction with a particular machine, or apply the judicial exception at all. (See Supp. Appeal Br. II at 6–8.) Rather, as Appellant’s arguments emphasize, the mass spectrometer and protein database provide inputs to the mathematical formula.

Furthermore, there is no assertion that Appellant’s invention improves the collection of data in the protein database, or improves the manner by which the set of sample proteins in which the peptides may be found is collected. The mathematical analysis of the data collected from the protein database via the spectra information does not provide input back to the

database and it does not change the contents of the database. (*Id.*; *accord* Appeal Br. 8.) In sum, there is not a “technological” improvement.

Such is consistent with the fact that the problem facing the inventor was not how to digest peptides in order to determine proteins within a sample, nor how to better use a mass spectrometer to observe peptides within a digested sample. Rather, as the Specification indicates the problem was to address the potential for the prior art’s “calculation of high (false positive) protein confidence[] values” (Spec. ¶ 29) when evaluating the data. Thus, the focus of the claims is the improved mathematical analysis. Appellant does not appear to dispute that, asserting that “[t]he patentable technological improvement provided by claim 1 is a specific method of calculating protein confidence values from peptide confidence values obtained from mass spectrometry data.” (Appeal Br. 14–15.)

That leaves us with the question of whether the processor, which applies the judicial exception to effect the calculation steps, imposes a meaningful limit on the judicial exception. Appellant does not assert that the processor is anything more than a generic computer component. It is the law that “simply, implementing a mathematical principle on a physical machine, namely a computer, [i]s not a patentable application of that principle.” *Mayo*, 566 U.S. at 84 (discussing *Gottschalk v. Benson*, 409 U.S. at 71); *see also In re Downing*, Appeal No. 2018-1795, slip op. 9–10, and n2 (Fed. Cir. Dec. 7, 2018) (unpublished).

Appellant has explained that the process carried out by the processor achieves an improvement over steps a-e alone (Shilov Declaration⁶ ¶¶ 29–32, 36–42), which steps a-e are admitted to be the conventional system and manner employed for calculating protein confidence values in proteomic analyses (Shilov Declaration¶ 14). That improvement is derived not just from the use of Bayes law in step g, but through the addition of step f, prior to implementation of Bayes law. (*Id.*) In step f, a protein with the largest protein confidence value is removed from the set of proteins determined in step c and one or more peptides corresponding to the protein from the set determined in step c is removed and then in step g the protein confidence value is recalculated based on Bayes law. (*Id.*) As the Specification explains it, this inserts information “about the sample or about the relationships across peptides” into the calculation of confidence values that did not exist in the prior art calculation model. (Spec. ¶¶ 29–30.)

Irrespective of the improvement to the resulting data analysis, step f is a data gathering step, like steps a–c that the generic processor carries out. Thus, it too is pre-solution activity; it simply narrows down the data upon which Bayes law is applied. Determining values for variables used in mathematical formula does not save a claim from abstraction. *In re Richman*, 563 F.2d 1026, 1030 (1977) (“[N]otwithstanding that the antecedent steps are novel and unobvious, they merely determine values for the variables used in the mathematical formulae used in making the calculations. [They] do not suffice to render the claimed methods,

⁶ Declaration of Ignat Shilov filed August 30, 2016. This was the second Declaration of Mr. Shilov filed during prosecution of the Application on appeal. (Appeal Br. 3.)

considered as a whole, statutory subject matter.”) (cited with approval in *Flook*, 437 U.S. at 595).

Thus, the additional elements recited in the claim, namely the mass spectrometer, the protein database, and the processor, do not reflect an improvement in the functioning of the processor, or an improvement to mass spectrometers or protein databases, or otherwise integrate the exception into a practical application. *See* Guidance at 55. For the foregoing reasons, therefore, we do not agree with Appellant that the additional elements reflect an improvement in the technical field.

Appellant argues that the improvement in the identification of proteins in a sample is like the improvement in computer animation in *McRO, Inc. v. Bandai Namco Games Am. Inc.*, 837 F.3d 1299 (Fed. Cir. 2016) and therefore the claim is not directed to a judicial application. (Appeal Br. 16–17.) We do not agree. In *McRO*, “the claimed improvement [was] allowing computers to produce ‘accurate and realistic lip synchronization and facial expressions in animated characters’ that previously could only be produced by human animators.” 837 F.3d at 1314. “The claimed rules in *McRO* transformed a traditionally subjective process performed by human artists into a mathematically automated process executed on computers. *Id.* [at 1313–16].” *Fairwarning IP LLC v. Iatric Sys., Inc.*, 839 F.3d 1089, 1094 (Fed. Cir. 2016). In short, in *McRO* the patent claimed an improvement in computer animation. The additional elements, here, do not solve a technological problem in the proteomic analysis field, nor do they improve upon the technological process of peptide digestion for proteomic analysis. Rather it is the application of the specific mathematical calculation in step g that results in improved identification of proteins in the sample, i.e. an

improvement in data analysis. Thus, we find that claim 1 is directed essentially to a method of calculating, using mathematical formulae.

Appellant further argues that claim 1 does not preempt the calculation of protein confidence values (Appeal Br. 18) and the additional requirements of the claim do not preempt the use of Bayes law (Supp. Appeal Br. II at 9–10) and thus, the claims should be deemed directed to patent eligible subject matter. We do not find this argument persuasive. Preemption is sufficient to render a claim ineligible under § 101, but its absence does not require a conclusion of patent eligibility, as noted by the Examiner (Final Action 4). *Athena Diagnostics, Inc. v. Mayo Collab. Servs., LLC*, 915 F.3d 743, 752 (Fed. Cir. 2019) (citing *Flook*, 409 U.S. at 71–72 (holding claim involving mathematical formula invalid under § 101 that did not preempt a mathematical formula); *Ariosa Diagnostics, Inc. v. Sequenom, Inc.*, 788 F.3d 1371, 1379 (Fed. Cir. 2015); *In re BRCA1- & BRCA2-Based Hereditary Cancer Test Patent Litig.*, 774 F.3d 755, 764 n.4 (Fed. Cir. 2014)). As just discussed, claim 1 is directed to an abstract idea because it recites only the collection of data, using standard equipment in proteomics, and applying mathematical equations to that data to analyze that data.

STEP 2B

We next turn to Step 2B to evaluate whether the claims provide an inventive concept. Guidance at 54.

As noted above, the process carried out by the processor includes a set of unconventional steps that results in an improvement over the prior art proteomic analysis: namely steps f and g, which are repeated in step h. As noted, it is this unconventional gathering and processing of the data, that achieves a reduction in the false positive protein identification. (Shilov

Declaration ¶¶ 14, 29, 40–41.) As the Guidance indicates, such unconventional data gathering in combination with a specifically recited application of it can render a claim patent eligible under § 101 despite the fact that the judicial exception is not considered to be integrated into a practical application. *Id.* at 55 and n.39 (citing *Exergen Corp. v. Kaz USA, Inc.*, 725 F. App’x 959, 966 (Fed. Cir. 2018).) Thus, while we agree with the Examiner that the claim is directed to data manipulation, the inventive steps involved in gathering the data for use in the Bayes law calculation, i.e. step f which narrows the data in a particular way and which new data set is employed in the recalculation using Bayes law to determine protein confidence values, under the Guidance is sufficient to render the claims at issue patent eligible under 35 U.S.C. § 101. *Compare with SAP*, 898 F.3d at 1168–69 (

all of the claim details identified by InvestPic—including in the claims that emerged from reexamination—fall into one or both of two categories: they are themselves abstract; or there are no factual allegations from which one could plausibly infer that they are inventive. In these circumstances, judgment on the pleadings that the claims recite no “inventive concept” is proper.)

Thus, we reverse the Examiner’s rejection of claims 1, 3, and 4 under 35 U.S.C. § 101 as being directed to non-statutory subject matter.

REVERSED

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte IGNAT V. SHILOV

Appeal 2017-011343
Application 13/697,707
Technology Center 1600

Before ERIC B. GRIMES, FRANCISCO C. PRATS, and
RACHEL H. TOWNSEND, *Administrative Patent Judges*.

PRATS, *Administrative Patent Judge*, concurring.

I concur with my colleagues that the Examiner’s rejection should be reversed. In my view, however, the rejection should be reversed under Revised Step 2A, Prong 2, of the 2019 Revised Patent Subject Matter Eligibility Guidance, 84 Fed. Reg. 50 (January 7, 2019) (“Memorandum” or “Office Guidance”).

The Office Guidance provides that we proceed to the analysis under Revised Step 2B *only* if, under the analysis under Revised Step 2A, a claim (1) recites a judicial exception and (2) does not integrate that exception into a practical application. *See* 84 Fed. Reg. at 54 (“When the exception is so integrated [into a practical application under the analysis in Revised Step 2A, Prong 2], then the claim is not directed to a judicial exception (Step 2A: NO) and is eligible. This concludes the eligibility analysis.”).

I agree with my colleagues that, under Revised Step 2A, Prong 1, steps d, e, and g of Appellants' claim 1 recite mathematical equations. I find, however, that under Revised Step 2A, Prong 2, the system recited in Appellants' claim 1 integrates the abstract ideas into a practical application because claim 1 requires the system to include a specific machine, a mass spectrometer, and the system is limited to analyzing protein spectra obtained from that machine. *See* Claims App'x at i–iii.

Because, in my view, Appellants' claims integrate the abstract ideas into a practical application, I would reverse the Examiner's rejection without reaching Step 2B of the Office Guidance.