

# Shahbozbek ABDUNABIEV

---

## 1 Personal Data

PLACE AND DATE OF BIRTH: Andijan, Uzbekistan | 30 December 1991  
ADDRESS: Via Degli Ulivi 35, 10156, Turin, Italy  
PHONE: +39 351 9898223  
EMAIL: [shahbozbek.abdunabiev@polito.it](mailto:shahbozbek.abdunabiev@polito.it)



## 2 Work Experience

JUNE 2019 - PRESENT | [Research Assistant \(Marie-Curie fellow\) at POLITECNICO DI TORINO, Turin, Italy](#)  
*Research*

My main responsibility is to work on the development of innovative, mini, biodegradable radiosondes to be used inside warm clouds (1-3 km altitude). I focus on the application of sensor fusion algorithms and filters to track precise trajectory of the radiosonde, floating inside cloud. The radiosonde board is equipped with a set of sensors for tracking fluctuations of pressure, temperature, humidity, velocity and position in a Lagrangian way. Then, sensor measurement data will be sent to ground stations using long-range/low-power radio transmission protocol. The data acquisition techniques and filters used to obtain precise fluctuation dataset from sensor readings.

APRIL 2016 - MAY 2019 | [Teaching assistant at TASHKENT TURIN POLYTECHNIC UNIVERSITY \(TTPU\), Tashkent, Uzbekistan](#)  
*Higher Education*

Teaching bachelor degree courses such as Algorithms and Programming (data structures and algorithms, advanced C programming), Computer Architecture (general computer organization and x86 assembly language), Object-Oriented Programming (object-oriented programming basics with Java), Database(database theory and SQL basics). Preparing lecture, practice and lab materials.

JULY 2018 - MAY 2019 | [Back-end Developer at DATASITE TECHNOLOGIES, Tashkent, Uzbekistan](#)  
*Software development*

I worked as back-end developer in Datasite Technologies software company. We developed with our team software solutions (Java, Spring Boot, PostgreSQL) for WING Delivery Management Company (Dubai, United Arab Emirates). I focused on automatic report generation of package delivery statistics for different time intervals (hour, day, week, etc.), suppliers, customers and regions.

APRIL 2017 - JULY 2018 | [Visiting teacher at ANDIJAN MACHINE BUILDING INSTITUTE, Andijan, Uzbekistan](#)  
*Higher Education*

Teaching bachelor degree courses in the joint educational project with Tashkent Turin Polytechnic University.

NOV 2016 - MARCH 2017 | [Teaching portal operator at TASHKENT TURIN POLYTECHNIC UNIVERSITY \(TTPU\), Tashkent, Uzbekistan](#)  
*System administration*

Teaching portal administration, working with users (students and professors).

### 3 Education

- MARCH 2016 **Master's Degree in COMPUTER ENGINEERING**  
POLITECNICO DI TORINO, Turin, Italy  
Thesis: "A Fusion Detection Algorithm Targeted to Gene Expression Outliers"  
Advisors: Prof. Andrea ACQUAVIVA, Prof. Elisa FICARRA
- NOVEMBER 2013 **Bachelor's Degree in COMPUTER ENGINEERING**  
TASHKENT TURIN POLYTECHNIC UNIVERSITY, Tashkent, Uzbekistan  
Thesis: "Tools for Agile Software Development"  
Advisor: Antonio VETRO

### 4 Publications

- 2020 | *"Turbulent transients of monodisperse and polydisperse distributions of water drops through unstable borders of cloudy environments."*  
AUTHORS: Mina GOLSHAN, Mattia TOMATIS, Shahbozbek ABDUNABIEV, Federico FRATERNALE, Marco VANNI, Daniela TORDELLA  
To be submitted to INTERNATIONAL JOURNAL OF MULTIPHASE FLOW  
An open question in atmospheric physics is the formation of clouds and the as-sociated unsteady processes of nucleation, condensation, evaporation, collision and fragmentation of water droplets. These processes mainly take place in the fully turbulent background air flow peculiar of cloudy environments. In the present study, we use direct numerical simulation to study the temporal evolution of a perturbation localized on the turbulent layer, that typically separates a cloud from the surrounding clear air.
- 2018 | *"A fusion detection algorithm targeted to gene expression outliers using RNA-Seq data."*  
AUTHOR: Shahbozbek ABDUNABIEV  
ACTA,TTPU (SCIENTIFIC-TECHNICAL JOURNAL OF TURIN POLYTECHNIC UNIVERSITY IN TASHKENT), Volume 8 | Issue 2, pages 21-24  
Nowadays there exist many bioinformatics tools that analyse sequencing data to identify genetic aberrations. The genetic aberrations can be amplification, mutation, copy number variation, fusion and so on. And they may cause pathology such as cancer. The identification of driving mechanism of pathology may lead us towards personalized or precise medicine. Personalized medicine is a medical model that uses genetic information of person's disease to diagnose or treat the disease.

## 5 Conferences

- MAY 2020 | *"Progress on the development of innovative, floating, biodegradable radio-probes for atmospheric monitoring inside warm clouds."*  
AUTHORS: Miryam PAREDES, Shahbozbek ABDUNABIEV, Marco ALLEGRETTI, Giovanni PERONA, Daniela TORDELLA, EROS PASERO, Flavio CANAVERO, Andrea MERLONE, Chiara MUSACCHIO  
Abstract accepted at THE GENERAL ASSEMBLY 2020 OF THE EUROPEAN GEOSCIENCES UNION (EGU 2020)  
In an attempt to address these knowledge gaps, this work presents the advances of an experimental method for measuring in-situ the influence of turbulence in cloud formation and producing an infield cloud Lagrangian dataset by means of the development of ultra-light biocompatible radio-probes. With a target weight of less than 20 grams, these innovative devices are carefully designed to float and passively track small-scale turbulence fluctuations in warm clouds and neighboring air. Each mini radio-probe embeds a set of compact size microprocessors, controllers and sensors for the measurement of atmospheric parameters inside clouds (e.g. velocity, acceleration, vorticity, pressure, temperature, humidity) after been released into the atmosphere.
- NOV 2019 | *"Innovative, mini, biodegradable radiosondes to track small-scale fluctuations in warm cloud and clear air environments."*  
AUTHORS: Shahbozbek ABDUNABIEV, Tessa C BASSO, Daniela TORDELLA, Miryam PAREDES, EROS PASERO, Flavio CANAVERO  
Presented by Shahbozbek ABDUNABIEV in THE 72ND ANNUAL MEETING OF THE AMERICAN PHYSICAL SOCIETY'S DIVISION OF FLUID DYNAMICS (APS/DFD 72)  
The innovative, ultralight green radiosondes presented here are designed to passively track fluctuations of temperature, humidity, pressure and velocity for several hours on isopycnic surfaces in cloud and clear air environments at altitudes between 1-3 km. To equalize the buoyancy force to the weight of the system, the balloon is filled with a mixture of helium gas and air. The sonde incorporates various set of sensors and a long range/low power radio module, which makes it possible to track fluctuations. A Lagrangian set of data can then be obtained by fusion of GPS (Global Positioning System) and IMU (Inertial Measurement Unit) sensor output. GPS and IMU data can be integrated using the Kalman filter, where GPS provides the periodic updates for removing drifts in the IMU output.

## 6 Postgraduate Training

- SEP 2018 Training on Mathematical Engineering for ECCUM teachers  
**University of Primorska**, Koper, Slovenia  
Certificates obtained: Attendance
- JAN 2017 MATLAB and COMSOL training for ECCUM teachers  
**University of Primorska**, Koper, Slovenia  
Certificates obtained: Skills declaration

## 7 Languages

- UZBEK: Mother tongue  
ENGLISH: Fluent  
RUSSIAN: Good Level  
ITALIAN: Basic level

## 8 Professional skills and competences

- Programming (C, FORTRAN, JAVA, Assembly)
- Writing software programs for microcontrollers
- Designing a sensor data acquisition system
- Sensor data fusion

- Working with parallel computing environments (CINECA, HACTAR, CASPER)
  - Statistical analysis (FORTRAN, MATLAB, Python)
  - Graphic design (Gnuplot, GIMP, Veusz, Draw.io)
- 

- Teamwork
- Commitment
- Communicable

## 9 Interests and Activities

Research: Sensor fusion, Position tracking, Machine Learning, Distributed Networks, High Performance Computing

---

Technology, Open-Source, Programming

---

Reading, Football, Travelling

Abstract Submitted  
for the DFD19 Meeting of  
The American Physical Society

**Innovative, mini, biodegradable radiosondes to track small-scale fluctuations in warm cloud and clear air environments** SHAHBOZBEK ABDUNABIEV, TESSA C. BASSO, DANIELA TORDELLA, Politecnico di Torino, MIRYAM PAREDES, Envisens Technologies s.r.l., Politecnico di Torino, EROS PASERO, FLAVIO CANAVERO, Politecnico di Torino — Modelling clouds depends on a variety of chemical and physical processes. These processes range from the nanometer scale, where nucleation, coalescence and rain formation take place, to airflow dynamics which can range up to kilometres. Turbulence plays an important role in the behaviour of these processes and can be noted on different scales. The innovative, ultralight green radiosondes presented here are designed to passively track fluctuations of temperature, humidity, pressure and velocity for several hours on isopycnic surfaces in cloud and clear air environments at altitudes between 1-3 km. To equalize the buoyancy force to the weight of the system, the balloon is filled with a mixture of helium gas and air. The sonde incorporates various set of sensors and a long range/low power radio module, which makes it possible to track fluctuations. A Lagrangian set of data can then be obtained by fusion of GPS (Global Positioning System) and IMU (Inertial Measurement Unit) sensor output. GPS and IMU data can be integrated using the Kalman filter, where GPS provides the periodic updates for removing drifts in the IMU output. This data set can be of help in developing stochastic models to account for turbulence effects on cloud formation.

Ruth Teferi  
APS

Date submitted: 09 Aug 2019

Electronic form version 1.4



## Progress on the development of innovative, floating, biodegradable radio- probes for atmospheric monitoring inside warm clouds

**Miryam Paredes**<sup>2,3</sup>, Shahbozbek Abdunabiev<sup>1</sup>, Marco Allegretti<sup>2,3</sup>, Giovanni Perona<sup>3</sup>, Daniela Tordella<sup>1</sup>, Eros Pasero<sup>2</sup>, Flavio Canavero<sup>2</sup>, Andrea Merlone<sup>4</sup>, and Chiara Musacchio<sup>4</sup>

<sup>1</sup>Department of Applied Science and Technology, Politecnico di Torino

<sup>2</sup>Department of Electronics and Telecommunications, Politecnico di Torino

<sup>3</sup>Envisens Technologies s.r.l.

<sup>4</sup>Istituto Nazionale di Ricerca Metrologica di Torino

Characterization of clouds is still a challenging task for weather forecasting and climate modeling. This is because clouds depend on interdisciplinary natural processes, ranging from the micrometer scale, where particles and droplets collide, to the thousand-of-meters scale of airflow dynamics. Turbulence has an important role in cloud formation and rain initiation since it helps rain droplets to evolve through coalescence and collision processes. Unfortunately, the effects of turbulence mechanisms are not yet well understood and there remains a need for further clarification.

In an attempt to address these knowledge gaps, this work presents the advances of an experimental method for measuring in-situ the influence of turbulence in cloud formation and producing an infield cloud Lagrangian dataset by means of the development of ultra-light bio-compatible radio-probes. With a target weight of less than 20 grams, these innovative devices are carefully designed to float and passively track small-scale turbulence fluctuations in warm clouds and neighboring air. Each mini radio-probe embeds a set of compact size microprocessors, controllers and sensors for the measurement of atmospheric parameters inside clouds (e.g. velocity, acceleration, vorticity, pressure, temperature, humidity) after been released into the atmosphere. To reach a buoyancy force equal to the weight of the system, the bio balloons containing the electronics are appropriately filled with a mixture of helium gas and air. During the flight, the smart radio-probes acquire, pre-process, store, arrange and transmit the obtained data to different receiving and ground stations located on earth through a dedicated radio transmission link. Due to the radio-probes' physical constrains and the environmental conditions that can be found inside warm clouds, a power-saving and long-range wireless communication technology has been selected and tested.

The development of the first operational prototypes for both, the radio-probes and the receiving stations, are presented together with results of the first measurement experiments both, in

laboratory and field campaign.

1-6-2018

## A Fusion Detection Algorithm Targeted to Gene Expression Outliers Using Rna-Seq Data

Shahbozbek Abdunabiyev

*Turin Polytechnic University in Tashkent*, shahbozbek.abdunabiev@polito.uz

Follow this and additional works at: <https://uzjournals.edu.uz/actattpu>

 Part of the [Computer Engineering Commons](#)

---

### Recommended Citation

Abdunabiyev, Shahbozbek (2018) "A Fusion Detection Algorithm Targeted to Gene Expression Outliers Using Rna-Seq Data," *Acta of Turin Polytechnic University in Tashkent*: Vol. 8 : Iss. 2 , Article 4.

Available at: <https://uzjournals.edu.uz/actattpu/vol8/iss2/4>

This Article is brought to you for free and open access by 2030 Uzbekistan Research Online. It has been accepted for inclusion in Acta of Turin Polytechnic University in Tashkent by an authorized editor of 2030 Uzbekistan Research Online. For more information, please contact [brownman91@mail.ru](mailto:brownman91@mail.ru).



ACTA TTPU

III. ENGINEERING SCIENCE



# A FUSION DETECTION ALGORITHM TARGETED TO GENE EXPRESSION OUTLIERS USING RNA-SEQ DATA.

Shahbozbek Abdunabiyev

*Turin Polytechnic University in Tashkent*

## Abstract

Nowadays there exist many bioinformatics tools that analyse sequencing data to identify genetic aberrations. The genetic aberrations can be amplification, mutation, copy number variation, fusion and so on. And they may cause pathology such as cancer. The identification of driving mechanism of pathology may lead us towards personalized or precise medicine. Personalized medicine is a medical model that uses genetic information of person's disease to diagnose or treat the disease.

The fusion detection tools are a subset of the bioinformatics tools that are targeted to find gene fusions. Usually, they have long execution time and work on the whole dataset to find all possible fusions. In this work we have designed and implemented target based fusion detection pipeline that works on a single gene. We had the sequencing data and the target gene that is highly expressed as input. We used alignment tools, statistical analysis, filtering and data mining techniques to find possible fusion partners.

*Keywords: bioinformatics, genomics, cluster, mutation.*

## 1 Introduction

Cancer is caused by changes (alterations: translocations, deletions, amplifications and inversions) to the DNA within cells. The DNA inside a cell is packaged into a large number of individual genes, each of which contains a set of instructions telling the cell what functions to perform, as well as how to grow and divide. Errors in the instructions can cause the cell to stop its normal function and may allow a cell to become cancerous [1].

Alterations happen often, but the human body can correct most of them. Depending on where in the gene the alteration occurs, it can be useful, harmful or not important at all. So, not all alterations are relevant for formation of cancer and one alteration alone is unlikely to lead to cancer. Usually, it takes chain of alterations over a lifetime to cause cancer. Gene fusions are important events in cancer formation from DNA alterations.

Gene fusion is the event that two genes form a hybrid transcript in the DNA transcription (RNA formation). Nowadays, development of the Next Generation Sequencing (NGS) technologies creates good opportunity to detect gene fusions. NGS technology reads DNA nucleotides and produces fixed length fragments (string of nucleotide letters) which are in two forms: single-end and paired-end (often

called RNA-Seq reads). In order to obtain paired-end reads NGS technology sequences both ends (5' and 3') of DNA, which is not the case for single end [2].

Nowadays, there are several fusion detection tools that detect fusion events from paired-end RNA-Seq reads. They map paired-end reads to references (genome, exome, transcriptome) and try to detect if read pairs are mapped to two different genes. Mapping process provides the first list of fusion candidate genes. Consequently, tools determine the exact location where genes are fused by finding reads that partially mapped on both genes. The following tools are examples which adopt this general mechanism: FusionSeq, deFuse, ChimeraScan, Bellerophon and soon. Even if they share the same general idea, they differ in type of filters and intermediate steps which they apply to decrease a number of false fusion events.

Complexity of available tools is very high due to complex filtering techniques, operations on large sequencing dataset and annotation of all possible fusion events with known genes [4]. As we stated in the beginning, not all fusions are relevant in cancer development. Typical consequence of gene fusions at the RNA level is strong variation of gene expression. It is possible to obtain the most relevant genes (outliers) by means of data mining techniques applied to gene expression analysis.

In order to reduce complexity of fusion detection process, we designed and implemented fusion detection pipeline targeted to outlier genes. In our implementation we used BOWTIE2, BLAST+, BedTools tools for alignment and annotation, Python, awk and Bash scripting skills for filtering and join operations. For execution and testing the pipeline, computational resources were provided by HPC@POLITO [6].

## 2 Methods

We provide pipeline workflow selected outlier gene (target gene) and it finds possible fusion candidate genes in two phases: alignment and filtering-annotation phases. The following sections highlight basic steps and details of the pipeline workflow.

### 2.1 Phase 1: Alignment

The section focuses on details of computational steps of the alignment phase of the pipeline workflow. Figure 1 shows the schematic flow of this phase. The alignment phase provides a set of possible fusion candidate reads by aligning RNA-Seq data on target gene, genome and exome in different steps.

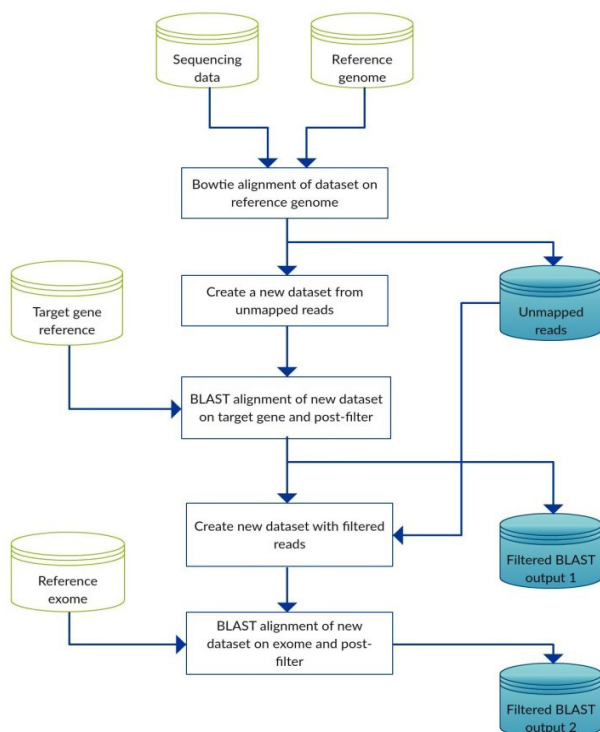


Figure 1: Alignment phase of the pipeline workflow.

**Reference genome alignment.** Aligning RNASeq reads to a reference genome is the first step in many comparative genomics pipelines, including pipelines for fusion detection. Many fusion detection tools exploit Bowtie2 alignment tool [7] for the initial sample alignment. Because, it is fast and memory efficient for aligning large datasets on long references. For this reason, we selected Bowtie2 and used it in this step. As a result, we obtain a set of unmapped reads and we discard all reads that are mapped to reference genome.

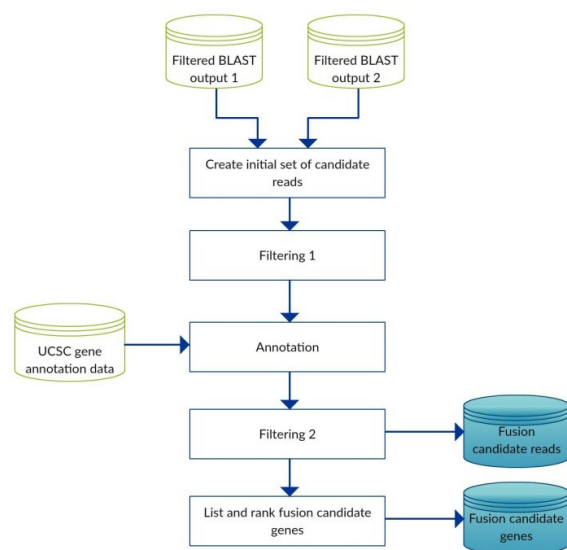
**Target gene BLAST alignment.** The new dataset generated from unmapped reads is aligned subject to target gene with BLAST+ alignment tool [3,5]. Then, output of the BLAST is filtered to get reads that are partially mapped to target gene. Firstly, duplicate alignments are removed (in some cases BLAST reports duplicate alignments). Then, we filter out alignments with alignment length above predefined threshold and all further hits of the same read are also discarded. After that, read ids are extracted from filtered BLAST output and they are used to create a new dataset from the set of unmapped reads, which is generated in the previous step.

**Reference exome BLAST alignment.** Starting from the new dataset generated in the previous step, we run another BLAST alignment on reference exome. We apply the same filtering criteria as before to obtain reads with partial alignments. Moreover, alignments on target gene are excluded from BLAST output. So, we keep alignments related to other genes, which are possibly fusion candidate partners for the target gene.

### 2.2 Phase 1: Filtering-annotation

The second phase of the fusion pipeline workflow is the filtering-annotation. In this phase, we examine alignments generated in the previous phase for finding possible fusion events. In the meantime, we annotate them with known genes in order to identify involved genes in fusion event. Therefore, cascade of filters are applied on the set of alignments. Figure 2 shows flow schema of this phase, where we start with alignments and generate a list of fusion candidate genes and corresponding reads as a final result.

**Create initial set of candidate reads.** In the previous phase we stored filtered BLAST alignments of target gene and exome. In this step, we join two datasets based on read identifier. As a result, we generate the initial set of fusion candidate reads, where the two parts of the read mapped on different genes.



**Figure 2: Filtering-annotation phase of the pipeline workflow**

**Filtering 1: Overlapping and coverage reads extraction.** One of the most important step of the pipeline workflow is to identify properties of reads that are involved in fusions. That is why, previously generated candidate reads are analyzed to get most promising candidates. We keep reads that two parts of the read are consecutive or overlap with each other in terms of read coordinates. Moreover, the two parts should cover the read length with given threshold (e.g 80% coverage). Both the coverage threshold and overlapping window size can be tuned based on dataset.

**Annotation.** For annotation purposes we used UCSC and RefSeq known genes annotation database. Since there can be gene aliases, the database is modified by removing gene aliases. As a result we keep only the most generic genes in terms of genomic coordinates. Then, the set of reads generated in the previous step is annotated with modified annotation database

**Filtering 2: Extracting reads along fusion breakpoint.** Starting from annotated set of reads, we apply another filter for ranking candidate genes based on significance. Firstly, we remove candidate genes which have annotated reads less than given threshold. Then, we identify possible fusion breakpoints and candidate reads with remaining set of reads. Finally, fusion breakpoints are sorted subject to a number of supporting reads and corresponding fusion candidate gene is extracted for each breakpoint. As a result, we obtain a sorted list of fusion candidate genes.

### 3 Results

Firstly, we tested the pipeline with TCGA-CA-5254 dataset with ~ 80 mln of 48bp long reads. In this case, BCAR4 is selected as a target gene and results are validated with deFuse results. In the test, we identified fusion BCAR4-ZC3H7A fusion which is common with deFuse. The deFuse provides 27 supporting reads along fusion breakpoint. Our pipeline provides 30 supporting reads for fusion and 20 of them are common with deFuse output. Then, there was an another test with TCGA-AA-3520 dataset with ~ 30 mln of 76bp long reads. For this dataset, we selected FLVCR2 as a target gene and obtained results are validated with MapSplice results. The pipeline found out FLVCR2-RPS24 fusion, which exists in MapSplice output. There are 11 supporting reads reported in MapSplice output, while the pipeline provides 25 reads. MapSplice reported fusion breakpoint as chr14:76062166 for FLVCR2 and chr10:79796970 for RPS24. Our pipeline resulted as following: chr14:76062160 for FLVCR2 and chr10:79796970 for RPS24 with 10 supporting reads along junction.

### 4 Conclusion

Results show that implemented pipeline provides similar results as available fusion detection tools. Moreover, our pipeline introduces some innovations as follows:

- Target based fusion detection.
- Less complex filtering processes, dataset and computation time.
- It is independent of read types (paired-end, single-end).

In the future, the pipeline can be optimized by increasing sensitivity. Moreover, web service based version of the pipeline can be introduced. As a result, we will achieve a unique framework for fusion analysis of outliers (genes or any genomic intervals).

### References:

1. DNA replication. DNA replication — Wikipedia, The Free Encyclopedia. 2018. URL: [https://en.wikipedia.org/wiki/DNA\\_replication](https://en.wikipedia.org/wiki/DNA_replication) (visited on 06/06/2018).
2. Help me understand Genetics. Genetics Home Reference. 2018. URL: <https://ghr.nlm.nih.gov/primer> (visited on 06/06/2018).
3. Christiam Camacho et al. "BLAST+: architecture and applications". In: BMC Bioinformatics 10.1 (2009), pp. 1–9. ISSN: 1471-2105. DOI: 10.1186/1471-2105-10-421. URL:

*Abdunabiyev Sh. / ACTA TTPU 2 (2018) 21-24*

<http://dx.doi.org/10.1186/1471-2105-10-421>.

4. Francesco Abate et al. "Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer". In: BMC systems biology 8.1 (2014), p. 97.

5. S. Altschul et al. "Basic local alignment search tool". In: J Mol Biol 215 (1990). DOI: 10.1016/S0022-2836(05)80360-2. URL:[http://dx.doi.org/10.1016/S0022-2836\(05\)80360-2](http://dx.doi.org/10.1016/S0022-2836(05)80360-2).

6. HPC@POLITO. Computational resources were provided by HPC@POLITO, a project of Academic Computing within the Department of Control and Computer Engineering at the Politecnico di Torino. 2016. URL: <http://www.hpc.polito.it>

7. Ben Langmead and Steven L Salzberg. "Fast gapped-read alignment with Bowtie 2". In: Nature methods 9.4 (2012), pp. 357–359.



O'ZBEKISTON RESPUBLIKASI  
Toshkent shahri  
"O'ZAVTOSANOAT"  
Aksiyadorlik kompaniyasi

РЕСПУБЛИКА УЗБЕКИСТАН  
город Ташкент  
Акционерная компания  
"УЗАВТОСАНОАТ"

## TURIN POLITEKNIKA UNIVERSITETI

100095, Toshkent sh, Olmazor tumani, kichik xalqa yo'li 17 uy, tel.: +998712461018, fax.: +998712467082.  
x/r: 20 208 000 904 790 690 001 "Acaka" bank TShF, MFO 00416, STIR 301249598, XXTUT92110. e-mail: info@polito.uz. www.polito.uz

16.02.2017 № 8/02-185

To Whom It May Concern:  
Dear members,

It is my pleasure to recommend Shahbozbek Abdunabiev for admission to your program. Due to his outstanding performance in the work, I am delighted to hear that he is interested in attending for your program, and I am equally delighted to assist him in this process by writing this letter to recommend him to your program. I have worked very closely with Mr. Abdunabiev during the several years while he has been enrolled as a student of Tashkent Turin Polytechnic University and in his academic career as a trainee-teacher. Shahbozbek has excelled in this role and maintained one of the highest levels of productivity and study for an assistant over the years tenure with the University. Shahbozbek produces a high volume of work while maintaining high standards for quality and accuracy. Mr. Abdunabiev possesses the ultimate "can do" attitude while taking on all tasks with a positive energy and a smile. His upbeat personality and engaging personal style enables his to interact effectively with students and staff. Mr. Abdunabiev is very well organized and keeps track of the details necessary to coordinate events of this kind and run an efficient office. Mr. Abdunabiev takes initiative to go beyond the expected parameters of his job and study. There will be no unpleasant surprises and I am confident he will fit in and add to office morale.

I volunteered to write this recommendation for Mr. Abdunabiev because I am very grateful for his contributions to our university and very confident that he has the intelligence, work ethic and communications skills to add value wherever he works or studies. Please feel free to contact me if you have any questions about him. Mr. Abdunabiev has been an outstanding person, and I am delight to encourage and assist him in pursuit of his goals. Participating to your program will help him both in research and in the international experience that can remove any barriers to future successes. I have deepest personal and professional respect for him, and sincere belief that he will bring his unique energy, optimism, passion and tireless creativity to your program. I strongly recommend him for acceptance to your program without reservations. Feel free to contact to me if you have further questions.

Yours Sincerely,

Sharipov Kongratbay Avezimbetovich

First Vice-Rector, Tashkent Turin Polytechnic University

Kichik khalka yuli str. 17, 100195, Tashkent, Uzbekistan

Tel.: +99871 246-70-82

E-mail: k.sharipov@polito.uz





Tashkent 28/10/2013

## EVALUATION LETTER

To whom it may concern

This letter is to serve as my formal recommendation for Abdunabiev Shahbozbek. As a Senior Professor at Politecnico di Torino, I am basing this evaluation on my personal knowledge of this student, who successfully completed my courses in Computer Architecture and Algorithms and Programming at Turin Polytechnic University in Tashkent (TTPU), where I also teach. I have known him for six months and feel that he is a deserving candidate for your Master and PhD program.

Abdunabiev Shahbozbek's results in courses suggest a very responsible and motivated student. He attended my lectures regularly, participated actively, completed his assignments within the prescribed time frame, demonstrated a high level of interest in the study of my discipline, and obtained excellent marks in the end-of-course examinations (the maximum one).

He has talked with me about his goal of attaining higher education, and I have enjoyed seeing such enthusiasm in an undergraduate.

Since his classmates, my fellow teachers, and I will always hold him in the highest esteem, I sincerely recommend as the ideal candidate for higher studies at your University.

I believe Abdunabiev Shahbozbek's strong academic abilities and his clear dedication towards studies make him a very strong candidate for your Master and PhD program. I sincerely recommend him as an ideal student for higher studies at your university.

Sincerely yours

Angelo Serra

Full professor of Computer Science Engineering  
Faculty of Information Engineering

**Angelo Serra**



Dear Sirs/Madams,

I am very pleased to write a letter of recommendation for **Shahbozbek Abdunabiev**. I highly recommend Shahbozbek for PhD position of your University.

I have worked alongside with Shahbozbek for a past year in the following courses: Algorithm and Programming, Computer Science. As a professor and colleague I have had opportunity to observe his teaching activities, skills, interaction with students and colleagues and evaluate Shahbozbek's knowledge of the subject matter. He is outstanding person on all respects. Shahbozbek has proven that through hard work, competence and team work can accomplish task in timely manner with excellence.

Shahbozbek can plan teaching process, create new materials and learn while teaching. He has made his contributions in teaching process by organizing interesting classes and engaging students in Information Technology field.

Shahbozbek has shown his interests on research during projects of University, Republican and International level. He is highly intelligent and has good analytical skills. His participation on ECCUM (Mathematical Engineering, Erasmus+) project demonstrated his ability to come a detailed understanding of the practices of another person. Moreover, he showed his motivation to study and enter new research field and made his contributions with his creative ideas and study reports while attending seminars and conferences in the framework of the ECCUM project.

Shahbozbek presented his sincere research motivation on Computer Engineering field by attending Republican level projects on "Development of Agro-Robot" and "Application of ICT in Education System". Participating in PhD program will help him both in research and in the international experience that can remove any barriers to future successes.

Shahbozbek is keen to study and explore new ideas while working in our University. He is well equipped to grow from challenges he is presented with. His teaching ability, competence, working ability with team and strong computer science skills prepare him for your PhD program. I strongly endorse making Shahbozbek a PhD student at your University.

Sincerely,

Kasim Khusanov,

Associate Professor of the Department of Natural and Mathematical Sciences  
Tashkent Turin Polytechnic University

+998 90 329 80 19

k.khusanov@polito.uz

