Scientific Report

First name / Family name	Victor Chukwudi Osamor
Nationality	Nigerian
Name of the *Host Organisation*	University of Warsaw
First Name / family name of the *Scientific Coordinator*	Jerzy Tiuryn
Period of the fellowship	17/03/2014 to 16/03/2015

I – SCIENTIFIC ACTIVITY DURING YOUR FELLOWSHIP

My scientific activities during the tenure of my fellowship include:

1. Thorough reading activities of different text and publications on histone modification, mechanisms and existing algorithms that enhance the study of epigenetic controls.

2. Getting acquainted with an in-house program called TACO for dimer prediction.

3. Writing programs in python to plot the tag density of 5 cell lines on a genome-wide scale.

4. Writing programs to compute various features like left and right overlap, 100% containment, no overlap between called MACS peaks of Bam file in Histone Modification data and DNA-seq data.

5. We evolved an experimental design for combinatorial analysis of histone markers (H3k4me1, H3k4me2, H3k4me3, H3k9ac and H3k27ac) across 9 human cell lines namely GM12878, H1hESC, K562, HELAS3, HUVEC, NHLF, HMEC, NHEK and NA-H. The analysis was comprehensively done for a total of 31 experimental set-up for each cell line targeted at replacing DNase-seq with ChIP-seq histone modification data in TACO (Transcription factor Association for Complex Overrepresentation) dimer prediction tool.

6. The experimental design is shown in the table below where "+" symbol represents a histone mark whose MACS peak were used directly as a singular modification or in combination with other modifications for each specific experiment.

EXPERIMENTAL DESIGN

CELL-LINE: H1hesc

Histone Modification(HM)	**CODE**	**HM1**	**HM2**	**HM3**	**HM4**	**HM5**	**Peak DATA INPUT**
Histone Modification type		**H3K4me1**	**H3K4me2**	**H3K4me3**	**H3K9ac**	**H3K27 ac**	
EXPERIMENTS							
1	HM123	+	+	+			Peaks combined, sorted & Merged
2	HM1	+					Used directly
3	HM2		+				Used directly
4	HM3			+			Used directly
5	HM4				+		Used directly
6	HM5					+	Used directly
7	HM12345	+	+	+	+	+	Peaks combined, sorted & Merged
8	HM12	+	+				Peaks combined, sorted & Merged
9	HM13	+		+			Peaks combined, sorted & Merged
10	HM14	+			+		Peaks combined, sorted & Merged
11	HM15	+				+	Peaks combined, sorted & Merged
12	HM23		+	+			Peaks combined, sorted & Merged
13	HM24		+		+		Peaks combined, sorted & Merged
14	HM25		+			+	Peaks combined, sorted & Merged
15	HM34			+	+		Peaks combined, sorted & Merged
16	HM35			+		+	Peaks combined, sorted & Merged
17	HM45				+	+	Peaks combined, sorted & Merged
18	HM124	+	+		+		Peaks combined, sorted & Merged
19	HM125	+	+			+	Peaks combined, sorted & Merged
20	HM134	+		+	+		Peaks combined, sorted & Merged
21	HM135	+		+		+	Peaks combined, sorted & Merged
22	HM145	+			+	+	Peaks combined, sorted & Merged
23	HM234		+	+	+		Peaks combined, sorted & Merged
24	HM235		+	+		+	Peaks combined, sorted & Merged
25	HM245		+		+	+	Peaks combined, sorted & Merged
26	HM345			+	+	+	Peaks combined, sorted & Merged
27	HM1234	+	+	+	+		Peaks combined, sorted & Merged

28	HM1235	+	+	+		+	Peaks combined, sorted & Merged
29	HM1245	+	+		+	+	Peaks combined, sorted & Merged
30	HM1345	+		+	+	+	Peaks combined, sorted & Merged
31	HM2345		+	+	+	+	Peaks combined, sorted & Merged

7. The investigation was done for thresholds of 500-30000bp and assessment was made to ascertain how much quality prediction we might be compromising for substituting DNase-seq with ChIP-seq histone modification data in TACO for the prediction of transcription factor dimer.

8. We evaluated our results using DNase result as a gold standard to measure the performance of our prediction for both Weakly Cell-Type Specific and Strongly Cell-Type Specific algorithms.

9. We also further compared the predicted TACO dimer count to the experimentally proven dimers that exist in literature.

10. Most of these scientific activities have their results now accepted for publications in various journals and conferences as listed in the publication section.

II – PUBLICATION(S) DURING YOUR FELLOWSHIP

The list of my publications and pending manuscripts include:

1. Osamor V.C., Chinedu S.N., Azuh D., Iweala E.E.J., Ogunlana O.O. (2015). The interplay of post-translational modification and gene therapy. Drug Design, Development and Therapy (Accepted for publication).

2. Osamor VC, Tiuryn J. (2015). Analysis of replacing DNase-seq data with histone marks in computational dimer prediction. The 24th Annual Computational Neuroscience Conference, July 18-July 23, 2015, Prague, Czech. BMC Neuroscience (To appear – Accepted for publication)

3. Osamor VC (2015). Sourcing brain histone modification data for identification of hypersensitive sites. The 24th Annual Computational Neuroscience Conference, July 18-July 23, 2015, Prague, Czech. BMC Neuroscience (To appear – Accepted for publication).

4. Osamor VC, Tiuryn J. (2015). Combinatorial dimer prediction in 9 cell-lines: Substitution of DNase_seq in TACO (Transcription factor Association from Complex Overrepresentation) Algorithm (Tentative title) – Pending Manuscript.

III – ATTENDED SEMINARS, WORKHOPS, CONFERENCES

During the tenure of my fellowship, I attended the following seminars and conferences:

1. ABCDE Seminar IV, 23-24/10/2014, Pisa, Italy

2. I attended European Molecular Biology Organisation (EMBO) workshop on Computational Biology at Goniadz, Poland, 20-22 February 2015.

3. Also arising from my work are two research results accepted for presentation at the 24th Annual Conference of Computational Neuroscience (CNS 2015) in Prague, July 18-23, 2015. I will present these results at the meeting.

IV – RESEARCH EXCHANGE PROGRAMME (REP)

Bioinformatics is my area of specialty, and its an emerging field of Computer Science engaged by relatively few number of ERCIM research centres compared to other aspects of Computer Science. To this end, securing REP placements outside my host organisation for similar research activity was challenging especially when the choice is limited to ERCIM member centre only. After several attempts, I quickly reported the challenges to my Scientific Coordinator and we resolved to present the challenges and recommendations in our report. In a bid to avoid placements that will not add any relevance to my professional career, we decided to focus on the research at my host institution.

In this regard, I will suggest that REP placement be bundled with the award of the fellowship such that every individual will know where to visit from the onset instead of the fellows themselves begging for placement. This will also make fellows readily acceptable when institutions are mandated by direct correspondence through ERCIM's central administration for the purpose of receiving fellows for REP.