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MANA TOHU MĀTAURANGA O AOTEAROA

QUALIFY FOR THE FUTURE WORLD
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Scholarship 2015 Biology

9.30 a.m. Tuesday 10 November 2015

Time allowed: Three hours

Total marks: 24

ANSWER BOOKLET

Check that the National Student Number (NSN) on your admission slip is the same as the number at the top of this page.

Write your answers in this booklet.

Start your answer to each question on a new page. Carefully number each question.

Check that this booklet has pages 2–26 in the correct order. Pages 2–4 are blank and are to be used for planning. Pages 5–26 are lined pages for writing your answers.

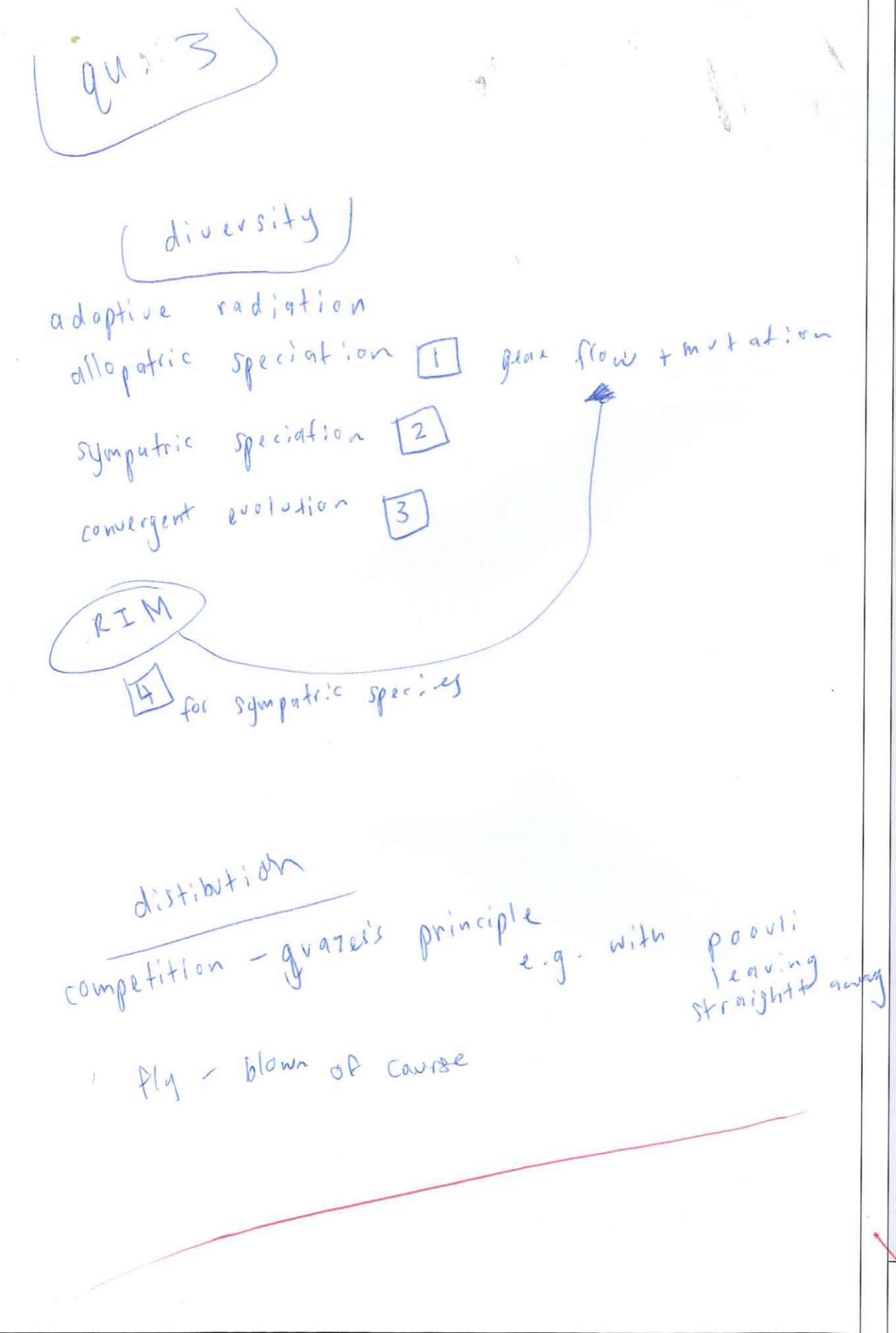
YOU MUST HAND THIS BOOKLET TO THE SUPERVISOR AT THE END OF THE EXAMINATION.

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There are many factors that can cause a species population to decline and possibly become extinct. Some species are highly specialised for the environment they live in and there may be low genetic variation within the species. This means that if the environment changes, for example with climate change, destruction of habitat or introduction of a parasite, predator or competitor, the species ~~is~~ does not have the genetic information within the gene pool to adapt to these changes. An example of this would be H. neanderthalensis, that were out-competed by H. sapiens (competitor) or possibly were too thickset and were not adapted to the increasing temperatures in the interglacial period. Population numbers can also decline if the habitat becomes over-populated so there is not sufficient resources to support ~~the~~ the species. Especially if the organisms are very large, such as Dinornis, a large amount of resources is required to support 1 individual so the environment can only support a few. This over-population could lead to death of many individuals by starvation as well as lack of suitable breeding sites and nesting sites. All these will prevent genes being passed onto the next generation so numbers in the population will decline. If the population is very small and isolated (or the population has bottlenecked previously e.g. modern day cheetahs) then there will be low genetic diversity. This means that one disease could wipe out the entire population, or many members of it, thus leading to population

define.

There are a number of possible reasons today as to why the rate of extinction has become so high, mostly related to human interference. As the human population continues to grow rapidly, more and more land is cleared for humans to live on and to grow resources on such as plants, animals and materials like cotton. This means there is much less available land for other populations to live in so their populations will decline and they may become extinct e.g. in the Amazon Rainforest land is cleared to produce Palm Oil, endangering species that previously lived there. Humans also destroy habitats such as the ocean with oil spills endangering fish species that can lead to their extinction. Humans only allowing plants and animals desired for commercial use to live on land also decreases diversity of the environment so less species, for example secondary and tertiary consumers, are supported by it (only ones that feed on commercial crops which is not all species). Finally, humans introduce species into habitats where they did not previously exist, these species can out-compete or exploit native species, causing their extinction. New Zealand is a prime example of this. Cats, possums, dogs and rats have been introduced that exploit the native bird populations such as kiwi and takahae. The introduction of rats by Maori may have led to the extinction of moa like *Pachyornis*, species like *L* as they eat the eggs/juvenile birds or for smaller species, animals like cats can catch the mature birds. Species like the possum

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consume large amounts of bush land that native wildlife feeds on, lives in and hides in. This can lead to a higher rate of extinction today. As well as introduced species, humans have also hunting species for food and then exploited the population. This may have been another contributing factor to the extinction of moa as the arrival of Maori people in New Zealand meant that moa were now hunted so had predators in contrast to when they were the dominant herbivore.

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cloning would be a technique humans could use to restore a moa population. This would be done by extracting DNA from a large number of moa remains (such as skeletons), both male and female to form a population that could breed and would have sufficient genetic diversity. Firstly, an egg cell from a surrogate mother of a closely related species such as emu or ostrich (as also ratites, common ancestor) would have to be taken and the DNA within it removed. Then, the DNA from a somatic cell of a moa would be injected into the egg cell and fused by an electric shock. A further electric shock would stimulate mitosis to occur begin. When a sufficient number of cells had formed, the cells would be inserted into the surrogate mother and the process would continue as if she was growing an infant of her own species. Once a large enough population was established, the moa could be released into the wild.

There are a large number of biological implications that could result from doing this. Firstly, it would be hard to get a very large range of genetic diversity so the implications of the founder effect would apply. The population would be subject to genetic drift, so alleles could become fixed or lost. This would make moa very susceptible to certain diseases that could wipe out almost all of the population. There will also be diseases present today that moa will have little or no resistance to so the population could die out. The population dying out would mean that the production of the species would be a waste of resources as cloning does not have 100% success rate and is expensive. Resources may be better spent preventing existing endangered species like short-tailed bat, kiwi and falcons from becoming extinct. Moa are also likely to be poorly adapted to the environment, further increasing their chances of becoming re-extinct. They are adapted to a cooler environment than is present today (with the planet is further into the interglacial period and possibly amplified with global warming) so may be weakened because it places extra stress on them so less likely to survive. They are also poorly adapted to survive with predators such as rats and possums. Unless the park is protected and free of these pests, the species that may have contributed to moa extinction in the first place may do so again. Moa cannot fly, so unlike species of bird that have managed to survive, Moa may not (could be similar to kiwi that struggled but were as it is bigger). The

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idea of starting with smaller species such as Pachycornis is intelligent of Mallard, as these species are more likely to survive as they require less resources. The habitats Moa lived in are still present today in New Zealand - shrublands, forests and grasslands (presumably also in the forest park) so ~~the~~ Moa would have some chance of surviving in that respect. However, the species likely introduced (Pachycornis or similar) lives in dense forest. Rimutaka may not be sufficiently dense for the moa survival. Also, moa, even the smaller one, will still consume a large amount (as Moa is a dominant herbivore) of present bird species, leading to their extinction. This would be counter productive.

Thus, I believe moa is not a goer (we should not bring them back). This is because there are many factors that increases the chance that moa would not survive, meaning it would be a waste of resources - other endangered species protection should be prioritised. Also, moa may have an adverse effect on other bird species present in the area due to competition for resources (as there is less present than before human introduction to New Zealand) meaning bringing back the moa would be counter-productive.

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Question 2

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Approximately 80,000 to 40,000 years ago, a mutation would have occurred in the Denisovan population in the EPAS1 gene that prevented over production of haemoglobin. This must have occurred in Denisovans as H. sapiens from Africa do not contain the variant and thus the mutation must have occurred outside Africa (could not have been the descendants of Denisovans). It is possible that this mutation was also present in Altai Neanderthals, but unlikely as these would have then interbred with Europe Neanderthals possibly, which then contributed DNA to African and European modern humans who do not possess the EPAS1 variant. This mutation would have been an adaptive advantage as not having thickset blood leading to hypertension, conceiving difficulty, low birth weight, increased mortality and chance of strokes and heart attacks, means that you individuals are less likely to die and their offspring are less likely to die. Thus it is more likely their genes will be passed onto the next generation so the EPAS1 variant would have a greater frequency in the population. This variant would only have been an advantage because at least the Altai Denisovans lived in alpine areas so individuals that didn't possess the variant would have more likely died from the causes above (as there is 40% less oxygen on the Tibetan plateau, for example). The variant is possibly not a disadvantage to individuals living in lower land areas (with higher percentage oxygen) such as south-east China. This is seen by the

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fact that 90% of Han Chinese living in lowland China possess the rare variant, showing that survival in lowlands with the variant is still possible. This would have meant that the variant was less likely to be removed from the population, thus this also accounts for the presence of the gene variant.

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0.2% of SE Asia DNA of Denisovans entered Asian modern human DNA (and 3-6% Oceanic). This would have been by interbreeding between Denisovans and modern humans in the areas above. The SE Asia Denisovans must have interbred with Altai Denisovans and carried the gene (as Altai Denisovans did not interbreed with modern humans), further supporting the idea that the mutation does not have an adverse effect when oxygen concentrations are higher. Modern humans in Asia, for example, that had ancestors who interbred with Denisovans and thus possessed the variant EPAS1 gene would have had an adaptive advantage in the alpine areas of China against modern humans that did not possess the variant. They would have had a greater chance therefore of passing on their genes to the next generation. This explains the very high 87% of the variant in the high altitude area of the Tibetan Plateau's Han Chinese populations. The reasonably high 90% frequency in lowland China can be explained in a number of ways. Firstly, these lowland H. sapiens ancestors would have interbred with SE Asia Denisovans. Although it may not have given them a large

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adaptive advantage, the mutation would not have given a significant disadvantage, thus remained present in the population. The frequency of the variant could have been made higher with interbreeding between Tibetan populations and Han Chinese in lowland China as there is ~~a~~ a higher frequency of the variant in the Tibetan population, thus interbreeding with the Tibetans would have increased the frequency of the variant of the gene in modern humans in lowland China. The same reasons as above would explain the identification of the variant gene in Nepalese Shepards, as Nepal is geographically close to the Tibetan plateau. However, there is a much lower frequency of the gene. This could be because the Nepalese did not interbreed with Denisovans - the Altai mountains are geographically Tibetan plateau's high altitude may have to some degree geographically isolated the Nepalese from the Denisovans in South East Asia (and it is ~~generally~~ in general a fair distance away). This means the only way the gene would have entered the Nepalese Shepard population would have been through interbreeding with Tibetans. This may have been ~~due to cultural bonding etc.~~ very limited too.

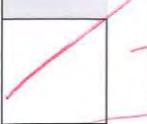
Above reasons can also be used to explain the small presence of the gene variant in the Mongolian population. Due to the large geographic distance between the Tibetan plateau and Mongolia, there was unlikely to have been much interbreeding between individuals in the two areas. This would significantly

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decrease the chance of the variant entering the population (as that is where the chance from acquiring it from other modern humans is highest with 87% of the population possessing it). They may have gained the small frequency of the variant through interbreeding with Han Chinese in lowland China (the low frequency of the variant in the Han Chinese means there would be a lower chance of the Mongolians acquiring the gene, so the low frequency is explained). Mongolians may have interbred with Denisovans, but if this were the case a much higher frequency of the variant would be expected so this is unlikely.

Finally, the variant is not present outside East Asia. This is explained because the variant became present after Asian and Oceanic modern humans interbred with diverged geographically from European and African modern humans. Presumably there was little interbreeding after this geographic divergence occurred (supporting Out of Africa/Eve theory). This means there was no way the gene variant could enter modern human populations in Europe and Africa. Also because the Denisovans that possessed the variant gene only interbred with Asian and Oceanic modern humans. Most likely Neanderthals did not possess the gene variant as they did not interbreed with European and African modern humans. Thus the distribution of the EPAS1 gene variant is explained.

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L+PA⁺ LN+HV LAJL⁺
Sj + Ad⁺ (LJ+3 P-Sj)⁺ Poly. Pmjv⁺

Question 3ASSESSOR'S
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A primary process that would have resulted in the distribution of honeycreepers would have been intra and interspecific competition. Initially, the population would have dispersed due to population expansion and because there were vacant niches on the other islands because the islands had only just formed (5mya and the rose finch arrived ~7-5mya). Because birds can fly (unlike mammals and reptiles generally) they would have been among the very first secondary (or tertiary if they feed on bugs) consumers to inhabit the islands. This begins to fulfill the requirements for adaptive radiation: the divergence of a species into a large number of other species to occupy different niches (the different islands and micro-habitats on them). This ~~mostly coincides~~ is caused by population dispersal or invasion of new habitats due to competition or environmental change. There is "great phenotypic diversity" and "at least 56 species of honeycreepers are known to have existed" showing that many species were indeed produced. They occupy at least 6 different islands so different niches, they have one common ancestor and the radiation coincides with environmental change of the production of islands at different times, as well as likely competition as they are all birds ~~species~~ so occupy similar niches. Gause's competitive exclusion principle states that no 2 species can live in the same habitat if they have the ~~exact~~ same niche. One species will either be eliminated or move away. If only allopatric speciation

(DNj)
(DNG)

occurred, then this principle would not apply (only intraspecific competition would have caused the distribution). However, if sympatric speciation occurred (will be discussed later) then the principle could apply - interspecific competition could have contributed to the distribution. However for sympatric speciation to occur, the species would likely have different niches meaning the principle would not apply. An example of a ~~species~~ population occupying a different island is the poouli, which early on moved to occupy Maui island, whereas the rosefinch/honey creeper ancestor likely occupied the Kauai island. This ~~was likely~~ allopatric speciation as no poouli are present on Kauai island (suggesting they evolved into the new species after leaving Kauai). However, it is possible poouli were once present on Kauai island but were outcompeted, this sympatric speciation would have occurred.

Allopatric speciation is a process that contributed to the species and phenotypic diversity of the honeycreepers. Allopatric speciation occurs when populations become separated by a geographic barrier that prevents gene flow, in this case predominantly water between islands. With no gene flow present, mutations that occur in one population will not be spread to the other. Because the different islands would have had different selection pressures, different adaptations would have been selected for. This means that non-geographic isolating mechanisms can develop so that the species become so different even if they are no longer geographically isolated, they will not be able to produce

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so speciation has occurred - they are different species

fertile offspring. This may be because they are behaviourally isolated (individuals do not recognise / accept courtship rituals of the other species), they are anatomically isolated (cannot physically mate), they are ecologically isolated (different niches), temporally (are active at different times) or the hybrids are inviable - the chromosomes are not compatible (or hybrid breakdown may occur). These reproductive isolating mechanisms.

* They may have become geographically isolated in the first place if they were blown to another island or if the islands were connected at one point during a glacial period, for example one million years ago approximately.

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account for the diversity in phenotypes (with anatomical isolation particularly), as well as accounting for the species diversity

DRJ

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An example of where allopatric speciation may have occurred is between the Maui creeper and Kauai creeper. They both descended from a common ancestor on O'ahu island, but then both became geographically isolated on different islands - Maui and Kauai.

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Sympatric speciation is where populations are not geographically isolated but tend to occupy slightly different niches. This results in a low level of gene flow between them, thus having the same effect as allopatric speciation. An instance where this could have possibly occurred is between Akohakohé, ~~and~~ Iiwi ~~or~~ and ~~for~~ Aparante. All three birds derive from a common ancestor and all three occupy Maui island. It is possible that they once were all geographically isolated so and they expanded their populations to occupy the same island's allopatric speciation occurred, but it is also possible that they evolved into different species while all on Maui island (or Iiwi diverged from the ancestor of Akohakohé and Aparante on one of the other three islands and then Akohakohé and Aparante became geographically isolated). In any way, there is a possibility sympatric speciation was a process that resulted in the diversity of honeycreepers (in terms of species diversity).

Another possible ~~process~~ pattern that will have resulted in the diversity of phenotypes is ~~from different evolutionary branches~~ coevolution. When species are subject to similar selection pressures due to being in similar environments, natural selection (the process here, most likely directional) shapes similar adaptations in the

species. This is possibly what has occurred between Akēpa and I'iwi (~~or~~ apapane). These 2 species last common ancestor was almost 3.5 mya so there has been much time to accumulate different mutations (they are technically not from different evolutionary branches but the effects of it still apply). More closely related species to Akēpa such as Kākā Akēpa and Hawaii creeper all have dull colours. However, Akēpa exhibits the same brilliant red phenotype as I'iwi (and to some extent Apapane), much more distant relative. Thus it is likely Akēpa developed the red phenotype independently to I'iwi (and thus has the effect of different evolutionary branches) because they were in similar environmental niches (both occupy O'ahu, Maui and Hawaii islands). The red phenotype is likely an adaptive advantage on these islands. This could be because red is a warning colour so being red prevents any predators consuming the birds (this is Mullerian mimicry - multiple species using the same warning colour). If birds with these warning colours did not get predated, they would have survived and passed on their genes to the next generation.

Mullerian mimicry is also possibly present with a large number of the honeycreepers using the warning colour of yellow. Maui creeper and Maui parrotbill have very similar colour markings. They both live on the same island (similar niche shaping similar adaptations) and have a last common ancestor.

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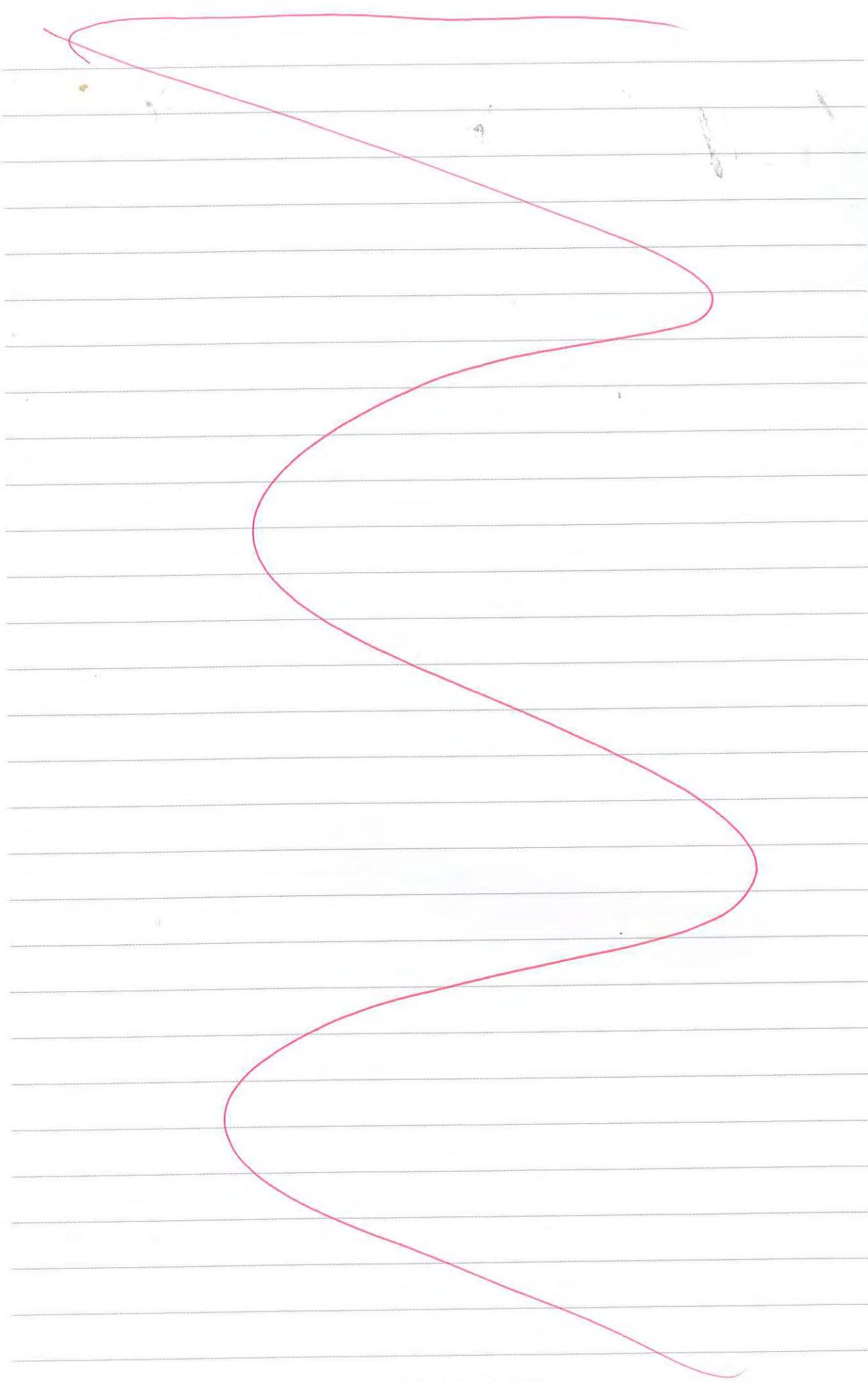
almost 5mya. Much more closely related species to each bird do not have the same warning colours, suggesting once again the species ~~do~~ evolved the warning colour (or colour good for camouflaging in the foliage of Maui Island) separately no Mullerian mimicry and the effect of convergent evolution is seen here resulting in the diversity of honeycreepers on the Hawaiian Islands.

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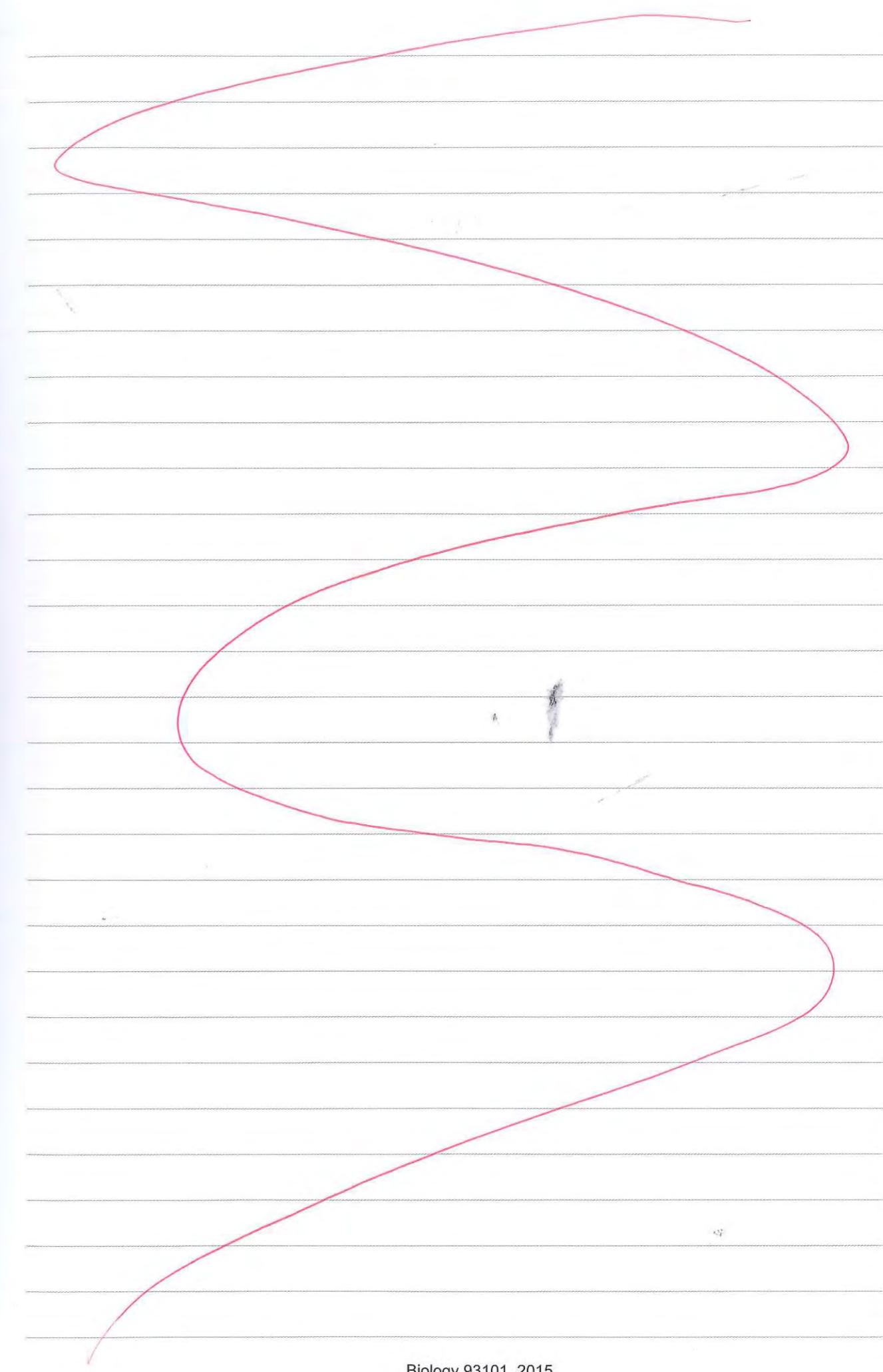
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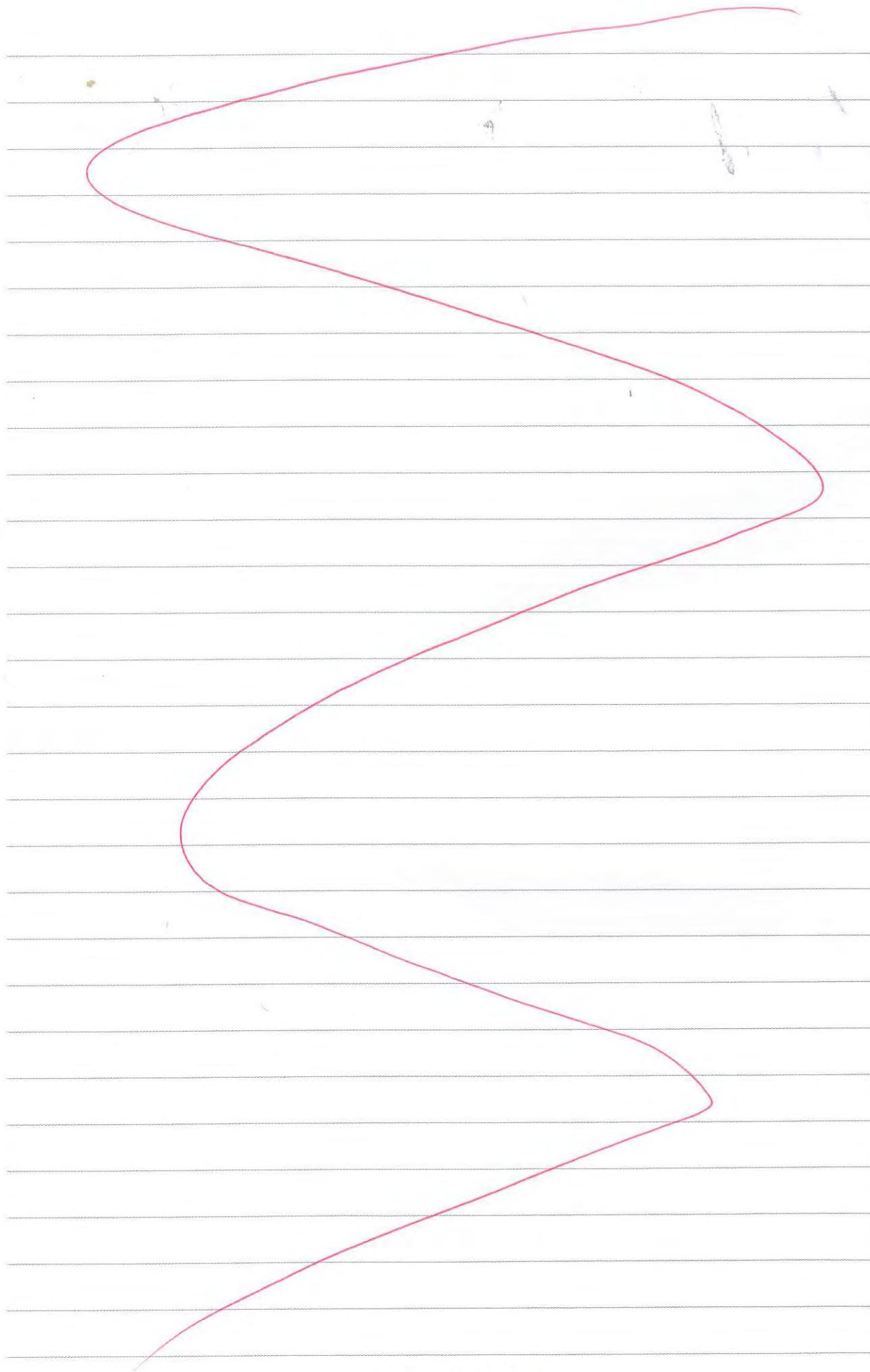
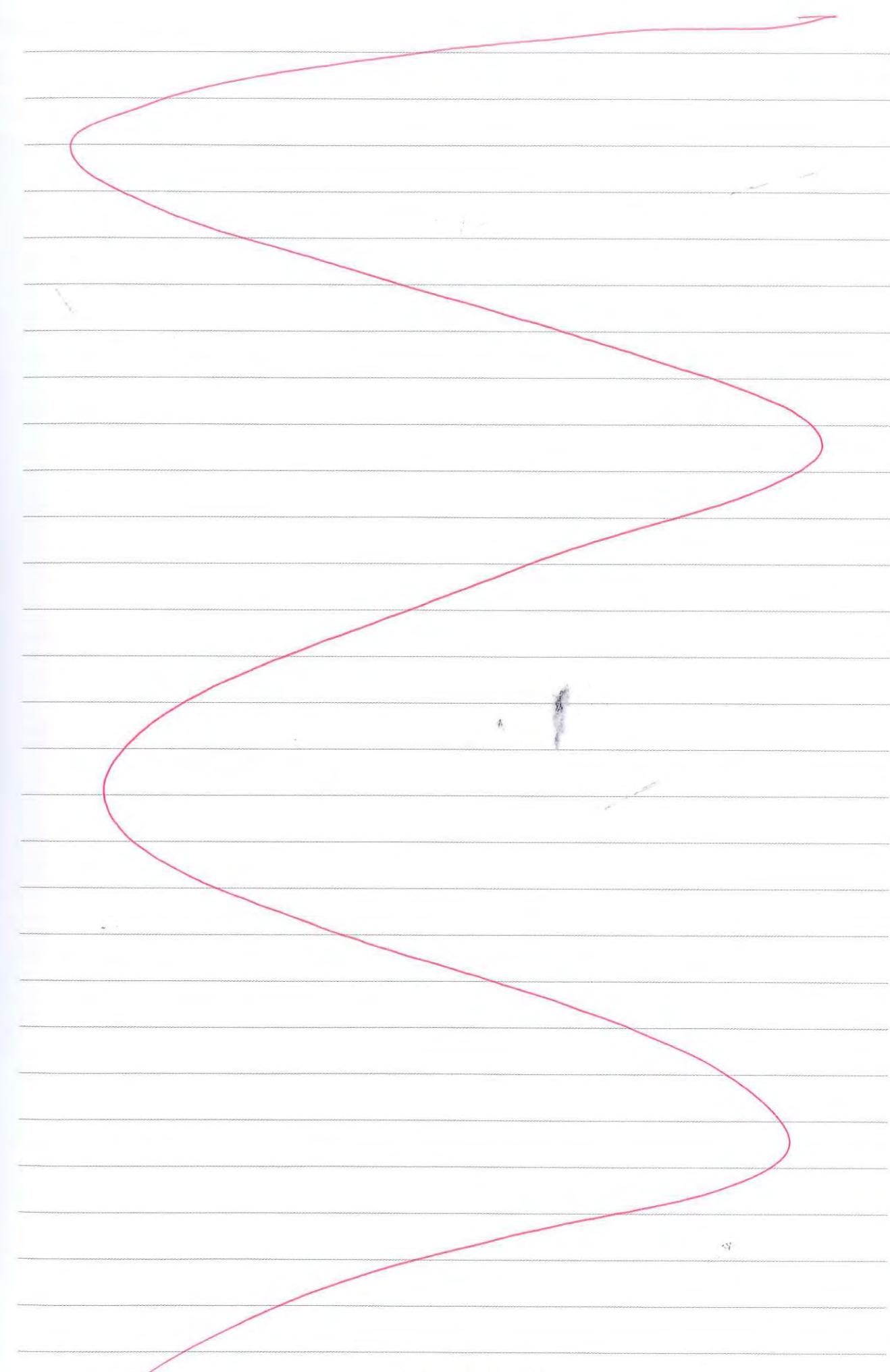
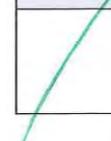
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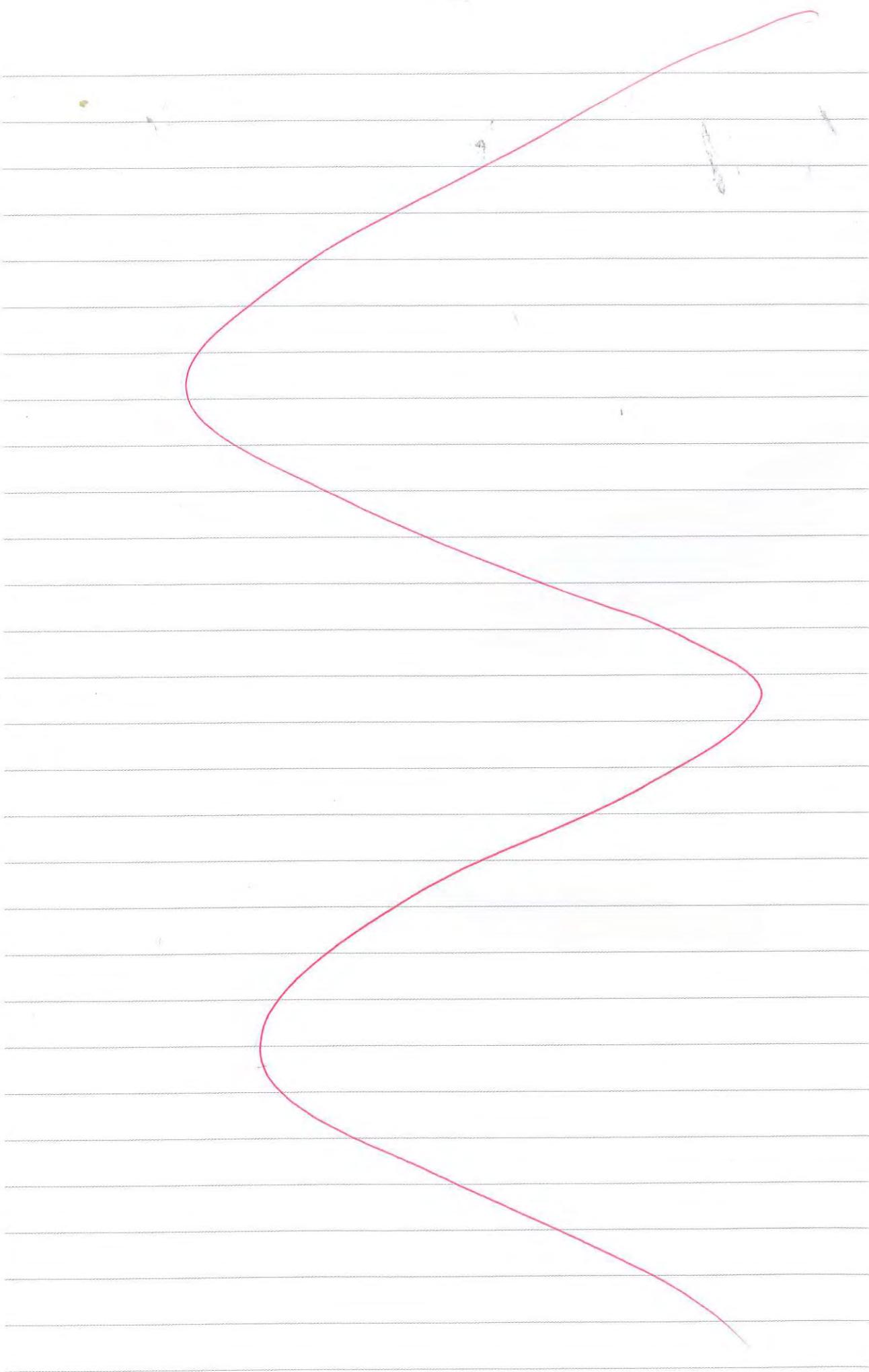
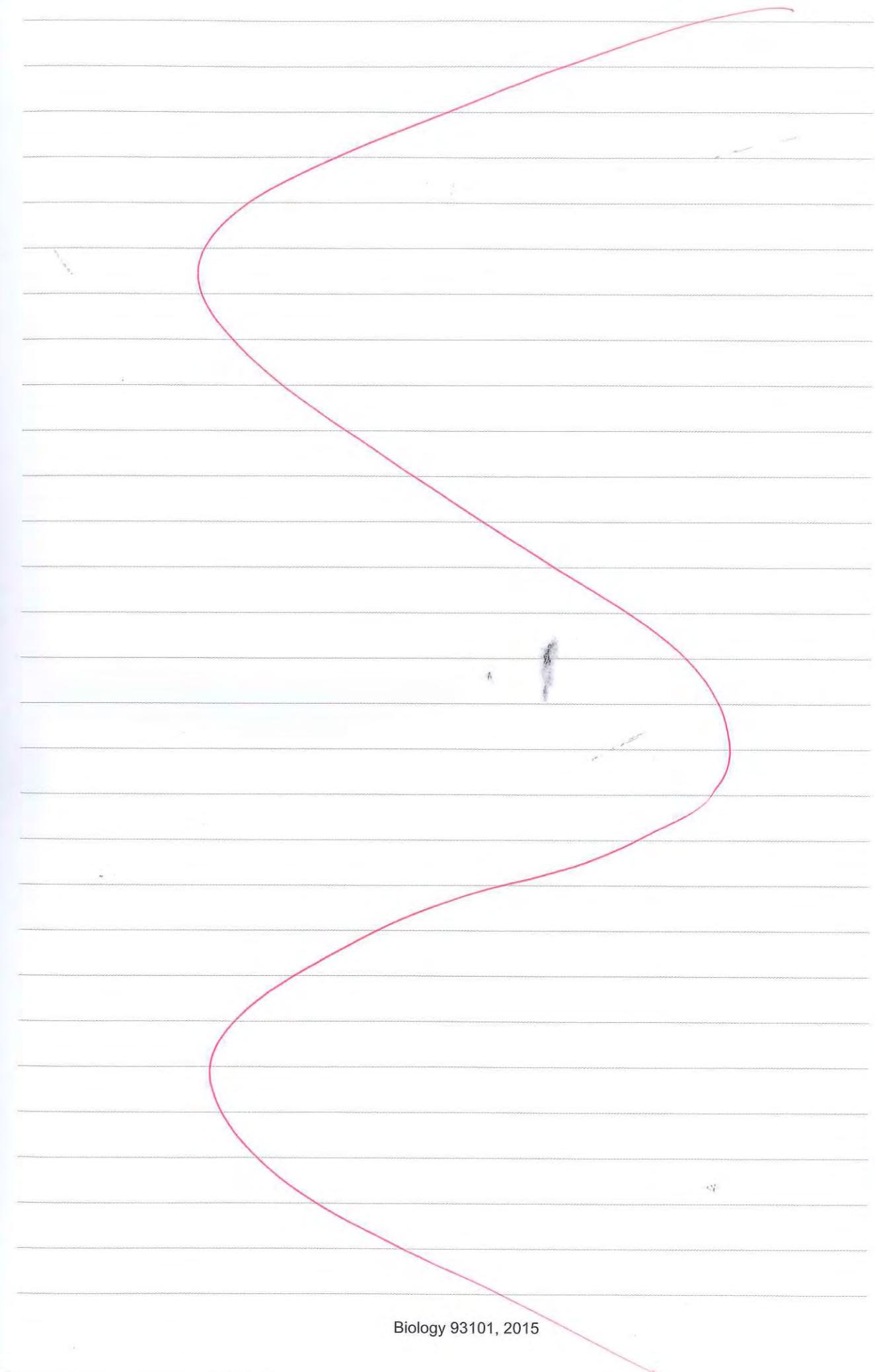
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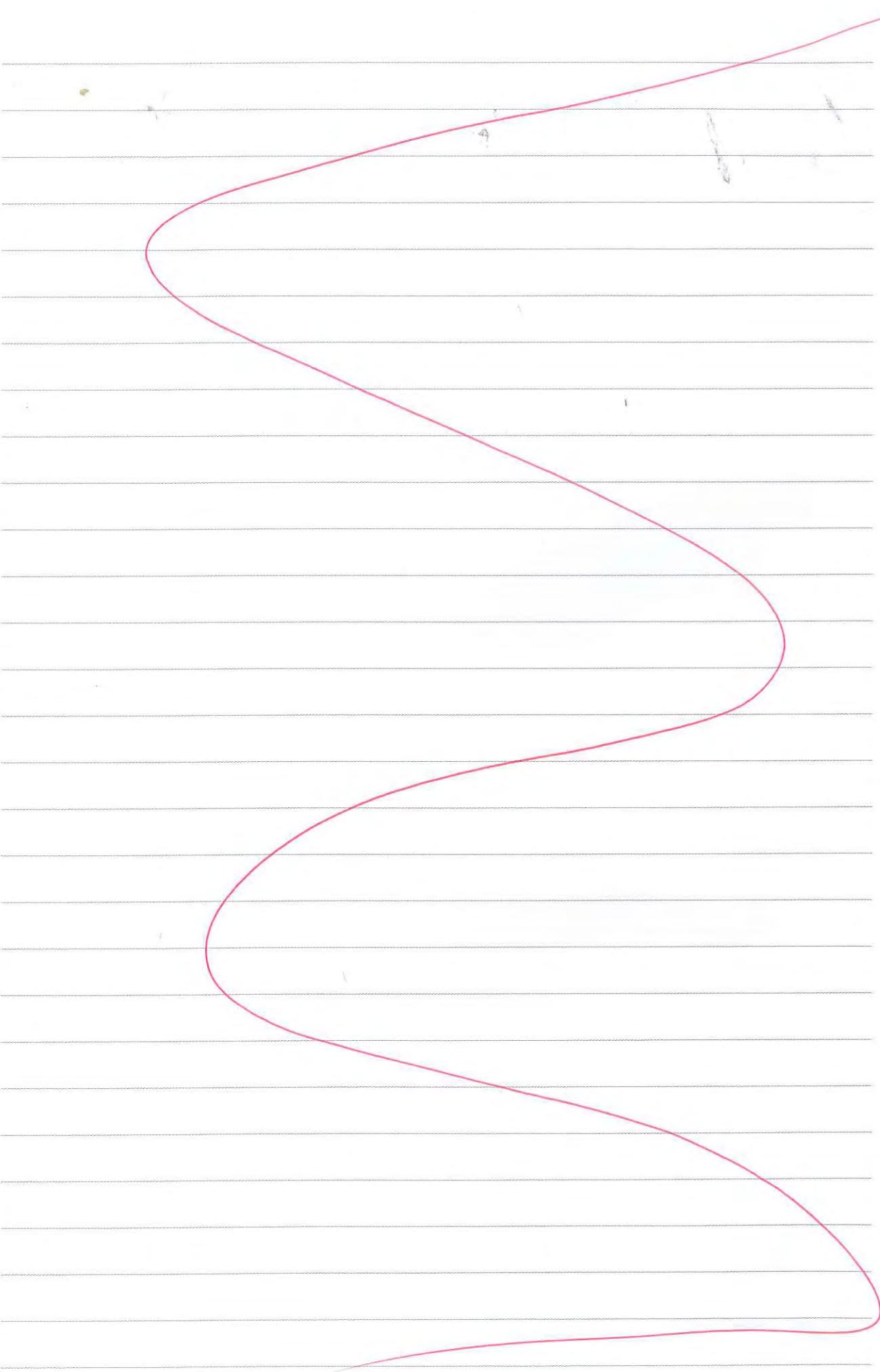


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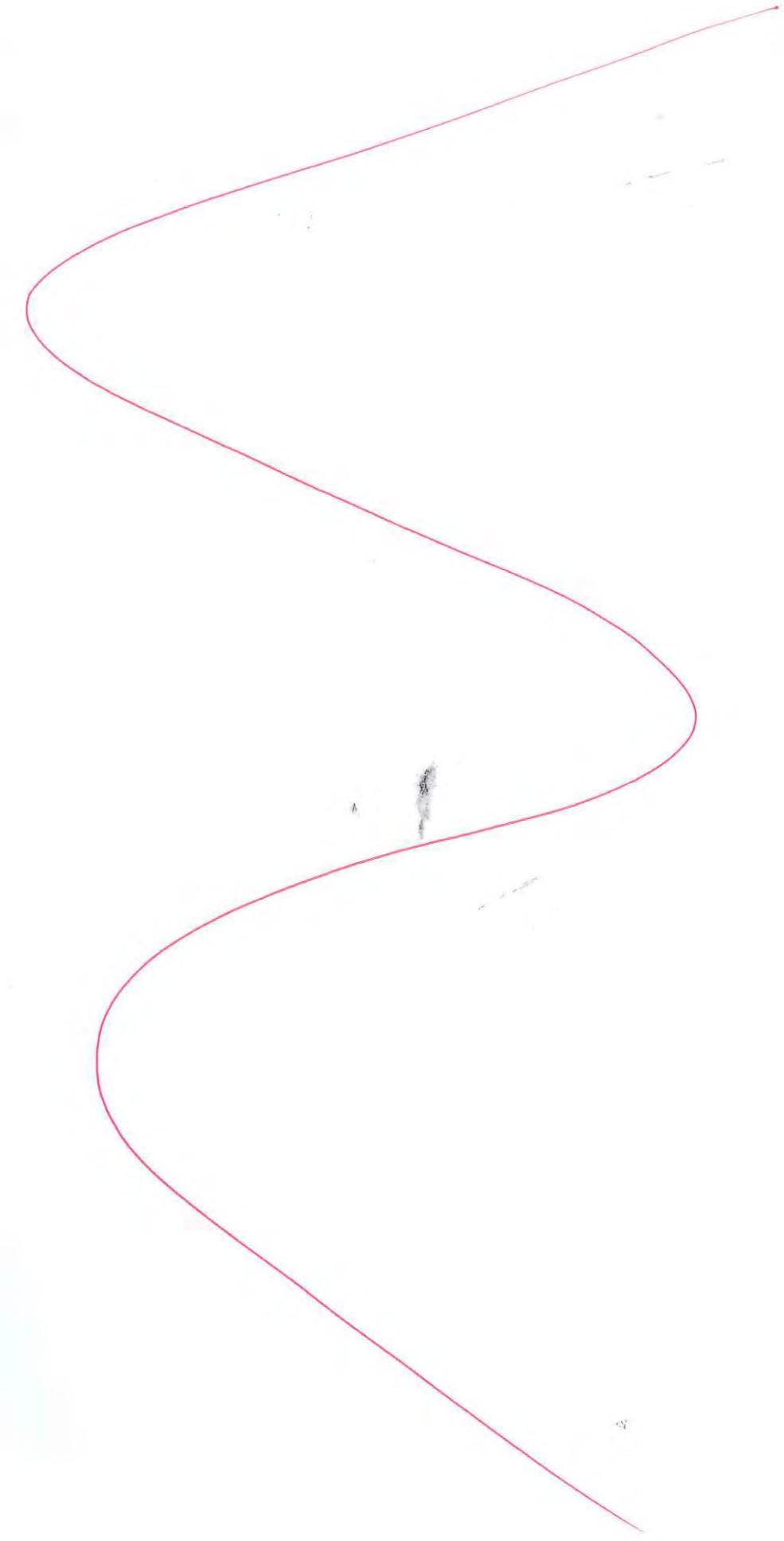
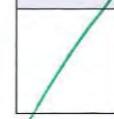
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